

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GCGTTGTCGT CGATGATTAA TAAAGTATGG GTATACCATT AAGAATAACG CTACCCAAAT	60
gAkTGCTAGT GACGTGCCGC CAATGACATC TGAAAAGTAA TGTGCATGAA AATAAAGGCG	120
ACAAAATAAT ATGCTAAGCC ATAATATTCC CATAACQAC GCACTCAACA CTTTTGTTAT	180
TGTCTTAGCA GCAAGTGAAA TAATAATGAT CATTAAAGGCG AAATATAATA ATGTGCTGGC	240
GTTGGAATGT CCACTCGGAA ATGAAAAGCC TGTATCAACG GCTAAATGAT TATATGGTCT	300
TGGACGTAAT ACAGTATCTT TAATTAATTT GTTCATGATG ACACCTGAAA CCAAATATGT	360
CACAAACCAA ACCGCTAAAT GCCTCTGTTT AATAAACAGT ATGATTGTGA CGATAATGGA	420
AATCAACACG ACACCTTTGA CATCTCCAAT TTCCGCACTA AACGTCATAT AGTAATTAAA	480
CAAATTGTTA ACATACTGAC GTTGTGGCTC ACCGAAATAA TCTGTAAACC ATGTTAATGA	540
TCCCATATCT ATATTTTTAA GCCATTCTTG ATTTGTCACT ACACTGTAAA ACATACCTAT	600
AAATACAATC AGCGCGATTA AAAATAAAGG CACTGTcATT TTCGGTGATG TTAATTTTTT	660
ATCTATCATC TTACAATCTC CTCGTATCAT CATTTTCATT TTACAAATGT TATCCATAAT	720
ATCAATGTGC CACAAATTTT ACTTTACCGA CAATATCAAA ATT E AAAAGT TCATATTGTT	780
ATGTATATTG CAAATAAAAC ATTGTATAAT TGAAATAACA ATATTTTGCT ATTTTCAATT	840
TAGTACGATT TATATTTATT ATACAGAGGG GGTAAGGCGT ATCAATAGAG TTATTTTTGT	900
CTATATAGCG TTAATCATTa CATTAGTTAG ATTCTTTACC CCTATTCATC CATCATTTTC	960
AAATTTGATT TACTGGATAT TTGTATTATA TTTTATTCTT ATTATACTAT GCGTTATCGG	1020
TTTCAAGGCC GAAAACTTA TTGCAACAAT GGTCAATTATA CCTAATTTTT TAGGAATACT	1080
TTATCGATTA TATGCCTACG TCACACATAT ACTCTTTATG TAAAAGGATA GTGGGCATGT	1140
CTCGCAACAA ATATGCTTGC GTCGA A TTGT CACCATTTCGC AAATTTTATG ACATACGCCT	1200
TTCACGGGCT ATATTCAGAC CCACGCATTC ATCCACGTAA TAAACACATC ATGTAATAGA	1260
AAAACAGCAC ACCCAAATAT ATGGCGTTGC GCTGTTTAAAC CAAGCATACT TCTATAGCTT	1320
TAATAAGCCA GCAGAAGCAT ACCTAACCTT CTAAATATG CTTTTCCAAA TATCCTCAA	1380
GTTTGAATAC GATAATACGT TCACCTGTAA CTGTACTTAA ATCACTATGG AAGCTCATCA	1440
CTTTGATACC TGTAATTTTA AAAATGATAT CATTCAAATC TTGCTCACCG GATTCAACTA	1500
ATTCAGAACG TGTTCGTTTA ATATTTAATA ATCCTTCATT CGTACTACAT ACACGATATT	1560
CAGCTGGOGT TAAGATACCT TGTA A ACTAA TAATCACCAT ATCTCTTAAA ATGTCTGATT	1620
TAACTGACAA GGAACCTCTG CCAAGGAAAT CTTTTTCCCA TTGCGTAATG GCTTTACTGA	1680
TTTCAGCTTC GATTTACCT TTCGTTCTTT TCATATCACT AACTCCAATA ATATTTAAAT	1740
TGATTACTTC ATCTTTGTAT CGTTATCACG AC A CAACTA TTACATTAAG TTTATCATTT	1800

TTAGTATATT	TTAAGAAGCT	AGAACATTGT	AGATATGATG	ATATATTAGT	TACTTAGCAT	1860
CGCAACATAT	CATCGTTAAA	TCCAACTTTT	AAAACGCCCT	TCCTCATTAA	CGCTCATTAA	1920
ACGCAGCCAA	TGATTAGACA	CCTTCCTAGC	GAAATGCTCA	TTATTCGCGA	GTAGTCTTG	1980
TACAACATAG	TCGGGTGCCT	GAATAACGAC	AAGTAAACGA	ATTGGCGAAT	GATACATCGT	2040
CCGATCAGCA	GCCATAACAG	ATTGCCATGA	TAAGCCATAC	ATCAGATCAC	TCGCATTACC	2100
TTGCATGACA	CCAACACCTG	ACGTGACGGT	TTGTGTCGCT	TTATTCCCAC	TTCCGTAAAA	2160
ATGCGGCGCA	ACTGTCGACG	CATAATATTG	TAAATTAATC	CATTGTGCCA	CAAGTGCCGG	2220
ACCAGAAATG	ATGGTATTTA	ATAATGTGCC	ATCTTTATCT	TTACGCCAAT	CATAATTGTG	2280
TAAAAATGTC	CGCCCTTCTA	AATCAATGCC	TTTTGTTAAT	TGGCGTCGTC	CAATTATAAA	2340
TGATGCATTT	TTAGCCAATC	CCCATTCTGG	ACGTACCTCACT	CCAATCAC	TCGCAAACCG	2400
CTGCGCTTCT	TCCACTGGAT	GATTACACAG	ACCAATCGTT	GGCAGTTTGT	CCAAACGTTT	2460
GCGATTGCG	TGtTCAGAAA	TCATCGGCAT	CGCGTCATTC	AATGATTCAT	ATGCATCTAA	2520
AGCAATAGAA	GATAATGTGT	CTGGCACATA	TACCCATGCC	AACGTATCAG	TAGACGTATG	2580
ATGTTCTGCT	ACCGCAAAAA	CAGTTGTCTC	TGGAATATAC	ACACCTGATT	GTTTTAATCC	2640
TTGTCTGACA	TTTGACGAT	TACATATCAT	CGCTAATAAC	TTAGCATTAA	AACCGCTTGA	2700
TGCGCCACCA	CAAGCCCCAC	ATTCAAGTGA	TGCATGATGT	GGATTATTGT	GAGAATGACT	2760
AGCATGACCT	GCTAACACAA	CGAACGGCGC	AAATGCTTCG	GTTAAATCCA	TCAATTTCAA	2820
CGCTTGTAAC	GCGAAATCAA	TTTGCTCTTG	CTCAGTAAAT	CCAACAGGTA	AGTCTGATGT	2880
TCGGTCAAAC	TCACGATCAA	TCGTCAACTT	TGTTTCAGGC	TTTTTCAACC	ACTTTTGT	2940
TATTTTTTGT	AAAGACGCGC	GACTTTTTTCT	AGGCATAATC	GAATTGAA	TGGTACTTAA	3000
GCTTAAAAAT	GGCCCACTTA	ATTGAGGCAA	TAACAGACTA	GGCATGACAT	TATTTTTTCAT	3060
CAATTTAAAT	GTGTAAAACA	TCGATGACAT	TGTCTGTTGC	TGTTGTGCGAT	AAACATTCAT	3120
ATCGTAGCGG	TCTGCAAATT	CTTTAATGCG	ATATGCCGGC	GGTACCATGA	CAGGTAATGA	3180
ATCATGTTTG	AATTGTTTCGT	CTACGGCATC	TTTTTGAATA	GGTAATCCAA	AGAAGCCTGC	3240
AATACCAATC	GTTTCAAAGG	GCCCTGCTGC	TTCGATATGT	CTACGAAATG	GTTCTGAACG	3300
AACATCTATA	CAAAATGCAA	TTTGCGCTTT	CGTTGATGTG	CCCATCTGAT	TTAGCTCGCT	3360
ATTATTTTCA	TCAACTGCTT	GTGTGTCATT	TAACAATACT	GAATGTGGCT	GATTAGCGTT	3420
ATCATTTTCT	GAGACATTTA	CTTGTTTAC	ATCTAATGCG	CCCGCCACAC	TTTCATGACC	3480
TGCTTTAATT	TTTTGTTTTA	ACTGAGATTC	GTATGTCATT	TCCCAGGCAA	TTAGCCATAA	3540
ATTTTTAAAT	ACATTTTTAT	TCATAGTTGC	TGCAAAATGA	ATAAACGTTT	GAATTCATT	3600

GACGTCATGT TGTAGTAATA CATCGCTAGG CATATCACTG TAGTAACACC ATGATGCAAC	3660
AGTTTGCTTA AACCAATTTT CCGATCTACT TTCACAATCT TTAGCGACTG ACTTAAACTC	3720
ATCACCAACT AGCAATTGTT CGACAACTAA CCGAATTGCC AAATAATCCG TTAACAAATG	3780
TTGTTCAAAG TGATGCTGTT GTGAACGGTA ATACAACATA CCTGCCCAAC CCGGTAACGC	3840
CAAAAAGATGT CCTTCAACAT AAGCTTGGA GTCTTCCTGA TCTATTGAAA AATGAGTTAA	3900
TACTGACTCT ATCGTCATTT CAGGATCATT GGGTAAGCCT TTAATCACTT GGCCTGTGC	3960
TTTAGTAAAA CTATGGTCAT GTTGCCTAA ATGCAACAT GCATGGTAAA AACTTTGcTC	4020
ACGCTTCGGC ATTGTCCAAC TCGATAGAAA TTGATCGATA TAAAGTTTCG TCCATTTAAT	4080
CATTTGACGA TTCCTTGTT CGCTAAGTGG CTCACCTTGT TCATCTATTA TTGCATCACT	4140
CATCGGACGT ACATCATAGT GATGATATGA TTCAGCCATA TCACGTTTTG ATTTTTCTAA	4200
TAGTAGATCA GCAACAACAT CAACATTTGA ATGATTGATA TATGATGCAG GTACGTCTTT	4260
TAATGTTTTA ATGTTATCAA TATAAAGATT GATGTAGTGT TGCGGGATAT TGTAGTGATG	4320
TTCAAGTAAC ATATCAGTAA CAAGTTGATT AAAGACACTT TCATCTAATT CACCACGTGC	4380
CACAGCGCTT TCTATTAATG CTTTATTTGG GAAAATATCC ACATCTCGAA CATCACGTAA	4440
CCATTTTGCG ACATCTTCAA ACGTATCCGC TTCTAATCCT TCCCATGGAT TTCGTGCTGC	4500
AAAAATCGAA ATTGGTGATA ATGGTGTAAT AACACGTTTC GCATTTTCAA TGACTGAATT	4560
GATATTTAAC TGTGTTGTCA TACCTTTCAC CTCCTATAAA TACTCTTCA AATAATTGCG	4620
ATGACTTTCT ATCGCTTTTCG AGCGTGCTTC ACCTAGATTA ACTAACCACA CGTACAATAC	4680
CGCAAAAGCC TTAGAGTATC GATGCCGCGC CACCCAAATA CTTAATAAAC TGCCAAAGAT	4740
TAAATAACA AACTAATGA TGACACTCAC TGTAGGCGGC GTTGTCGCAT GTGTTGTTAT	4800
ATTTTGTAAT ACAGCGTAAA AATAATTATG TGTGATGACG TAGATAAATG TCACGATTGC	4860
AATCAAAATC ATACCAACAA GACGTGCCAT GCGTCCTTTA CTAAAGGCTA CCATTTGATT	4920
CCAAGATACA AGTAATGACC ATCCTAGAAT GAGTGCACTT AACACTTCAT ATGCACTTCT	4980
GTCCTACTC ATCCAAAATA GAAATCCAC GATAATAGCT AATACACGTC CCATGACAAT	5040
CCAGCCATAA GCGTCTTTAG CAGATGCTTG TTTTGGAATA TTGAATCGCT TCACGATAGA	5100
ACCTGATTGT AAAAATAATG TTGCTTTAAA AATACCGTGC AATATTAAAT GAATAATCGC	5160
TGCTGAATAT ACACCCAATG CACATTGAAC TAACATAAAG CCCATTTGAC TATCGTAGA	5220
GCCCACTAAT TGGCGTTTAT AGTCAACTTG AACTAAGCTA ATACCCGATC CTAACAATAC	5280
AGAAATACTA GAAAGGATAA GTAATAATGA TAACGCAAAT CCATTATCAA ATATCGGCGC	5340
AAAACGAGTT AGAATAACAC CACCTGCATT CACAATTCCT GCATGCATAA TTGCCGATAC	5400
TGGCGTTGGT GCCGTTACAG ATTCAATCAA CCATCGATGA AAAGGAAATT GTGCTGCCGG	5460

TATCATGACA	GCTAATACAA	GTAGTACATT	CGTCAACAAT	GACCATGTCTG	GATGAACTAT	5520
ATGTTGTGGT	ACCCGCCACT	CGCCAGTCGC	AATATAAATA	GTTACAATTG	CTCCAACGAA	5580
TGCAAGCCAA	CCACATAAAA	ATGTCATGCT	TGTAATTTTC	GCAGACTCAC	GTGGCACTTT	5640
CCAAAAACGA	TTAACGTTCA	TCAGCAATGT	TAAACATAAT	AATGTAATAC	CCCAGCAGAG	5700
TGCCATCAGT	CTTAAGTCTT	CAGACATCCA	TGCTAAAGAT	GCAAACGACG	TAATCGCAGT	5760
GAACAATGGA	AAGTAATGTC	TATAATGATG	ATCACCTAGT	AAATATCGCA	TTGAAAAC	5820
TTGAATAATA	AAGCCAAGCG	CCATTACAAA	GCCAGCTAAT	AACCAAGATA	AACGATCTAT	5880
TTTAAATGGA	CCTAAGACAT	GTTGACCATG	AATACCGAAA	AAGCCAATGA	CTGCAAATAA	5940
TACTGGCATG	ACTAGTATGT	ATAAATGTAA	TTAATATAT	CTCATTGGCA	TAAGTGGTGC	6000
TAAAAACAAC	AAGCCACTTA	TCAATGCAAT	GATAAGCGCA	ATAACAAACA	GTGAAAATAG	6060
CAATTGAAAA	CTTAACACTG	CATAACCTCC	TTATTTCTAA	TCTCTCGCAT	AATTGCTTAT	6120
GTATAAAAAT	AAAAACCTAC	AATAGTAGAT	TCTGTACATA	ATGGCAGAAA	ATTTACTATT	6180
GCAGGTTTCA	GTTTAACTAG	ACACTGCATC	ACGGTACGTT	GATATACCTT	GTTGCAGTGT	6240
TCTCTTTAAG	CGTGCTCCCA	TGCACATATG	TATATAAAAT	GTTACTTCTG	TCTGTTCAAT	6300
TCATCTTCAT	AAATATGCTT	TGCCTAGACG	AGACCTAACG	TGTTATTCGT	TTTAAACTTA	6360
TACATAAAAA	TATAATTAAA	TTTCTGCTTC	ATGTCAAATT	CATGAGCTTA	ACCTCTATTA	6420
AACCAATGAT	TGTAAAGATT	TTGTAAATGC	ACCTGTACAG	TTAGGCAGTA	TTTCCCGTCC	6480
TTTTAAATA	AAAAATTCGC	AGTTATGATC	ATAACAATTC	AAGTTAGGAA	AAAAATCAAT	6540
TACGCACAAG	ATAACTATGT	ACAATGAAGT	TAAGTCATAA	GCAAAGGAGG	TAATCTTAAT	6600
GGGTATCATC	GCTGGCATCA	TTAAAGTTAT	CAAAAGCTTA	ATCGAACAAT	TCACTGGTAA	6660
ATAAGATTTT	ATAACAAACA	AAGGAGGTCT	TTCACATGGG	TATCATTGCA	GGAATCATT	6720
AATTCATTAA	AGGATTAATT	GAGAAATTCA	CTGGTAAGTA	AGTTATAAAA	ATCTCATAGA	6780
TATGAACATC	TTATTTGAAG	GGGGCCATTC	ACATGGAATT	CGTAGCAAA	TTATTCAAAT	6840
TCTTTAAAGA	TTTACTTGGT	AAATTTTTTAG	GTAACAACTA	ATCTCAAACA	TTAACGATCA	6900
ACAACTCATC	ACTATGTTAA	ATCAACATAC	AGGAGGACAA	AACGATGGCT	ATTGTAGGTA	6960
CTATCATTAA	AATCATCAAA	GCAATTATCG	ACATTTTCGC	AAAATAATTT	AAGCGAATTG	7020
AATACTTAAA	ATTCTCAGGC	CACTATACCA	ATAGGGATGG	TGGCTTTGCT	TTGTGTTGAT	7080
TTATTGATGT	GAGGTGAGTC	TTGTTAGTTT	GTTGCAAATA	AATGGTCTTG	GTGTTTTTTG	7140
TATAGGACGT	TCTTAGTGGG	ACATACGGAA	TATTCGTGAT	CTTTGTAGTC	TGACGCGTTA	7200
TATTTTTGTG	GCGTGTTTTA	TGTTTGATAC	TCGAGTTCTG	AGACATTCAT	GATTTGGCAT	7260

GCGAAATCTT AATGATTTTC ATGATCTAGC GCAAGATATA TTGGCCACGT GCGGAATTGC	7320
GTTGCACGTT TAGACTGAAA CACTCGTGTG ACCGTAAGTG TTAATAGTAC ATTGATAGCT	7380
GCATTTACTT CACTCATTTT TATGACTGTT AAACAATGAT TGTACCTTCA ATTAAGTT	7440
GGTACGATGG TTTTGCCATT TTTCATCAAC GTAAATATAA AAAGGACTAA GACACATACA	7500
TGTCCTAGCC CTATGGATAA AATGCAAATT TCTGCTTTAT CAAAACCTATC ACACCTTTAGA	7560
TAGATTGAAA ACAAAAAGAT CCTAAGAACA CCTTAACCTT TTATTAATTG TCATAAATTG	7620
CAAACAATTA AGCCACAATT CAAAATGAT TATACTTCAT TCAACTTATC GTGCTGGTCT	7680
AATTTGCCAT TGATATGGAT CTTCAAATTG TTGCCAATCT GCATCAATTT CTTGCGCATT	7740
GACTAAGCAT GCGTCGAGTT CTTTTGTAA TTTTCTTCA TCTAATTCTG TACCAATAAT	7800
GACAAATTGT GTATGACGAT CGCCATATTC TGGATCCAT TCAGCTGCGA CATCTTGACG	7860
TTCTGCTAAT ATTTGTGTTT GTTGCGCTTC AGACATACTA GCCACCCAAT ATGTAAGTGG	7920
ATGAATATTG CAAGATGACC CTGCTTGAGA TAATAAACAT GCTACGTGAT TGTATTGTGC	7980
TAGCCATACG ATACCTTTTG ATCGAACGAC ATTATTTGGC ATGCTTTCTA ACCAATCATT	8040
GAACCTTTTA GCATGGAAAG GTAGACGACG TTTATATACA AACGATGATA TACCATATTC	8100
TTCTGTTTCA GGTGTATGCG ATGCATGCCC ACCAGACTCA AGTTCTTTGA TCCATCCTGC	8160
TGACTCGCTC GCTTTTTCAA AATCAAAAACG CTGCGTATTC AAGACTTCTT TTAAATCTAC	8220
TTCAGAATTT GTTGTCTTA TAATTTTAGC AGTCGGTTGC AATGCGCTTA ACATTTTTTC	8280
TAACTTCGCT AGTTCTTCTT CACTAATTAA ATCAATTTTA TTAATAATCA ATACATCACA	8340
AAATTCAACT TGGTCAATTA ATAAATCAGC AATCGAACGC TCATCTGTTT CGTCAACGCT	8400
TTGATCACGA TCCATCAATA AATCTTCTGA GTTGATGTCA TGTEGAAGC GGTTAGCATC	8460
CACAACTGTA ACCATTGTAT CTAAACGGCA AATCGCTGTA AGATCAATGC CAAGTTCATC	8520
ATCAATATAT GAGAAAGTTT GTGCAACAGG TACTGGCTCT GAAATCCCTG TTGACTCAAT	8580
AACAATTTGA TCGATGCCAC CTTTTTTCAC TAAACGCTCA ACTTCTTTTA ATAAATCGTC	8640
TCTAAGTGTA CAACAGATAC AACCATTAGA AAGTTCGACT AATTTTTTCAT CTGTACGCGA	8700
TAGTCCCACA CCATCTGCGA CAAGATCTTT ATCGATATTT ACTTCACTCA TATCATTTAC	8760
AATTACCGCG ATACGTCGAC CTTCTCGATT TTGTAAAATA TGATTTAACA ACGTTGTCTT	8820
CCCCGAGCCT AAATAACCAC TTAATACCGT AACTGGAATT TTAGCATAT ATATACCCTC	8880
ACTTCAATTT ATTTGTAAAT AGGAATAATT CTGTTTTACA TTATATAGGA GCGTTTCCTC	8940
TTTCGCAATC TTCGATAATA AAAAAATAGT AACTTAATT AAATTATTGA GCGCTTTACT	9000
TTATAATGGA GACAAAGATA TATCTCACGA AAGAGAATCG AGGTGTATAA AATGTTATT	9060
TGTCATTTTA GTTTTATATG TTAAGGTAT TGCATTTATT CTAATCAGTG TTTTGGTTC	9120

AAAGACTGAA GGATTATCTA CGAAACATAC TTTATATACC ATTGGCAGTG CTATTATAAC	9180
GATTGCTATT TTCATTTCAA TTGGCTATGC CATTCAATAC TTAAGTGCAG CGCTTTATGG	9240
TTTGTAAGGT GAAGGTGATG AGTAACGGGT AGTTCGGGAG AGGTAACTT GCGTTGATTT	9300
TGATAAAGTG ATCATAGCTT TTAGTACTTG AGGATTTTTA TTGTTGCTGT TACGAATGTG	9360
GTCATGTTTA ATGCGGGACA GTAATTTAAG TTGTTTTTTT ACAATTGAGA GTGTGATATT	9420
TCGATTCGGT TCGAATTACT TTACATGGGA ATATATAAA TAAAAAGAA GCGGCCTAGT	9480
GTCAGTTGTG AATATACTGA ACATTGGTCG CTTTATTTAG TAGTATGATA TGTAGTTTAG	9540
CTATTAATTT TTTTCAGGTC ATCCTTAATG CTGTCTATCT CAGACATGGC ACTTTTAACC	9600
CAATCTCCTT GAGCTGCACC TTTAAAATTA GCTTTAAAAG ctTCGCAATG TTGCGCCAT	9660
TGTTCAATTA ATACTTTTTT TTCACCTTTT AATCCGTTTT CAATATCTTT GTATTTATGC	9720
TTATGTTTCA GTGCAATAAC TGTGCGAATA TTTTCTTTTT GCGCTTCCAT TTTAGATATG	9780
AGATTAAGTG TTTCTACTGT AGTACTTATA TCTGGCATTG TTAAGGTCAT ATCTGGTTCT	9840
ATTAGAGTCA TTTAATCTCC TCCAAATTAT CAGTCACTTA GCTTATCTAA CTGCTTTTCA	9900
TAAGACTTTT TTAAGTCTTC TTTATATTCT TCTAATTTCC CATTCTTGCT TTCTGA	9956

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TTTCTTTTAA CAGaTTTATC cCATTAAATTG TTCTACAAGC CCACGaTGAG CAATATCATT	60
TTTAGCAACC ATTAATAAAC CAGAAGTATC CATATATATA CCGTGAACAA TACCTGGACG	120
AATTTCTCCA TTAATACCTG ACAAATTTTT AATTTGATAC ATTAAACCAT TAACTAATGT	180
ATTGGTATAA TGCCCTGGTG ATGGATGAAC TACCATGCCT TTCGGTTTAT ATACAACTGC	240
AACATCGTCA TCTTCATAAT AAATATCTAA ATTTAAATTT TCAGGTAGAA TATCAGCTTC	300
AACCACTTCT TTTTCAGTGA CAACTATATG ATCATTAAGT TTCACTTTAT AATTAGATTT	360
AACAACCTTA TCGTTTGCAA CGACTAAACC TGCTTTAATC CAATCTTGTA TCTGGTTACG	420
AGACCAATCA TTATTTAATT CAGGCAGCAA CTTATCTACA CGCATACCTG TTTGTTCTTT	480
ATCTGTAATG TTAAATTGAT AAGTCTCCAT TACTTAACCT CTTCTCCTT TTTATTGGAA	540
GTATCCTTTA ATAAGGCAAT AATAATTAAT ATTACACCAA TTGTTAAACT TGAATCTGCG	600

ATATTAAATA TTGGAAAATC ATAACCAAAA ATATTTGTAT CAATAAAGTC AACAACTTCT	660
CCTGTTAAAA TTCTATCAAT AAAGTTTCCA AGTGCACCTG CAAAAGTAA ACTAATAGCA	720
ACTTGCATAA ACAAATTATA TTGAGCATCT TTAATAAAGA AATATACTAA GGCTATTAAT	780
ATAATAATGG TAATAATAAA GAAAAATGTC ATTTTTCAC TCAATATTCC CCATGcAGCA	840
CCATTATTTT GATGTGaTGT TATGTTTAAA AAGTGCGGTA TCACTTCAAA TGAATCTCCA	900
ATTTTCATTG TAGTAGCTAT AATATATTTA GTAACCTGGT CAAATATAAC GACAAATACT	960
GCTATTAAAA TGGAAGTGCC AATAAAATAT TTTTGTGCA TTTTCGTTCC TCCAATCAAT	1020
CGTCCATGAG ACAACTCTTT ATATTATAGC TTACACCTGC TAATAAAAAA AGTAAGCATA	1080
TTACATTAAA TCTAATGTTA CTAACtCAAT ACTTGATAAA CTACTATGTT TTGACATTAA	1140
ATATGAACTT AATTATTCAT TTATCATATT TAAGATGACA TTAAAAATTA GGAAAGCAGG	1200
CTGGAACATA AATCCCTAAA AAGACAGTAG TAAGATATTT TCTAATTAAA AATTATCTTA	1260
CTGCTGTTCT CTATTTATAC AATACTTCGT ATTGAATGGC TTCGCTATGCCcATCTGGCA	1320
CATTACTGTA AAATTCTATA AATAGAATTT TTGATGATGG GTCCCTTCCT AGGGTGCCGT	1380
CTCAGCCTCG GtCTTCGACT GGCACTGCTC CCTCAGGAGT CTCGCCATTA ATACTACGTA	1440
TTAACATGTA ATTTTACTTT TAAATACTTT AAAAAATAA GACATGAATC GTCTACACTT	1500
AATTGGACAA ATTCTATGAG AATAGATATT GTTAATTTAA GAAAGTAGGC TATTTTGAGT	1560
TtCACTCGAA TGTCAGTTCG AGGAATAAAT AAAGTTAAAC GAGAGCTAGG TTTTGTATTA	1620
ATGGCAATTA ATATAAGGAA AATAGCAGCT CAACGAGCTG TACATTATAA AATACATATC	1680
AAAAAAGCTG ATTTCTATCA AATAATTAAT AaATCAGC TTTTTTACAT TGCCTAAGAA	1740
CTTAATGTCC CAAGCCCTAA AACTTGTTGT TATTTATTTG ATTTAGCAGC GATACGTTTA	1800
TATCTTAAGT ACATAAATGC TAAAAGTATA AACCAAATCG GAATAAAATA AATTGCACGT	1860
CTTGTATCAA CATTAATAAA TAATAACCCG AACACAAAAA TGAAGAATAC AAATATTAG	1920
TAGCCCATAT ATTTGCCACC TAATAGTTTG TACGTAGCAT TTTTATGTAG ATCTGGGTTT	1980
TTACGACTAT AATTGATATA TGCAATGATA ATCAGACCCC ATACAACTAA AAATAACACT	2040
GTAGAGATGG TAGTCACATA CGTAAATACT TTTGTGCAT CTGGGAAAAAT ATAGTTTAGT	2100
AATGCTGCCA CAAGTAATAA TGCTGATGAA GCAAAGATTG CAACATGTGG AACGCCATAT	2160
TTATTCGTCT TAGAAAAGTT CGGAGGTGCT TGtyGTTGAC TTGATAAACC GaAAAGCATA	2220
CGGCTATTTG AGAATATACC ACTGTTACAT GATGAAGCAG CAGCGGTAA TACTACAAAA	2280
TTAATCAAGC CCGCAGCAAA CGGAATTCCG ATCAATGCGAATrATTTTnC GAATGGACTG	2340
TTATCAGGAT CAACTTGCTG CCAAGGGGTA ATAGACATGA TAACCGCTAA CGCCCCAACG	2400
TTnnATATTA A	2411

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GnGAATTATT TTTAATAATG AAAGGATTAC TTnCATGGGT TTTTACTAGG AnTACCCAGA	60
AGGTCAAAAT ATTTTTGATG CGCTAAGTCA ATATGAAGTT AAGCGACGCG GCGATATGGA	120
AGAGGATCCA TCATATAAAC AACTCATTTC TTATTGTTTA CTTGAAAATG AGCATGGCGA	180
GATATTAGTG TATGAACGAT TATCTGGCGG TGGAGAAGCT CGATTGCATG GACAATCTTC	240
AATAGGTGTA GGCGGTCATA TGAATGATGT TCCAGGAGCA GAATCTATTA ACGAAGTATT	300
GAGAGTTAAT GCACAGAGAG AATTAGAAGA AGAAGTAGGT TTAAGTGAGC AAGATTACACA	360
AAATATGGAA TATATCGGTT TTATTAATGA CGATAATAAT GAAGTGGGCA AGGTACATAT	420
TGGTGTTGTA TTTAAATCA CTGTAAGTAC GAATGATGTA GAECTAAAG AAACAGATAC	480
TTTACGAATA AAATGGGTTG AAAAAGGCAA CATAGAGTCA TATGATGATT TCGAAACGTG	540
GAGTGCATTA ATCCTTCAAG ATTTATAATC AAACGAGGTG ACATATATGT CAGATATTAT	600
TCCAG	605

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

TTTATTAGCA CATCCAAACT ATTCATATGT TGGACAATTT TTAAACGAAC TAGGATTTAA	60
AAATGCATTA AGTGACGATG TAACAAAAGG TTTAAGTAAA TATTTGAAAG GACCTTACTT	120
ACAATTAGAC ACTGAACATT TAGCTGATTT AAATCCAGAG CGTATGATCA TTATGACAGA	180
TCATGCTAAA AAAGATTCTG CTGAATTCAA GAAGTTACAA GAAGATGCAA CATGGAAAAA	240
GTTGAATGCA GTTAAAAATA ATCGCGTGGA TATTGTTGAC CGTGATGTTT GGGCAAGATC	300
TCGTGGCTTA ATTTCTTCTG AAGAAATGGC TAAAGAACTT GTTGAATTAT CAAAAAAGA	360
ACAAAAGTAA GGTGGAAGTA AATGGCTATA AAAGAAATAA GTAGCCATC TGCCATAGAT	420

CATAAAAGAA AAAGACGCAC AACACTCACG TATATAGTGA GTTTGTGCTT TCTTTTTATT	480
TGTATATATT TAAATATGGC GATTGGTTCT TCGAAAATTA ATTTTAGCGA TATCATTCAC	540
TATGTTACTG GTCATACAGA TACGAAAGCA ACGTTTTTAT TGCATAATGT ACGTATGCCA	600
AGGATGATTG CAGGGTTATT TATTGGCGGT GCATTAGCGG TATCTGGTTT GTTAATGCAA	660
GCAATGAC	668

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

ATAÇAAAAAA ACATATCGAA AATAAAGCTA AAAGAACTA TCAAGTTCCA TATTCAATTA	60
ATTTAAATGG TACATCTACA AACATTTTAT CGAATCTTTC ATTTTCAAAT AAACCTTGGA	120
CAAATTACAA AAATTTAACT AGTCAAATAA AATCAGTACT GAAGCATGAT AGAGGTATTA	180
GTGAACAAGA TTTAAAATAT GCTAAGAAAG CTTATTATAC TGTTTATTTT AAAAATGGTG	240
GTAAAAGAAT CTTACAGTTG AATTCAAAAA ATTACACAGC AAACCTTAGTTCATGCGAAAG	300
ATGTTAAGAG AATTGAAATT ACTGTTAAAA CAGGAAGTAA AGCGAAAGCA GACAGATATG	360
TACCATACAC AATTGCAGTA AATGGCACAT CAACACCAAT TTTATCAAAA CTTAAAATTT	420
CGAATAAACA ATTAATTAGT TACAAATATT TAAATGACAA AGTGAAATCT GTATTAAAAA	480
GTGAAAGAGG CATCAGTGAT CTTGACTTAA AATTTGCGAA ACAAGCAAAA TATACAGTAT	540
ATTTCAAAAA TGGAAGAGAA CAAGTAGTGA ATTTAAATC AGACATCTTT ACACCTAATT	600
TATTTAGTGC CAAAGATATT AAAAAGATTG ATATTGATGT AAAACAATAC ACTAAATCAA	660
AAAAAAATAA ATAAATCTAA TAATGTGAAA TECCAGTAA CAATAAATAA ATTTGAAAAC	720
ATAGTTTCAA ATGAATTTGT GTTCTATAAT GCAAGCAAAA TTACmATTAA TGaTTTAAGT	780
ATAAAAC	787

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

AAAGTAAAAA TAAATCTCCC TTTTAACTT TCGTTTCTGC CATAGCCATT GCTTTTCTG	60
TGATAGTTGC TACAATATCT TTTCTTTCAC GGTTAAAATG TTCAACTTGT TCTGCTAAAA	120
ATGCAGCTTC TTCTTCGACG TCAGTCATCA ACAATTCGCa AGCTAATGAT GCGTCATCTA	180
AACGACCTAC AGCATTAAGT CTAGGTCCAA TAATAAAACC AATTGTTTCT TCATCAATAT	240
TGTCATTGTA TCCCGCTTCT TTTAGCAATG CTTTAACAGA GGTCGGACAT TGATCATTTA	300
AGACTTTTAA TCCTTGTTtTC ACTAATGATC GATTTTCATC AGTTAAGGAT ACTAAATCCG	360
CAATGGTACC TATCGCAACT AATGCTTTAA AATAATCAGG TACATTTtCA ATCAATGCTT	420
GTGCTAATTT GTATGCAACA CCTGCACCAC ACAATtTTG GAACGGATAA TTAAACGATG	480
GATGCATTGG ATGTACGATT GCATATGCTT CTGGTAATGT ACTACCAATT TCAT	534

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GGTGAGTCAA ATTAAATGAA TCTAATAAGT CATAACTATC TATTTGTAAT GTGCAACGCT	60
TAACGCATAT ACAAATGAA TGTGCTGATA ATGATTTACT CAAATTAAAA GGTGATTTT	120
ATTCAATGAT GAATGAAAGT TGCCTTTTTA TTTTGGTAA AAGTTAATGC GTCAGTGAAT	180
TGTGTAAGTT TTTCAAAAAG TAAAAAGAAA TAATAAAGGT GAATTATTAG AATTCCArAA	240
ATAATTCATT ACATTCATAA AGCATTTTAC AAATGGTAAG AAAATGAGTG TTACAAATCT	300
AAATATTGCA AAAGAAGCTG ATTTAGTCAC AAAAAATGTC CTATGTAATA ATTCGAGAAA	360
GATGCACTAT ATACGGTCTT CTTACTATTC AAATGTAAAA GTTGCTTATT TGC GTGGCTT	420
TTTGTTTTAT AAAAGTATAA AATTTTACTA TAATATATCT TG TAGAGAAC AATGAAATGA	480
CAGACTTATA AAACAAAATA GTAAGCTATG CTAATTTTtA TACAAAAAAT ATGTATAAAC	540
ATAGCAAAC TATTACTTT GATACAAAAA TG GTTGTAAT AAATATTTAT CGATATGACG	600
ACTTGAATAT GATAAAGTGA CATATTTATG TATATGACTA TTTCGCAAAA TGTAATCGAG	660
G TAGAATTTT T TGACAATTC TGTCAGTTTA TAAGATGTTA TAAATATGTA GTGTATAAGG	720
AGGCAAACAA GATGACTGAA GAATTCAATG AATCAATGAT TAACGATATT AAAGAAGGTG	780
ACAAAGTCAC TGGCGAGGTA CAACAAGTTG AAGACAAGCA AGTTGTTGTT CATATCAACG	840
GTGGTAAATT TAATGGGATT ATTCCTATTA GTCAACTATC TACGCATCAT ATTGATAGCC	900

CAAGTGAAGT	TGTAAGAGAG	GGCGACGAAG	TTGAAGCATA	TGTCACATAA	GTTGAGTTTG	960
ATGAAGAAAA	TGAAACTGGA	GCTTACATCT	TATCTAGAAG	ACAACTTGAA	ACTGAGAAGT	1020
CTTATAGTTA	TTTACAAGAA	AAATTAGATA	ATAATGAAAT	CATCGAAGCG	AAAGTAACAG	1080
AAGTAGTTAA	AGGTGGTTTG	GTTGTTGATG	TAGGACAAAG	AGGTTTGTT	CCGGCTTCAC	1140
TAATTTCAAC	AGACTTCATT	GAGGATTTCT	CTGTGTTTGA	TGGACAAACA	ATTCGTATTA	1200
AAGTTGAAGA	ATTGGATCCT	GAAAATAATA	GAGTCATTTT	AAGCCGTAAA	GCAGTTGAAC	1260
AAGAAGAAAA	CGATGCTAAA	AAAGATCAAT	TATTACAATC	TTTAAATGAA	GGCGATGTTA	1320
TTGATGGTAA	AGTAGCGCGT	TTAACTCAAT	TTGGTGCATT	TATAGACATT	GGCGGTGTTG	1380
ATGGTTTAGT	GCATGTATCT	GAACTTTCTC	ACGAACATGT	TCAAACACCA	GAAGAAGTAG	1440
TTTCAATTGG	TCAAGATGTT	AAAGTTAAAA	TTAAATCTAT	TGATAGAGAT	ACAGAACGTA	1500
TTTCATTATC	AATCAAAGAT	ACGTTACAA	CACCTTTCTGA	AAATATTAAA	GGTCAATTCC	1560
ACGAAAATGA	TGTCATTGAA	GGTGTCTAG	TAAGATTGGC	AAACTTTGGT	GCATTTGTTG	1620
AAATTGCACC	AGGTGTACAA	GGACTTGTAC	ATATTTCTGA	AAATTGCACAC	AAACACATTG	1680
GTACGCCAGG	TGAAGTGTTA	GAACCTGGTC	AACAAGTAAA	TGTTAAAATA	TTAGTATTG	1740
ATGAAGAGAA	TGAAAGAGTA	TCACATCTA	TTAAAGCAAC	ATTACCAAAC	GAAGATGTTG	1800
TTGAAAGTGA	TCCTTCTACG	ACTAAGGCGT	ACTTAGAAAA	CGAAGAAGAA	GATAATCCAA	1860
CAATTGGCGA	TATGATTGGT	GATAAACTTA	AAAATCTTAA	ACTATAATTT	AATATTTAAT	1920
AGTCAACTCC	ACATGTTTAT	GATTGcATGT	GGAGTATTTT	TATGTAACAA	AATATACTCG	1980
GAATGATAAC	GTGGgACAAA	TTTAACTAAG	TGTTTAAAAA	GATArAGTTT	TAAGTGcGa	2040
tTTTTATCAT	TACAGTAATA	AACTCATTTT	GAATACACAG	TCTCATGTGA	TATTATTAAA	2100
AAGATATaAG	AAAGAGAGGA	AGTTAGCTTA	TGACAAACC	TATAGTAGCT	ATTGTAGGTA	2160
GGCCTAATGT	AGGTAAATCT	ACAATTTTTA	ATAGAATAGT	TGGAGAACGT	GTTTCGATTG	2220
TGGAAGACAC	GCCAGGTGTA	ACACGAGATC	GTATTTATTC	TTCAGGTGAA	TGGTTAACAC	2280
ATGATTTCAA	TATTATTGAT	ACAGGTGGTA	TTGAAATTGG	TGATGCACCA	TTCCAAACAC	2340
AAATTAGAGC	GCAGGCAGAA	ATCGCCATAG	ATGAAGCGGA	TGTTATTATT	TTTATGGTTA	2400
ACGTGCGTGA	AGGATTGACA	CAAAGCGATG	AAATGGTCGC	TCAAATTTTA	TACAAATCTA	2460
AAAAACCGGT	CGTATTAGCG	GTTAACAAAG	TAGATAATAT	GGAAATGCGT	ACAGACGTGT	2520
ATGATTTCTA	TTCATTAGGA	TTTGGTGAAC	CGTATCCGAT	ATCAGGGTCA	CATGGTTTAG	2580
GTCTTGGTGA	CTTGTTAGAT	GCAGTTGTTT	CTCATTTTGG	TGAAGAGGAA	GAAGATCCTT	2640
ATGATGAAGA	TACAATTCGA	CTATCCATTA	TTGGACGACC	AAACGTAGGT	AAATCAAGTT	2700
TAGTAAATGC	TATTTTAGGT	GAAGATCGCG	TTATCGTTTC	TATGTTGCA	GGGACAACGA	2760

GAGACGCTAT TGATACAGAG TATAGTTATG ATGGACAAGA TTATGTTTTA ATCGATACTG	2820
CTGGTATGCG TAAAAAAGGA AAAGTATATG AATCAACTGA GAAATATTCA GTATTAAGAG	2880
CTTTAAAAGC GATTGAACGT TCAAATGTTG TTTTAGTGGT CATAGATGCA GAACAAGGCA	2940
TCATTGAACA AGATAAACGT GTTGCAGGAT ATGCACATGA ACAAGGTAAA GCAGTCGTGA	3000
TTGTCGTAAA TAAATGGGAT ACTGTGGAAA AAGATAGTAA AACGATGAAG AAATTTGAAG	3060
ATGAAGTACG TAAAGAATTC CaATTTTTAG ATTATGCACA AATTGCTTTT GTGTCTGCTA	3120
AAGAACGCAC AAGATTACGT ACATTATTCC CTTACATCAA TGAAGCAAGT GAAAACCATA	3180
AAAAACGTGT TCAAAGTTCA ACTTTAAATG AAGTTGTTAC TGATGCAATT TCCATGAACC	3240
CTACACCAAC AGACAAAGGT AGACGTTTGA ATGTCTTTTA TGCAACACAA GTTGCTATAG	3300
AACCACCGAC ATTTGTTGTA TTTGTTAATG ATGTAGAATT AATGcATTTTTCTTATAAAC	3360
GCTATTTAGA GAATCAAATC CGTGCCGCTT TTGGTTTTGA AGkTACACCA ATTCATATTA	3420
TAGCTCGAAA GAGAAATTAA CGATTGGGGG ATAACAATGA CTAAAATTAC CGTTTTTGGT	3480
ATGGGAAGTT TTGGGACAGC CCTTGCCAAT GTTCTTGCAG AAAATGGACA TGATGTTTTG	3540
ATGTGGGGTA AAAATCAAGA TGCTGTTGAT GAATTAAATA CATGTCATAC AAATAAAAAG	3600
TATTTAAAAT ACGCGAAATT A	3621

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CTTTTCGAAA TTAGGATChG nGCTATCTTG GCCCAATTA CCAAGGGAAC TAnTGGCACC	60
AAATGGTGGC AATCGCCGTC CATTAAATc GGTCCAATTC TAGTACCGCC TGCTTCGATT	120
AATGctTCTT TCATCTCCAT GCCCTGTTGC TCATTATTAA TAACACGGTC TATTAACACA	180
ATGGCATTtTG TTACTACGAT TCCAATTAAC ATTAGCATAC CAATTAAACT TGGTACTGAT	240
ATTGTTTTCTC CTGTGATTAA TAGTGCAATA ATTACACCGA TAACTGTAAA TGtAAAAGAG	300
AATAAAATTG TAAATGGTGC TAGGCCACCT TTAAATGTAA TAACTAGGAT TAAATATACG	360
ATAATGATTG CAGCTAACAT TGCAAAGGCT AATTGTGTCA TTGCATTGTT AATATCATCT	420
GATGCACCAC CGATATTAAC CTTTACATTA TTCGTTTTAT CCAAATTATT TATTTTAGAC	480
ATCACTTGTC GTGTTGTGCC ACCCACATCT TTATTTGTTA CTTTAGCAGA TACCGTCGTT	540

GCATAATCTC CTTGTTCTTG CGTCAATTTA CTTGGTGTGCG TTGTTTTAAC TAACGTAGCG	600
ATATCTCCCA ATTTAATCGT ACCACCAGTC GGCTTTTTTCA AAG	643

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

TTTCAGGCyG TGCAAGGGCT TTTTCTTTTG CTTTTAAGAT TATGATTTAT CGTGCAAAGT	60
TAAGTGGTCG TATATAGTTT TAGTTTTAAA AAGGTAATTA AATAAAATAG TTTGCCGAGG	120
GAGATGTCAA AATGATTAAA ATACCTAGAG GGACGCAGGA TATTTTACCT GAAGATTCAA	180
AGAAATGGCG TTACATTGAA AATCAATTAG ATGAATTAAT GACATTTTAT AATTATAAG	240
AAATAAGAAC ACCAATTTTT GAAAGTACAG ATCTTTTTGC AAGAGGTGTT GGTGATTCAA	300
CCGATGTCGT ACAAAAAGAA ATGTATACAT TTAAAGATAA AGGCGATAGA AGTATTACAT	360
TAAGACCTGA GGGAACAGCT GCAGTTGTGC GTTCATATAT TGAACATAAA ATGCAAGGTA	420
ATCCAAACCA ACCAATTAAA CTTTATTACA ATGGACCGAT GTTTAGATAT GAACGTAAGC	480
AAAAAGGACG CTATCGTCAA TTAAATCAAT TTGGTGTAGA AGCTATTGGT GCTGAAAATC	540
CTAGCGTAGA TGCAGAAGTA TTAGCTATGG TTATGCATAT TTATCAATCA TTTGGATTAA	600
AACATTTAAA GCTTGTTATT AATAGTGTAG GGGATATGC GTCTCGAAAA GAATATAACG	660
AAGCGTTAGT GAaACACTTT GAACCAGTAA TTCATGAATT TTGTTCAGAT TGTCAATCAC	720
GTTCGCATAC AAATCCGATG CGAATTTTGG ATTGTAAAGT AGACCGTGAT AAAGAAGCGA	780
TTAAGACTGC ACCTAGAATC ACTGATTTCT TAAATGAGGA ATCTAAGGCA TATTATGAAC	840
AAGTAAAAGC TTATTTAGAT GATTTAGGTA TTCCATATAT TGAAGATCCT AACTTAGTTC	900
GTGGATTGGA TTATTATACA CATAACGCAT TTGAATTAAT GATGGATAAC CCTAACTATG	960
ATGGTGcCAT TACAACGCTT TGTGGTGGTG GCCGTTATAA TGGTTTATTA GAATTGCTAG	1020
ATGGTCCAAG TGAAACAGGT ATTGGTTTTG CGCTAAGTAT AGAACGATTA TTGCTTGCAC	1080
TTGAAGAAGA AGGTATCGAA TTAGATATTG AAGAAAACCT AGATTTATTC ATTGTTACAA	1140
TGGGTGATCA AGCAGATCGA TATGCTGTGA AGCTATTAAA TCATTTGAGA CATAATGGTA	1200
TTAAAGCAGA TAAAGACTAT TTACAGCGTA AAATTAAAGG ACAAAGAAA CAAGCAGACC	1260
GTTTAGGTGC CAAGTTTACA ATCGTTATTG GTGATCAAGA ATTAGAAAAT AATAAAATCG	1320
ATGTTAAAAA TATGACAACT GGTGAATCTG AAACAATTGA ATTAGACGCA TTAGTCGAAT	1380

ATTTTAAGAA GTAGAGAGGG CGTTAAAATA TGAGTAAGAG AACAACTTAT TGTGGATTAG	1440
TTACTGAGGC ATTTTtagga CAAGAAATTA CATTAAAAGG ATGGGTAAAC AATCGTCGTG	1500
ACCTTGGTGG ATtGATTTtC GTTGATTtAA GAGATAGAGA AGGAATTGTA CmAGTCGTGT	1560
TTAATCCTGC ATTTTCAGAA GAGGCaTTGA AAATTGCTGA AACAGTACGT TCTGAATATG	1620
TTGTAGAAGT TCAAGGTACA GTTACGAGC GTGACCcTGA AACAGTTAAT CCTAAAATTA	1680
AAACTGGCCA AGTTGAAGTA CAAGTTACAA ATATTAAAGT GATTAATAAA TCTGAGACAC	1740
CACCATTTTC TATAAATGAA GAAAATGTTA ACGTTGATGA AAATATTCGA TTAAAATACC	1800
GTTATTTAGA TTTACGTCGT CAAGAGTTAG CGCAAACATT TAAAATGAGA CbCAAATTA	1860
CACGTTCTAT TCGTCAATAT TTGGATGATG AAGGGTTCTT TGACATCGAA ACACCAGTAC	1920
TAACGAAGTC AACACCTGAG GGTGCACGTG ACTATTTAGT ACCATCTCGT GTTCATGATG	1980
GTGAATTTTA TGCATTACCA CAATCACCAC AATTATTTAA GCAATTATTG ATGATTAGTG	2040
GATTTGACAA ATACTACCA ATCGTAAAAT GCTCCGTGA CGAAGATTTA CGTGCAGATC	2100
GTCAACCTGA ATTTACACAA GTCGATATTG AAATGAGTTT TGTAGACCAA GAAGATGTGA	2160
TGCAAATGGG TGAAGAAATG CTTAAAAAAG TTGTAAAGA AGTTAAAGGC GTTGAAATTA	2220
ATGGCGCTTT CCCACGCATG ACATATAAAG AAGGATGCG TCGCTATGGT TCTGATAAAC	2280
CAGATACACG TTTTGAAATG GAATTAATTG ACGTTTCTCA ATTAGGACGT GATATGGACT	2340
TTAAAGTATT TAAAGATACT GTTGAAAATG ATGGTGAAAT TAAAGCAATT GTCGCTAAAG	2400
GTGCAGCTGa ACAATATACT CGTAAAGaTA tGGGaTgCTT TAACAGAATT TGTAaACaTC	2460
ymTGGtGCTA AgGtTAGCGT GGGGTAAAG TTGTGGGAAG GTGGTTTTGA CAAGGTCCCA	2520
ATGG	2524

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1507 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TCGTTGAGTA AAAGTCCAGA AAATTGGATG AGTAACTTG ATGATGGAAA ACATTTAACT	60
GAGATTAATA TACCGGGTTC ACATGATAGT GGCTCATTCA CTTTAAAGGA TCCAGTAAAA	120
TCAGTTTGGG CAAAGACTCA AGATAAAGAT TACCTTACCC AAATGAAGTC GGGAGTCAGG	180
TTTTTTGATA TTAGAGGTAG AGCAAGTGCT GATAATATGA TTTCAGTTCA TCACGGCATG	240

GTTTATTTGC ATCATGAATT AGGAAAATTT CTCGATATG CTAAATATTA CTTGAGTGCT	300
TATCCAAACG AAACAATTGT GATGTCTATG AAAAAGGACT ACGATAGCGA TTCTAAAGTT	360
ACGAAGACAT TTGAAGAAaT TTTTAGAGAA TATTATTATA ATAACCCGCA ATATCAGAAT	420
CTTTTTtACA CAGGAAGTAA TGCGAATCCT ACTTTAAAAG AAACGAAAGG TAAAATTGTC	480
CTATTCAATA GAATGGGGGG TACGTACATA AAAAGTGGTT ATGGTGCTGA CACGTCAGGT	540
ATTCAATGGG CAGACAATGC GACATTTGAA ACGAAAATTA ATAATGGTAG CTTAAATTTA	600
AAAGTACAAG ATGAGTATAA AGATTACTAT GATAAAAAAG TTGAAGCTGT TAAAAATTTA	660
TTGGCTAAAAG CTAAAACGGA TAGTAACAAA GACAATGTAT ATGTGAATTT CTTGAGTGTA	720
GCGTCTGGAG GCAGCGCATT TAATAGTACT TATAACTATG CATCACATAT AAATCCTGAA	780
ATTGCAAAAA CGATTAAAGC AAATGGGAAA GCTAGAACGG GTTGGCTGAT TGTTGACTAT	840
GCAGGATATA CGTGGCCTGG ATATGATGaT ATCGTAAGTG AAATATAGA TAGTAATAAA	900
TAAGGATTCA ATAATGATAT TAAGACGAGT ATGAAAATAG TTAGATTCTA ATTATTTTCA	960
CTACTCGTTT TTATTTTGAA AATAAGTAAT AATTCAACAA TATTATAAAT TGAACAGATT	1020
GTTTGTGAAA TTTTGTGATA TATTAAAGTG AAAAAGTGTT ATAAATTGAT AAATATATGT	1080
AATTAACAAA AACAAATCAT TTTAAAAAGA AGAGAGTTGT AAGATGATGa AACGATTAAA	1140
CAAATTAGTG TTAGGCATTA TTTTCTGTT TTTAGTCATT AGTATCACTG CTGGTTGTGG	1200
CATAGGTAAA GAAGCGGAAG TTAAGAAAAG CTTTGAAAAA ACATTGAGTA TGTACCCTAT	1260
TAAAAATCTA GAGGATTTAT ACGATAGGA AGGCTATCGT GATGATCAGT TTGATAAAAA	1320
TGATAAAGGT ACATGGATTA TAAATTCTGA AATGGTTATT CAACCTAATA ATGAAGATAT	1380
GGTAGCTAAA GGCATGGTTC TATATATGAA TAGAAATACC AAAACAACAA ATGGTTACTA	1440
mTATGTTCGAT GTGACTAAGG ACGAGGATGA AGGAAAACCG CACGACAATG AAAAAGATA	1500
TCCGGTT	1507

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

TACATGTTTC GGATGCTACT TTATTTAGTT TGAAGGGTGC ATTATGGACG TTAGCGCAAG	60
AAGTTTATCA AGAATGGTAT TTAGGATCGA AGTTGTATGA AGATGTTGAA AAGAAAATAG	120
CACGAACTAC TTTTAAGACA GGTTATATTT ATCAAGAAAT TATTTTGAGA CCAGTAGATG	180

AAGTTAAGGT ACTTCTGAAT GATTTAAAAG GTGCTGGTTT CGAATTAGGT ATTGCAACAG	240
GTCGTCCTTA TACTGAGACT GTTGTGCCAT TTGAAAATTT AGGATTGTTA CCATATTTTG	300
AAGCTGATTT TATTGCAACA GCAAGTGAT TTTTAGAAGC AGAGAATATG TATCCGCAAG	360
CACGACCATT AGGAAAGCCG AATCCTTTTA GTTATATCGC AGCTTTATAT GGTAATAATC	420
GCGATAAATA TGAATCTTAT ATCAATAAGC AAGATAACAT TGTAATAAAA GATGACGTAT	480
TTATAGTAGG CGATTCGTTA GCTGACTTAT TAAGTGCTCA AAAAATAGGT GCAAGTTTA	540
TTGGAACATT AACAGGTTTA AAAGGTAAGG ATGCTGCAGG TGAGTTAGAA GCGCATCATG	600
CCGACTATGT TATTAATCAT TTAGGTGAAC TTAGAGGTGT ACTAGATAAT TTGTAATTTG	660
ATTGTTGTTT GACAGCATAA CTTGTAGTGA ATGATTGAAC CAAAGGTTTC ATATTGAGTT	720
ACAATGAAAT TAATAATGAA AAAATGCCAA GAAGCAATGG AAGTAATCCA ATGTCTTCTT	780
GGCATTTTGA ATTTACATAA ATTGTTTATG ACTGTACCGT CAATTCAGTT GTGAAAATTT	840
GATTGTATTC ACCAACTTGT TTAAGTTCAT CAATTATATT GTTTGAAACA GGTTGATCAA	900
CGGATAAAAT CATTAGCGCA TCTCCGCCCC CTTCATTCT ACCTAAAGTC ATAGATGCAA	960
TGTTGATATT GTATTTACCT AACAATGCGC CAGTTTTTCC TACCATACCT GGAGTATCAT	1020
TATGATATGA CACAATTTGA TATTGATTTG GCTTTAAGTC TACAGAAAAA TTATTAATTC	1080
TAACAATTCT TGGACCGAAA CCTGTAAAGA CAGAAGCGCC AACTTTAACG GAATCGCnAT	1140
CGnTTGATAG TTCTACCTCT AAGTAGTTAC TAAAACCTGT CTCTGCTTTA TTATTTTCAA	1200
TATTTAATGT CACTTG	1216

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 867 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

ATCAAAATAT TTAAATAAT ATTGATGGTC ACATTGTAAA TrmAATAGAA AATAAATTTG	60
ATCAAATATT ACAAGAACCA TTAAATCCAT TAAATTATGA TACTGTCAGT GGATTAGCTG	120
GGATAGGGAG ATATTTGCTA AATAGAGTAG ATGAGAATGA ATTTAATGTT AAAGCATTA	180
AAAGCATATT AGTATACTTT AAAGATATTC AATATTCTAA AAATAGCTGG GTAGTCCCAC	240
AAGArAGTCA ATTTTTAGAG TCTGATAAAA ATTATTTTACTGAAGGTAAT ATCAATCTTG	300
GCCTTGCA CA TGGaGTGCTA GGACCGATGT CTTTATTTGC ATTATGCGTG ATTAAAGGAA	360

TTACGATTGA AAATCATCAG CACATATTAA AAGACATGTA CAAATTTATC ATGGACGAAA	420
AATTTTGTAA CCACGAAAGA TGGTTGCAGC GTTACGATTT AATTTCTGAA CGTAATCATT	480
TCAATTTTAT TCGGAATGGT TGGTGTATG GCAATACGGG TGTAATGACG ACGTTGTTTT	540
TAATCGGCCA AGCATTACAA GATGATGAAA TAATTAAAAT GTCTAAAAAA GTGATGCTAC	600
AAGTAGTAAA TGATAAAGAT GAAAATTTAA TAAGTCCAAC TATTTGTCAT GGATTGTCAT	660
CACAAATATT AATGTTAACA ATTATGAATT TGAATTTTGA ATTAAATGAA GTGTCTGATT	720
ATATCACTGT ATTAATAAAT AAAGTATTTT CTCATTATAA GGAAGATTAT CTGGTGAATT	780
TTATAGACAT TAATGAAAAT AAGCAAGATG TATTTAAAAG TAGGAAAAGT GGCCTTTTAG	840
AAGGTGAATT AGGGGTCATC TAACATT	867

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

TACCTTTTCT TtTAAATCAT TTTATATTTT CCCaCTAATA TCCGcTGtTA ATCaATCctG	60
ACATCCctTGT ATCaCTATGA CAATTAATTG TTAAATACAT GAATTTCTAC ATTTTATGAA	120
AAAATCCATT TTTATTACAA TTCAACACTT TATATGACAA CTTCATTACA GTTACTTTTA	180
TTGTTGATTG CTTACATTGT TTTCTAAAAA AAATTTGTTA TCATAATTAA CGTTGAATAA	240
AGAAAAAAT TAACCTGGGA GATAAAAATG GAATATAAAA AGATACTAAT TCGTTTATTA	300
ATTGCTTTTG CAGTACTTTT CTCAGCAGAT TTCACTTATC AATCCGTCGA ACAAACGCAT	360
CAATCGCATG CCGCAGTTAA TTATTATAGT AAAAACCAAT GTACATGGTG GGCATTTAAA	420
CGTCGCGCAC AAGTCGGTAA ACCTGTTTCT AATAGATGGG GCAATGCTAA AAATTGGTAT	480
TACAATGCAC GTAAATCAAA ATATGCGACT GGTCGTACAC CAAGAAAATT TGCTGTCATG	540
CAATCAACTG CAGGATATTA TGGACATGTC GCAGTTGTTG AACAAGTAA TAAAAACGGT	600
AGTATTAAAG TTTCAGAATA CAACTTTTAT CGCCCATTA AATACAATAC ACGTGTACTA	660
AGCAAAAAGG CAGCACGTAA CTTTAACTAT ATTTACTAAT CAAAAAACTT CTATCACGAA	720
CGCTTCAATT TCCTGTATGC GTGTGATAGA AGTTTTTATT TTATGAAATT ATATTATTAC	780
TTCTACAAAT TTCAAATTGC CGTAATTGAA CGTATATTTT TTCTTCAACT ATTATTTTAT	840
CTTTAGCATA ATCTATATAT AAAATTTTAT GCTATTATTT AAATAATTCT CTATAACTTA	900
ACATACGTTT TCGATATAAA CCTTGTTCTA AATCTCAATA ATTTTTTGCT GTTTTCATCG	960

TCATTAGTTA	AAAAAATAAT	TTAACTGAGT	TTTTGAGACC	TGTTTAAATT	GATGACTCAA	1020
AACCTTTATC	CCCTTTTCAC	TCGGTTTAAT	TGCTTTAATA	TTTAACACAG	TCTCATTGTA	1080
ATTTTGCTAC	TAAGTTTGAA	ATATTTTCGAT	TCGAATGTGA	AaATCATTTA	TTATTACTTT	1140
CGACAGCTAG	AAAAATATTG	TTAAACCAAA	ACTATAATTA	CCACTTTTAT	ATAGAATAT	1200
ATATAAATTT	TAACTTTGAG	ACAGAACTGC	TAGTCAGGTT	TATGAATATA	TTTCTTTAGT	1260
TTACTTGaTA	TACTTATTGG	TAAATCATTa	TTTATTTGAA	GAGCATTAT	AACAAAAAGT	1320
ATAATCCCAG	TTATAGCGAT	TCCATGACCA	TTTTTATCAG	TCAAAGATTC	ATCAACAAAA	1380
ACTTTTTGAT	AAATTTATAT	ATTTGTATAA	TTTATTATGG	TAGATATCTA	CACCCGTATC	1440
TATAACAGCT	ACAGTTATCA	TTGCGTCTTA	TCCAAATAGT	TTTTAAGAAA	TAAATATAAT	1500
TCATTAATAT	CATGGCTATT	TGTAACGTCA	GtGCTTaAGA	CCTTGTCAAT	TATTGTTTTA	1560
TCTGTTTCTA	AGAGCCCCTG	ATTTTCTGCA	TACATATTT	GTATATCGCT	GTTAATCTCA	1620
TTTAATTTTT	TAAATTTTTT	TCTAACCTTT	TTCAAAATAA	AATGCTCTTT	AATTCCATCT	1680
CTTAAATACA	TATAAATCTC	TATTATAATC	TCCATAAATG	TCATATCTCC	TCTCTCAAAA	1740
AACATTATAC	TCAATATATT	AAAAATAAGA	AAGGTTTTTT	CAGAATTTTT	AGTATTTTCA	1800
GATATTTATT	CTTAAGTATC	TTATTATTAC	TTCTTTTTTA	CGCTAGTGa	ATAATTAATA	1860
ATAATTGTAT	TTAAATGCAA	TGCTGTTGTT	CTTTCATACT	TACAAGCAAG	TCATAAGAAA	1920
TGAGAAATTA	AATTCTTATA	TGATGAATAA	ATGATGACTG	CAGAAGAAAT	TGCTAAAAAA	1980
GGAGTGGAGT	GAGGCATTCT	ACTGTTCATA	TTGTTAACAA	ATATCAAAAT	GATAGGAACT	2040
TGAAGAATCT	AAGACTGTTA	AAATCGAGAC	AAGAAGAAAC	TCGTTCCAAA	TTTGAATCCT	2100
ATAATGAATT	CGTCTCATGA	AGAAGTTATT	TACTTTTCAT	TAGACTGATT	TACTAATCAA	2160
AAAACCTCTA	TCACGAACGC	TTCAATTTCC	TGTATGCGTG	TGATBAAGT	TTTTATTTTT	2220
GTTCATATTA	ATTTATCTAA	GCGCTACGAT	GGaCTGACTT	AAACTTTTCT	TTAAAATCGC	2280
TATTGCCCAT	TTACTATTGT	TGTCTAATTT	CTTGTA AAAAT	ATGTTCCGCT	GCTTGTGTAT	2340
TTGCACGGGG	TTCTTTTTTC	AAAGCTTCAG	CTACTTTAGC	AATTTTCATCA	CCTTTTGCCC	2400
CTACAACGAT	AGCTAATGAT	TTATATTGTA	AACTCATATG	ACCTTGTTGA	ATACCTTCTG	2460
ACACAAGCGC	GCGACATGCT	GCAAAGTTTT	GCGCTAAACC	AACGGCAGCA	ACTACATGAC	2520
CTAATTCTTG	TGCTGACTCT	ACATTTAGTA	GCTCTAATGA	AGCTTTAGCA	ATTGGTAATA	2580
CTTTTGTACC	ACCGCCAACG	ATTGCCATG	TCATAGGCAC	TTCAATTGTA	CCAATCAATC	2640
GTTGACGATC	TTGATCGTAA	CGCCATGTAG	CAATACCACG	ATACTGTCCG	TCACGACTCG	2700
CGTATGCATG	CGCACTTGCT	TCTGCACCAC	GCGTATCATT	TCCTGTTGCT	AAAACAACAG	2760

CATGTATGCC ATTCATAACA CCTTTATTAT GTGTTGCTGC ACGATGAATA TCACTTGGG	2820
CCAATACAGA AGCACGTTCC ATTCGTTTGG CAACCTCTTC TCCAGTTCTC TCGCCCCTTG	2880
CTAAATCTTT AACATCAATT TCGCCTTGAA CTTTAACAAC GGACGCTGTT GCATGATTGG	2940
ATAAAATACT CATTAAAATG TCGCTTTGCG GAAATTCATT TTTTAAAAAT GCAGTTATGG	3000
CCTCTAAAAAT CGTATTAAGC ATATTAGCGC CCATAGCATC TTTTCGTATCA ACAAATACTT	3060
TTAAAGATAG TAACTGTTGC TCAGGAAATG TATCAATCGC TATACGTTGG TAACCACCAC	3120
CACGCGCTTT AATAGAAGGA TATGCCCTCAT CCGCAATTTT ATGAATTTGC TTTTCTAAAG	3180
CTTTAATGTC TGCTGATAAT TTTTCAGTAT CGTACGCC ATCAAAGACG ATTTGACCTA	3240
TCATAATACG TTCAGAAGAT ACCGTTTTAA ATCCGCCAGT CTGATTCACT AGCTTTGCAC	3300
CATAACTAGC TGCAGCGACA ACTGAAGGCT CTTCCACCAT CATAGGTACA ACATATGCCT	3360
TATCGTCCAC AATGATATTC GGTAATAATC CAACGGGTAA TGCACCTTGC GCGATGACAT	3420
TTTCAATTAA ACTATTGGCT ACTTCTTCAT CGATTAATGG ATGATTCAGT AAAATGTGCA	3480
ATTGTTCTTC TGATAACCAT TGCTTATCAA CCAATTGTTG TAACTTTTCT TTACGAGATA	3540
AATGTCGAAA ATTCTTATCT AAATTTTGCA TGGACGTACT CCTTTTACTT CACATAATTT	3600
TTAACATTTT AATCACTACT ATTTTTACCA CAAAATAACG TCATTCGTCT TAAAATTCAA	3660
TTGAATAATT GTCGTTTTGA CTTTAAAAATA AAACAAGGTA AATTAAAACG CTTACAAGAA	3720
ACGACAAATC ATTTTTTAAAT TTAGTATATT TCTTTGTATA AAATTAGCAT ATTCTGATAT	3780
GATACAAGTG TTGCTTTTAT AAATTTGAAA GGATGTAAAA CTTATGACA ATAGGTATCG	3840
ATAAAATAAA CTTTTACGTT CCAAAGTACT ATGTAGACAT GGCTAAATTA GCAGAAGCAC	3900
GCCAAGTAGA CCCAAACAAA TTTTAAATTG GAATTGGTCA AACTGAAATG GCTGTTAGTC	3960
CTGTAAACCA AGACATCGTT TCAATGGGCG CTAACGCTGC TAAGGACATT ATAACAGACG	4020
AAGACAAAAA GAAAATTGGT ATGGTAATTG TGGCAACTGA ATCAGCAGTT GATGCTGCTA	4080
AAGCAGCCGC GTTCAAATT CACAACTTAT TAGGTATTCA ACCTTTTGCA CGCTGCTTTG	4140
AAATGAAAGA AGCTTGTTAT GCTGCAACAC CAGCAATTCA ATTAGCTAAA GATTATTTAG	4200
CAACTAGACC GAATGAAAA GTATTAGTTA TTGCTACAGA TACAGCACGT TATGGATTGA	4260
ATTCAGGCGG CGAGCCAACA CAAGGTGCTG GCGCAGTTGC GATGGTTATT GCACATAATC	4320
CAAGCATTTT GGCATTAAAT GAAGATGCTG TTGCTTACAC TGAAGACGTT TATGATTTCT	4380
GGCGTCCAAC TGGACATAAA TATCCATTAG TTGATGGTGC ATTATCTAA GATGCTTATA	4440
TCCGCTCATT CCAACAAAGC TGGAAATGAAT ACGCAAAACG TCAAGGTAAG TCGCTAGCTG	4500
ACTTCGCATC TCTATGCTTC CATGTTCCAT TTACAAAAAT GGGTAAAAAG GCATTAGAGT	4560
CAATCATTGA TAACGCTGAT GAAACAACCTC AAGAGCGTTT ACGTTCAGGA TATGAAGATG	4620

CTGTAGATTA	TAACCGTTAT	GTCGGTAATA	TTTATACTGG	ATCATTATAT	TTAAGCCTAA	4680
TATCATTACT	TGAAAATCGA	GATTTACAAG	CTGGTGAAAC	AATCGGTTTA	TTCAGTTATG	4740
GCTCAGGTTT	AGTTGGTGAA	TTTTATAGTG	CGACATTAGT	TGAAGGCTAC	AAAGATCATT	4800
TAGATCAAGC	TGCACATAAA	GCATTATTAA	ATAACCGTAC	TGAAGTATCT	GTTGATGCAT	4860
ATGAAACATT	CTTCAAACGT	TTTGATGACG	TTGAATTTGA	CGAAGAACAA	GATGCTGTTC	4920
ATGAAGATCG	TCATATTTTC	TACTTATCAA	ATATTGAAAA	TAACGTTTCG	GAATATCACA	4980
GACCAGAGTA	GTCGGTGTAT	TTAAAAACACA	TATAATAAAA	CCTAAAAGCA	GCAGTAGAC	5040
CACTTCTAAT	TGAAATCGTC	TTACTGCTGT	TCTCTATTTA	TAACACTTCG	TATTGAATGA	5100
ATTCATTATG	CCTATTTGAC	ACATTATTGA	AGTTTTCTTA	ATGCCTGGAT	CCTTTATACG	5160
TTACGGCTTC	GTGCTATGTT	TTGGTACATA	AAGCTTTGAC	ATATCGATAT	TCTCCAACCT	5220
TAACAGCTTA	ATTTTATTAT	TAATCGTTCC	ACCGAACCTT	GTTAAGCTAC	CCGTTTTACC	5280
GACAACACGA	TGACATGGCA	CGATAATAGA	TAATGGATTA	CTTCCGACTG	CACCTCCAAC	5340
CGCTTGGGCT	GACATTTTTG	GCTTGTTAAG	CAGCTTGCCT	ACTTTTTTGG	CAATAGCACC	5400
ATACGTTGTT	AGAGTCCCAT	AAGGAACCTG	TCTTAATTA	TTCCAAACAC	ACTGTTGAAA	5460
ATGACTACCT	GTTGGCTTTA	AAGGTATTGT	GATTTTCAGG	TTGTCACCTT	TAAAATACGC	5520
GTCTAACCAC	TGTGTCGCCT	CTCTAAATAT	CGCTAAAGAC	GTATTTTCTT	CCCTAGTACC	5580
ATCACCTTGT	TGATTTTCAA	ACAAAACAGC	GGTCAGACTT	ACCCCATCAC	TCAAAGTTC	5640
CAATCGTCCT	ACAGGCGAAT	CATAGTAACT	CTTATACTCC	ATAAAAAATC	CCCCTTTTTT	5700
TAATCATACG	CCTTAATTGT	TAAATTAGAA	AATATTCATG	TTCACATTTT	TTAAAAATAA	5760
ATAAGTCGTC	AATTACGTAT	ATAAACACGT	AATACCAGCT	ATCACTTTGC	TGCAATATAC	5820
AGTTACATAT	CTTACTACAC	GTGCTAACCT	CTTACTTTGT	AAACCAAATC	TTAAATTAAA	5880
ATATTGAAAA	TGCAATGAAT	CCTTAATATT	TTATTAAACC	TATAATTACT	TATTAAAAAT	5940
AACACACAAT	ATTCATAAAG	TTTTAAAAAT	ATTCTGTTTT	ATCACCTACT	ATTAGTGGAA	6000
AAGTACAATT	GCAATTGTAT	ATAGTTTGCA	TAACGCTTCA	AAAGTATTT	CTTTTTTGTT	6060
TAGTTCAAAA	AAATTTAGAG	GTGATGTTAT	ATGAATAACG	GTTTTTTCAA	TAGCGACTTT	6120
GATTCAATTT	TTCGAAGAAT	GATGAAAGAT	ATGCAAGGTT	CAAATCAAGT	CGGAAACAAA	6180
AAGTACTATA	TTAATGGTAA	AGAAGTTTCA	CCTGAAGAAC	TAGCGCAACT	CACACAACAA	6240
GGTGGCAATC	ACTCTGCTGA	ACAAAGTGCG	CAAGcTTTTT	AACAAGCAGC	ACAAAGACAA	6300
CAAGGGCAAC	AAGGTGGCAA	CGGCAATTAT	TTAGAACAAA	TTGGTCGTAA	CCTTACGCAA	6360
GAAGCACGTG	ACGGTTTATT	AGATCCAGTC	ATTGGTCGTG	ATAAAGAAAT	TCAAGAAACT	6420

GCTGAAGTTT	TAAGTAGACG	AACTAA AA AC	AATCCTATAT	TAGTTGGAGA	AGCTGGTGT	6480
GGTAA AA CTG	CGATTGTTGA	AGGTTTAGCA	CAGGCAATCG	TTGAAGGAAA	TGTACCAGCA	6540
GCAATCAAAG	ACAAAGAAAT	TATTTCTGTA	GACATTTTCAT	CATTAGAAGC	TGGAACGCAA	6600
TATCGTGGTG	CTTTTGAAGA	AAATATTCAA	AAATTAATCG	AAGGTGTTAA	ATTTCACAA	6660
AATGCCGTAC	TATTCTTTGA	TGAAATCCAT	CAAATTATCG	G TTCAGGTGC	CACAGGAAGT	6720
GATTCAGGTA	GCAAAGGGTT	ATCTGATATT	TTGAAACCTG	CATTAAGTCG	TGGTGAGATT	6780
TCTATTATTG	GTGCAACAAC	ACAAGATGAA	TATCGAAACA	ATATTCTTAA	AGATGCTGCA	6840
TTAACGCGCA	GATTTAATGA	AGTGCTTGTT	AATGAACCAA	GCGCTAAAGA	TACTGTTGAA	6900
ATTTTAA AA AG	GTATTCGCGA	AAAATTCGAA	GAACACCATC	AAGTAA AA ATT	ACCAGATGAC	6960
GTATTAA AA AG	CATGTGTTGA	CTTATCAATT	CAATATATTC	CACAACGATT	ATTACCAGAT	7020
AAAGCAATCG	ATGTGTTAGA	TATTACAGCA	GCA AT TTTAT	CTGCGCAAAG	TCCAGCTGTC	7080
GATAAAGTTG	AAACTGAAAA	ACGAATTTCT	GAATTAGAAA	ATGATAAACG	TAAAGCAGTA	7140
AGTGCTGAAG	AATATAAAAA	AGCTGACGAC	ATTCAA AA ATG	AAATCAAATC	ATTACAAGAT	7200
AAATTAGAAA	ATAGTAATGG	TGAACATACT	GCTGTTGCTA	CAGTTCATGA	TATTTCAGAT	7260
ACTATTCAAC	GATTA AA CTGG	TATTCCAGTT	TCTCAAATGG	ATGATAACGA	TATTGAACGT	7320
TTAAAAAATA	TTTCTAATCG	TTTAAGAAGT	AAAATCATAG	GTCAAGATCA	AGCTGTAGAA	7380
ATGGTTTCAC	GTGCAATTCG	CCGTAATCGT	GCTGGGTTTG	ATGACGGCAA	CCGTCCAATT	7440
GGCAGTTTCC	TATTTGTTGG	CCCTACTGGT	GTTGGTAAAA	CAGAGCTTGC	TAAACA AA TTA	7500
GCAATTGATT	TATTTGGTAA	TAAAGATGCA	CTGATTCGAC	TTGATATGAG	TGAATATAGT	7560
GACACAACAG	CTGTTTCAA	AATGATTGGT	ACA AA CTGCTG	GTTATGTTGG	TTATGATGAC	7620
AATTCAAATA	CGTTAACTGA	AAAAGTACGC	CGTAATCCAT	ETCAGTCAT	TCTATTTGAT	7680
GAAATCGAAA	AAGCAAATCC	ACAAATTTTA	ACATTGTTAT	TACAAGTAAT	GGATGATGGT	7740
AATTTGACTG	ATGGTCAAGG	TAATGTCATC	AACTTTAAAA	ATACAATTAT	TATTTGTACA	7800
TCAAATGCTG	GCTTTGGCAA	TGGCAATGAC	GCTGAAGAAA	AAGATATTAT	GCACGAAATG	7805
AAAAAATTCT	TCCGCCCTGA	ATTCCTTAAC	CGCTTCAACG	GCATCGTTGA	ATTCTTACAT	7920
TTAGATAAAG	ATGCATTGCA	AGATATCGTC	AACTTATTAT	TAGACGATGT	ACAAGTTACA	7980
TTAGACAAAA	AAGGTATTAC	GATGGACGTT	TCTCAAGATG	CGAAAGATTG	GTTAATTGAA	8040
GAAGGCTATG	ATGAAGAATT	AGTGCACGT	CCATTAAGAC	GTATTGTTGA	ACAGCAAGTA	8100
CGTGACAAAA	TTACAGATTA	CTATTTAGAT	CATACAGACG	TTAAACATGT	GGATATAGAT	8160
GTTGAGGATA	ACGAATTAGT	CGTAAAAGGT	AAATAACGAC	ACTTTAACAT	ATCGCGCATC	8220
AAAAATGAGC	ATCAGGTCGC	CCTTGCCTGT	GCTCATTTTT	TTAATTATT	CCCTGGAAAA	8280

TGATTCGCTG	TGTGCTGTTC	TGTTCCACAA	CAATCACGAT	TAATGTCACA	TGTACCACAT	8340
TTTCCTTGTT	TTGAACGCTT	GAAAAATTTT	ACTAGTGTAT	ATAAGGCATA	TCCGAAAATT	8400
GCTAAAAAAA	TTAAAATGTT	AATAATGACT	GACACTTTAA	CCACTCCTTA	AACAAATAAA	8460
TGTCCGACTT	GATAAAAAAT	GAATGTTAAG	ACATATGCAG	TGACTAGAGG	ATAGGCAACT	8520
GCAAGTGCCG	TCCATTTCCA	TGAATAAGTC	TCTTTACGGA	TTGCTGCTAC	TGTAGAAACA	8580
CAAGGAATAT	ACAATAGTAT	AAATATCATA	AATGCATACG	CAGATAGCGG	TGTGAATTGA	8640
TTTTGAATCA	CATTAACAAG	GCCTGCATCA	CCTGATGAAT	AGATAATCGC	CATCGAACTT	8700
ACGATAACTT	CTTTTGCTAA	AAATCCTGGC	AcTAACGTAG	CACCTGCTTG	CCATGTTCCA	8760
AATCCGAGCG	GTTGCACTAA	CATACCAAAG	AAACTACCAA	CCATATGTAA	AAAACCTTGA	8820
TTGATATTCA	CATTGATACC	ATGTGGTCCT	ACATAACTTA	ATAGCCAAAT	GACTIONAG	8880
CCGCCAAAAA	TAAATGTACC	TGCTTTACGA	ACAAAGCCCT	TAGCCTTTTC	CCAAGTACTA	8940
CGCCACAACG	TTTTAATGGA	AGGCACACGG	TATGTTGGCA	ATTCCACAAT	AAAGATTGCA	9000
TTATCATTTT	TTAAAATCGT	CTTAGTAAGT	ACTGTACTGA	CTAAAAATGC	CATAATAATA	9060
CCTAAAACAT	ACAGGCTTAA	TACTACTAAA	GATTGATTCT	CTTTGAAAAA	GATACCTACG	9120
AACAACGCAT	ACACTGGCAG	TCTAGCAGAG	CATGACATGA	ATGGTGCAAT	TAATATCGTT	9180
GTTAAACGCT	CTTTTTCATT	TTCAATACTG	CGCGCAGCCA	TAATACTCGG	TACATTACAA	9240
CCAAATCCGA	TAATCATTGG	TATAAAAGAC	TTCCCGCTA	AACCGAACGA	TTCCATAATA	9300
CGATCCATTA	AAACCGCAAT	ACGTGCCATA	TAACCCGAAT	CTTCTAATAA	AGATATAAAG	9360
AAAAAGAGCA	CAACAATTTG	TGGTACAAAG	ACTAATACTG	ATCCTACACC	AGCAATAATG	9420
CCATCTGTAA	TTAAATCTTG	TAAAAATGGT	ATAACACCAA	GATAATTTCAT	AATCGTCTTC	9480
ACACTATCTG	TAAATGTACC	ACCTATAAAT	GCATCGAGTT	GATCCGACAA	AGGTGTGCCA	9540
ATCCATGTAA	ATGTAGTTTG	AAAGATCAAC	CACATAATTG	CTAGAAAGAT	AGGCATCCCT	9600
ATATATTTAT	GTGTTAATAT	CTTGTCTATT	CTAGAGCTGA	AATATTGCTT	ATCTTCATCT	9660
GGATACGTTA	CCACGTCTTG	CAATAACGTC	TCAATATAAT	GATTGCGTAT	ACGCTCCATC	9720
TCTCGACGAA	CAGATACAGC	CCCTACTTGT	TCAGCAACTT	GATCACGTAA	ACTCGACAAT	9780
TTATTTACAA	CCTCTGAATT	AAGTTCGTTT	GCAATTTGCA	TGTTATTTAA	TAAGAATTGA	9840
ATCGCAATAA	ACCTAGCTTG	ATACTTATCA	TGAGATGTCT	CTGTATTAT	TATTTGACAC	9900
ATATTTTTAA	TTGTCTCTTC	AATCTTCTCA	CCATAATTGA	TTTTAAAATG	CGGTTGATAC	9960
CCTTCCCCTA	GATGCTTTAT	TTCGCCAAGT	AAATATTTTG	TTCTTTTGCC	TGTACGTGCC	10020
ACAACCTGGAA	AAATAGGTGT	TTTTAACTTT	TTCATCAATT	TATGATAATC	GATTTTTATC	10080

CCGCGCTTTG TAGCTACATC AATCATATTT AATCCGATGT ATATTGGTTG ATTAAGTTCT	10140
AACAATTGTA CTGTTAATTG CATATTTCTT TTTAGTTGAC TCGCATCAAC AATGTTAATG	10200
ATTCCTGAAA ATGAATCGTT TAATAAATAG TCTGTCACTA CAGTTTCATC TTTAGAAATC	10260
GGCGATAAAT CATATGTACC TGGTAAATCA ATTAATTGTC CTACATTTTC TTTAAGTTTC	10320
CCTACTTTTT TCTCTACCGT TACGCCACTC CAGTTGCCTA TATATTCATA CGAACCAGTT	10380
AAAGCGTTAA ACAAAGATGT TTTACCAACA TTAGGATTTT CTAAAATACA ATAATTTTCC	10440
ATTCGTCCGG CTCCTATTCT TCTAATGCAA TAGAACAAGC ATCGCAATGT CE ATACTTA	10500
ACTGTTGTCC GTTTACTTCA ATAATACATG GCCCTTTAAA TAAACATTTT TGTTTAATCG	10560
TTATGATAGC GTCATCTGTT AACCCAAAGG CACTTAGACG ATACAACATA TTCTCATTAG	10620
CAATATCCAT TCGCTTTATT TTATAAGCCT TATTCATTTT ACCATTTTTA ATGTTTAACA	10680
TACTATTTTG CTCTCCTATT AGAAATAATA ATCATTATCA CTTAAAAATC ATAACCCTTA	10740
AAATTGTAGC TCGCAATACT TTATTTAAAT AATTTTCATT TTTTCATGTAA AATTTGTGAC	10800
ATTGCAAAAA TGT	10813

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

TGATGGATTA GCAGACATTT TACGAGCGAA TGGTTTCAAA GTGTTTGGTC CAAATAAGCA	60
AGCAGCTCAA ATCGAAGGCT CAAAATTATT TGCTAAAAAG ATAATGGAAA AATATAATAT	120
TCCAAC TGCT GATTATAAAG AAGTTGAGCG AAAAAAGGAT GCTTTAACAT ATATTGAAAA	180
CTGTGAATTG CCCGTTGTTG TCAAGAAAGA TGGGTTAGCT GCTGGGAAAG GCGTATTAT	240
TGCAGATACT ATTGAAGCAG CCAGAAGTGC TATTGAGATT ATGTATGGTG ATGAAGAAGA	300
AGGTACTGTT GTATTTGAAA CGTTTTTAGA AGGTGAAGAG TTCTCGCTAA TGACATTTGT	360
TAATGGTGAT TTAGCAGTAC CTTTCGACTG TATTGCACAA GATCATAAAC GCGCATTTGA	420
TCATGATGAA GACCAAATA CTGGTGGTAT GGGGGCTTAT TGTCCmgTAC CACATATTAG	480
TGACGATGTT TTAAmACTTA CAAATGAAAC AATTGCACAw CCCATTGCAA AGGCAATGCT	540
TAATGAAGGT TATCAATTCT TCGGTGTATT ATACATTGGT GCTATTTTAA CTAAAGATGG	600
TCCAAAAGTA ATAGAATTTA ATGCCCGTTT TGGTGATCT GAAGCTCAAG TATTATTAAG	660
TCGCATGGAA AGTGATTTAA TGCAGCATAT TATTGATTTA GATGAAGGAA AACGTACTGA	720

ATTCAAATGG AAAAATGAAT CTATTGTAGG GGTCATGTTG GCATCAAAAG GATATCCTGA	780
TGCATATGAA AAAGGGCATA AAGTAAGTGG CTTTGATTTA AATGAAAAC TTTTGTTAG	840
TGGATTAAAG AAGCAAGGTG ATACCTTTGT TACTTcAGGT GGTAGAGTTA TACTTGCCAT	900
CGGAAAAGGT GACAATGTAC AAGATGCACA GCGAGACGCA TACAAAAAAG TATCACAAAT	960
ACAAAGTGAC CATTTATTCT ATCGTCATGA CATTGCGAAT AAAGCACTAC AACTTAAATA	1020
AGTAAATTTA AAATACTAAG aTTAGCTATG AACGAATCTA TAACGATAGA TTTTTTCATA	1080
GCTTTTTTTAG TTGTAGAGTC TAGGACATTG ATTTCTGTAC CAAATTTGTG ATTATGCATA	1140
TGTAATACAA AAGAGGCGCC ACAACATGTT TGGATGAACA AAATAACATG TTTGTGGCAC	1200
CTCTTTTGTT TAGTATGGAA TAAATGGTTT TCTTTTTCTA TACATGAAT TTCTAATTTA	1260
GTATCTATAC AATTATGGAT AAAATTTAAC CTACACGACC AAGACGAACA TCATCTATGC	1320
CCGTGATGGG TAAGGTGATT GAACAATAAT ATGCCATAGT AATAATGGCA ATTAAACTA	1380
TAATAAAGAT TATATCTTTA TATGAGAAAG GTACGTTGTA ATAGTAAGTA CGAGGACCAT	1440
CTCTAAATCC TTTCGACTCC ATCGCAACTG ATAATTGATG TGCCTTTCTA ATATTTTGGC	1500
TTAATAGAGG TATAATTAAA TGCTTAAATC GCTTTAACCC TCTATAATTT GCCGCGTCTA	1560
TCATCTGATA GCGCATTTTT AAAGATCTGC GAAgcTGTat TAAAGAACTA ATCATTAAAG	1620
GTATCATACG AATGGCAGCC ATGAATGCAT AAGCAACTTT TGATTTAACC TTTAAATGTT	1680
GCATTAAACT ATAAAATATC ATGACAACCT GAGATGTAAG TGCGATTAAG ATACCGAAAA	1740
ATGAAATAGC AATGGTTCTT AATGATACAT GTAAACCACG AACTAAACTT TCTGTTGTAA	1800
TATGGATAAA TCCGAATTTT AAAATTGTAT GGCTACCATT CCCGTATAAA ACATGAACA	1860
GGGAAGAGAG TAATGCAAAG CCAATACTTA TAGTTATAAA AATTGCTGTA ATTTTAACT	1920
GAGTACCATT AAACATCAAT AAGAAAACTA ACATTAAGAT AGTGATATAA AGCATAAAAT	1980
CGAAATTATG CACAAATATA ATAAAGAAAA ATAGTATAAT TCCAAGAAAT AGTTTCGTTA	2040
TAATGTTGAC ATCATCAACA AATGATTGCC GAACTTTCCA TTGCTCATAC ATTCGTATCA	2100
CCATCACAAT CTAGTAACGC ACCATCTGAA ATTTTAAGTC TTCTTGATGG ATAACGTTCA	2160
ATTATTTTAT CGTCATGTGT AaCCATGACA ATACTTTGTC CCAAATTAAT TCGCTTTTGG	2220
AAAAGTTTGA TCAACTGGAA TGTATTATGG CTACCAAGTC CAAATGTCGG TTCATCTAAA	2280
AAGATAATAT CAGCTTTAGA ACTTAGTGCG GTAgcTACGC TAAGGCGTCG TTTTGGACCA	2340
ATAGACAACT CATAAGGATG TTGATCTTTT ACATTTTGTA AATCTAAAAG TTTTAAAAGT	2400
TGTATCGTTT CATCATCACT TTGATCTTTA GAAAGGTGAT TAAAATGAAT GTTAATTTT	2460
TCATAAACCG AATTTGTTAT AAATTGTAAT TCTGGGTTTT GATAAACTAG GTACATGTGT	2520

TTTGCTGCAT	GTTTAATTTT	TGTTAAACGC	TGATTTTCAA	AATAAACATC	ACCTTGATAT	2580
TTAATCAATT	GCATAATTGA	TTCAAGCAAG	GTTGTTTTAC	CACTACCATT	TGCCCCTGTA	2640
ATTGTAATCC	ACTCACCTAG	ACCAATTTCT	AAATCTGAGA	ATGAGAGCAA	TGTTGATTTA	2700
CCGCGAATAA	TACGTCCATT	TTTAAATTGT	AATAAGTGTG	AGTTTGTGTG	TGGAAAGTCA	2760
ACACGACTTG	GTGCGAATTC	CCATGCACGT	GGATGCCACA	CACCATATTC	ACTGAGTAAA	2820
TGAACATACT	TCTGTAATAT	GATTTTCAGGA	CATTCATCGG	CAATGATATT	TCCGTTATAA	2880
TCCATCAAAA	TGACGCGGTC	GACATGATTC	CAGATGTGTT	TAACCTTTATG	TTCAACGATT	2940
ACAACCGTTT	GATCTTCCCA	AAGTTCAATT	AGTTTAGTCC	ATAAATCTTC	TGTTGCTTGA	3000
ACATCTAACA	TTGCTGTCGG	TTCATCTAAA	AACAATGTTT	TTGATTGTTG	AAGAATGGTT	3060
TCAACAATTG	CCAATTTCTG	TTTCATCCCG	CCACTTAAAT	CTTTGATATA	CGTTTCAGGG	3120
GTAACATTTA	AATTGACCAT	ATTTAAAGCA	TTGATAATTA	ACGCATCCAT	GTCTTCACGT	3180
GGTAATTGTC	TATTTTCTAA	AACGAATGCA	AGTTCCTCGT	ATACTTTTGG	CATACAAAAC	3240
TGGCTATCAG	GGTCTTGGA	AATAACGCCA	CTTAATGGGT	CAACGATTAG	TTCATCATAT	3300
TTCATAGGTA	ATTCAATTAA	ATTAGGAACA	ATACCACTTA	ATACATTCAG	AAGTGTACTT	3360
TTACCGCAAC	CAGAAGGACC	GAGTAAAAGT	ACTTTTTCTT	TGTCTTGAAT	AGTGATATTT	3420
AAATGATCGA	AAATTTTACG	TTGACCACTT	GGATATTTTA	ATCGTAAAC	ACTTACTTTT	3480
AACACTCTGA	ATGCTCCTCT	TATAAGTTGT	CGTAATCTTC	TTTAGCAGCT	GGTCTAAATA	3540
ATTTTGTTAC	GCCTGTCTTA	TCTAAAGCTT	TTACTAAAAG	GTAAGATAGG	ACGCCGGCGA	3600
CTACTGCACC	ACTAATTAAT	CTAAATACGA	TGAATAATGT	TAAGTTCCAA	CCTGCAACTT	3660
CATTTAAATA	ACCATAGAAA	TAATCTATCG	GGAAAGCCGC	GATTGCTGTA	CAAAAACCTG	3720
CTAACATAGC	TACCATAACT	GAACGTGATT	GATATTTAAA	AATTGCAAAG	ACAAGTTCAC	3780
ACGCTAAACC	TTGTATAAAA	GCGTAAACGA	TTGTCGGAAT	ATCGAAACGA	CCCATAATGA	3840
TAGTTTCGCC	GGCACCTGCA	GCAAATTCAG	CCAGTAAAGC	AATACCTGGT	TTTGAATAA	3900
TTAGATAGCA	GACAATCGCT	GCCATGAACC	AAACCCCGTT	TGTTAATTGT	TCGAGGTGAA	3960
GGCCTGTAGC	TTGCACACCA	TTGTAAACAA	ACCACCATAA	ATTGTAAATA	ACTGCGAATA	4020
CTACTGAAAT	AAGTACGGTT	ACTAGTATTT	CAGATAGCTT	TAAACCTTTT	GACATTTTA	4080
CATCCTCCTA	ATAAAAAAAC	GCACAACCAT	CCATAGGAAA	GTTATGCGTT	CACAATATAT	4140
ATTAGTAAAA	CATATGTATA	GTAACACTTT	CCTACGCTAG	TTCAAGCTAG	ATCAGGTTCA	4200
AAGGGTTTGA	GGGCAAGCCT	CATCTCAGTA	TAAAACACCC	CTAGTGTGTG	CGATTTATTT	4260
AATTAATTAT	ACTGTAAGAC	GTTTGTA AAC	TTATGTCAAT	AGGTTGTCTT	CATGAAATTT	4320
CGTTTAATTC	GATTTAAAAAT	TTATAATATT	AGCATTGGAT	TTAAATTGAA	GATGTAGTAG	4380

GAATGTTAGT AATTAAAGAT ATAAAAATAT GTGACATGTA ATAATATTGA GCTGATAAAT	4440
GAAGAGGGAT ACTTATCAAT CATACCTCTT TAACAAAGT GAAGAACCCG TGCATAATGG	4500
CTTACGAATT ATAGTTTATA AGGAAGAAGA GGGATACATG CGCCGAGCAC ATGCATAAAA	4560
GCCCCTAACA ACTAAAAGTT GTAAGGAAGG AGAGGGATAC ATGCGCCGAG CACATGCATA	4620
AAATCCCCTA ACAACTAAAA GTTGTAAGGG GATTTAAATT AATTTAGTGT ATCTTGATA	4680
TCTTGTTTTG kTTGaTTAAT ATCTTCTGTT TTTTCTTCTT TTTTATCTTT TAATTTTTCT	4740
TCAACTTCTT TAGCTTTTTT TGCTGCTTTT TTATTTTGAT TTTCAATTAGA CATGATTAAT	4800
TCCTCCCAA TTGGATAATT ATTTATATAT AAATCTTACC CGGTGTACT TTCGTTAAAC	4860
TTTTCTAAGT CTATAGCACT ATTTATTCAT TTATCTAAAG ACAACAACAT TAGATTAATA	4920
TATAATGATT TTGAGGTGAA CATAATGTCT TTTCTTAGGA AACACGCCGA AATTATTTTT	4980
AGCTATTTAA TCGGTmwCGT TcACTCTTCA CTGGkcTCAT TATTTTAATT AACTTGCCAT	5040
TAATTAAACA ATTAAATGGT GGTAAAAAAG TTGATACACA TGTTATAAT GTGTGGGAAT	5100
TTCTGAATGC ATTTTTCAGT GAAATTATTA AAGTAATGAG TCGATTTATA GGTAATTTCC	5160
CtATAGTTAG TGCAATTGTG ATAATTATAT TCGGTATTTT AGTTATGTTG ATTGGTCATA	5220
CATTACTTAG AACTATTAAG TATGACTATG ATATTTCTAT CTTTTTCTTA GTTATCGGTA	5280
TCATGTACTT TATTATTACT CTTATATTAA TGA CTCAAGT TTATGGATTC TTTGCAGTGA	5340
TTTTCATTAT TCCATTTACA ATTCATATAG GATATATCGT CTATAAAGAT GAATTGAATC	5400
AGGAAAATGT AAAAAATCAT TTCATGTGGA TAATTGTGAG TTATGGTATA AGTTACTTAA	5460
TTACACAAAT TGCATTGTAT GGCAGATTG ATGCTAATGA AATAGAGTCA ATTGATATCT	5520
TAAGTGTCAA TGCTTTCTTT ATAATTATGT GGTTACTTGG TCAAATGGCT ATTTGGAATT	5580
TCTTGTTCTT GCGCCGAGCT TTACCTTTAA CAAAGCAAGA ATTAGGTGAA GAGGAGCCAG	5640
AATTATCAAG AACAAGTAAA GGAATGTCA CGAATCAAAC TAAAATTCAC TGAAACAAC	5700
TCCAAGATAA GACTACAGAA TATGCACGTA AGACAAGAAG AAGTGTCGAT TTAGATAAAA	5760
TTAGAGCTAA AAGAGATAAA TTCAAAAAGA AAGTTAATGA TATTATCGAT ATTCAAGAAG	5820
ACGATATTCC TGATTGGATG AGAAAACCGA AATGGGTAA ACCAATGTAT GTCGAACAT	5880
TTTGTGGTGT CGTCATCTTT TTATTCACAT TTTTAGAATT TAATAATCGT AATGCATTAT	5940
TTGTATCTGG TGATTGGAAT TTATCACAGA CACAATATGT TATTGAATGG GTTACATTAT	6000
TAATTCTGTT ATTCATTATT ATCGCATATA TCGCTACAAC GTTAACTTTC CACTTGAAAG	6060
GTAAGTTTTA TTATTTACAA TTATTTATGG GGACATTTT ATTCTTTAAA TTGTTAACGG	6120
AATTTATAAA TATAATGATT CATGGACTAT TACTTTCAGT GTTCATTACG CCAACATTAC	6180

TATTAATGTT ATTGGCAATC ATCATTCTT ATTCGTTACA ATTACGAGAG CGACCATAAT	6240
TAAAAGCATT ATAAAAGTAC TATCTATTAA ACATTTTGAT GTGTACGCTA TAAGTTAGA	6300
ATATCTCTAA CTTACTTAGA TACAGGTCAA TGAAGTTTAT GGATAGTACT TTTTTGTAA	6360
CTAGATTTGA TTGATTGAGG TGATGTGAAT TAAGTATTGA rAATTGTATA CAAAGTTTTA	6420
GTGCAAATAA AATAGTTGAA AAGTTATCCA TTTGTAAAAT CAAGAAAAC AGTAAATAGT	6480
TGAAGCGACT TATGGaATTT GCGAAACGAT ATATAGTATT TCCTTTGTAG AAATTTmACA	6540
TATATCATTC AAATTACTAA TTTGTTAAAA TCAACAGTAA GATTAGAAGT AGATGATATT	6600
GAAATTTGGC AAACaAttTA ATCTATATAA AACTACAACG AAACACAGAA AGGAAGTTGT	6660
CAGATGAAAA TAGCAACTCT GAACAAAGGC AAAGAAACAAATATTTTAA TGGATATCCT	6720
TTAATTGAAG AAGAGGATAT CTATTCACAA GATCATTTAA AAGAAGGAGA TATTTTTCAA	6780
ATTGTGACTG ATAAATCACA ATAT	6804

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

aaaAGAGACG CATTaAAACA AGCTATACAA ATTATCGATA AATTAACATG GGGTGTTTAG	60
TGGTGGTTAA AGAAATTTTG AGACTATTAT TCTTACTAGC GATGTATGAG CTAGGTAAGT	120
ATGTAAGTGA GCAAGTATAT ATTATGATGA CGGCTAATGA TGATGTAGAG GCGCCAAGTG	180
ACTTTGAAAA AATCAGAGCT GAAGTTTCAT GGTAATAGCT ATTATCATTT TTGAATTAAT	240
TATATTAATG TGTGTAGCA TAGCACTGGA GGTGTTGTAA ATATGTGGAT TGTCATTTCA	300
ATTGTTTTAT CTATATnTTT ATTGATCTTG TTAAGTAGCA TTTCTCATAA GATGAAAACC	360
ATAGAAGCAT TGGAGTATAT GAATGCTTAT CTTTTCAAGC AGTTAGTAAA AAATAATGGT	420
GTTGAAGGTT TAGAAGATTA TGAAATGAA GTTGAACGAA TTEAAAAAG ATTCAAAGC	480
TAAAGAGAGG CGTTGGCTTC TCTGCTCTAT CyAAAATAAT GAAAGGAGCC saACATGTTA	540
GaCmAAGtCA CTCAAATAGA AACAATTAAA TATGATCGTG ATGTCTCATA TTCTTATGCT	600
GCTAGTCGTT TATCTACACA TTGGACTAAT CACAATATGG CTTGGTCTGA CTTTATGCAG	660
AAGCTAGCAC AAACAGTTAG AACTAAAGAA GATTTAACTG AGTACAATAA AATGTCTAAG	720
TCTGAACAAG CCGATATAAA AGATGTTGGC GGATTTGTCG GTGGATATTT AAAAGAAGGC	780
AAACGGCGTG CTGGTCAAGT CATGAATCGT TCAATGCTAA CACTTGATAT CGATTATGCA	840

GCCCAAGATA TGA	CTGACAT ATTAT	CTATG TTTTATG	ATT TTGCATATTG	TTTATATTCA	900
ACACATAAGC ATAGAGAGAT	AAGTCCAAGA	CTGCGTTTAG	TGATTCCCTT	AAAACGAAAT	960
GTAAATGCAG ATGAGTATGA	AGCTATTGGG	CGTAAAGTCG	CAGATATCGT	TGGCATGGAT	1020
TACTTCGATG ATACAACTTA	TCAACCACAT	AGGTTAATGT	ATTGGCCTTCA	ACTAGTAAC	1080
GATGCGGAAT TTTTCTTTAC	CTATGAAGAT	TTACCTTTGT	TAGACCCAGA	TAAAATATTA	1140
AATGAATATG TTGATTGGAC	TGACACATTA	GAATGGCCAA	CGTCTTCAAG	GGAAGAGAGT	1200
AAGACTAAAA GATTAGCAGA	TAAGCAAGGC	GACCCAGAAG	AAAAGCCGGG	AATTGTTGGT	1260
GCATTTTGTA GAGCCTATAC	GATAGAAGAA	GCTATAGAAA	CTTTTATTCC	TGATTTATAC	1320
GAAAAACATT CTACTAACCG	TTATACCTAT	CATGAAGGTT	CAACTGCAGG	TGGATTGGTG	1380
TTATACGAAA ATAACAAGTT	TGCCTATTCT	CATCATAATA	CGGATCCCGT	AAGCGGTATG	1440
CTTGTGAACA GTTTGTATTT	AGTACGCATA	CATTATATG	GTGCTCAAGA	TGAAGAACT	1500
AAAACAGATA CTCCGGTTAA	TCGACTACCT	AGTTATAAAG	CAATGCAGCa	AAGAGCGCAA	1560
AATGATGAGG TTGTTAAAAA	GCAATTAATT	AATGACAAAA	TGTCTGATGC	AATGCAGGaT	1620
TTCGATGAAn GAGAAAATAG	CGATGATGCA	TGGTCTGAGA	CGTTnGAAAT	TACTTCGAA	1680
GGTACTTTCA AAGCTAGTGA	TCCCAAATAT	AGAAATT			1717

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

AAGATTAGGC ATCAAGACAG	GGTCGCGATT	GTTTGAAATC	CCACATAGnA	ATGATATTTa	60
CaTTATCAAT CCaAGTATGC	GTAAATATCT	TAATGTTTCA	GTTGCTATTT	CTAAGATTGC	120
ATTGCGTTAT ATTCCACCTG	AAGATTTACA	CCAATATAGT	ATTGACGAAT	TTTTTATGGA	180
TGTTACTGAT AGCTATCATA	GATTTAGTTC	TACAGTACAT	GCATTTTGCG	AAAGACTTAA	240
ACGTGAAATT TATGAAGAAA	CAGGCATTTA	TTGTACTGTG	GGCATTGGTT	CTAATATGTT	300
ATTAAGTAAA ATTGCTATGG	ATGTTGAAGC	GAacAAGTc	AAAATGGTAT	AGCTGAATGG	360
CGATATCaAG ATGTACCAAC	GAAATTATGG	CCAATTCmGC	CCtTGCGAGA	TTTTTGGGGT	420
ATTAATCGTC GAACAGAAGC	CAAATTGAAT	AAAAGAGGAA	TTTTTACTAT	AGGAGATTTA	480
GCGAAATATC CATATAAATT	TTTAAAAAAA	GAGTTCGGTA	TTTTAGGTGT	TGATATGCAT	540

CTACATGCGA ATGGGATAGA TCAGAGTAAA GTACGTGAAA AGCACAAAGAT CAGCAATCCA	600
TCGATATGCA AAAGTCAAAT ATTAATGAGA GATTATCATT TTGATGAAGC AAAAGTAGTA	660
ATGCAAGAGT TAATTGAAGA TGTGCTAGC AGAGTTCGAG CAAGAAAAAA AGTGGCAAGA	720
ACGATACATT TTGCCTTTGG CTATAGTGAT GAAGGCGGTG TACATAAGCA ATATACTTTG	780
AAAGATCCAA CAACTTAGA AAAAGATATT TATAAAGTAG TAATGCATTT CGCAGATAAA	840
TTATGTAATA AACAAGCACT ATATCGTACG CTAAGTATAT CTTTGAGTCA ATTTATTAAT	900
GAGGATGAGC GACgTTAAGT CTGTTTGAAG ATGAATACCA AGCAAACGT GACGAATGTC	960
TAGCTAAAAC GATAGACCAA TTACATTTGA AATACGGCAA AGGTATTGTG TCCAAAGCAG	1020
TATCGTTTAC AGAAGCAGGT ACAAACACG GCAGATTAGG TTTAATGGCT GGACATAAAA	1080
TGTAATGACT ATACGGTTTA AGTAATATAT AACTGTGATT CGTATAAAAT AAGTCTCTAA	1140
AGATAAATAT TTCATATATC ACAATAGATT TTCACAATAA TATCTAAGAA TACATGGAAT	1200
TTATCAAAAG AGACTTAATA ATTATTGGAT ATAACAATCA AAATCACTCA ATGCTTGCAT	1260
ACCGCGTTCT CGGTCAGTAG GGTTTTTGAA ACTAATTTTT AAAGCACCGT ATATATCTTC	1320
GCGTACTTCT AAGATTCTTA AGT E CTTAT AGATATGTTA TGTA A ACTCA GGATATAAGT	1380
CACTTTACTT ATCATACCTG ATTCATCCGG AATGTCTACA TATAGATCAT ACGCmGtATT	1440
TAGTCCACCT AGTTGTTTAG CGGGTAGTGC GTCGCGATAC GATTTAGCTT GGGCAAAAAA	1500
TGATAACAAT TTTTCAGAAT CATTGCTTTC AATTAGTCTt TCTAAATCTTGAACTGACT	1560
TTTTAGCTGT CGAATCATTT CTAA A ATATA CGTTTTATTA CTCAAGGTGA TATCTTTCCA	1620
CATTTGTGCA TTACTACTAG CTATACGAGT GATATCACGA AAACCACCAG CTGCAAGTTT	1680
ATTA A CTAAA TGATGTtCTT GACCGTTCTT TTGACTAACA TGA A CTAAAC TAGATGCAAC	1740
GATATGAGGT AAATGACTTA CGACGCTTGT TACGTAGTCG TGTTCTTCAG CAGTAGTTAC	1800
AATAAATTTA GCAAGAGTAG GTGATAACAG TTCTTTTAAC GTGTTTG	1847

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

AACAAAAGGC ATAAGTTCGT GAATTAATGC GTATACAAGG ATAAAGCTTA TAACAGTAGT	60
AATTGTTGCT ATCAAACGAA CAACATA T T TCTATTTTCA GATAGCAATC GATTCACTAA	120
TCGATAATTT ACGTATACAA GAATTAACAA CAGCACAATA TAAACAATAA TCATATTTGG	180

CCCCATTTAA	TTTTTAAATT	TGTTTTCACA	TCATTTTCTA	CTTTATTATC	ATACTAATTT	240
TAAAGGCAAA	GGTGGACATC	GGCAACCTCT	CGTAAACTAT	TTATCAAAAA	TAACGTATC	300
TCATTGTTAT	GATATTTATA	AATCAATTCG	TTTTTATTAA	AGTCTTTTTC	AACAAGTTTG	360
TCACTATCTA	TTAAATAATC	ACGCATGCAT	CCTTTTAAGA	AATCATCTTT	ATAACTTGGT	420
GTGTACCATT	TTCCATCCTC	TTCAATGACA	ATGTTGCCAA	TATCAAATTC	AAGGACCTTG	480
CCGTCCTCTG	AAGT					494

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

GTCCATATTT	CCCGTCCAAC	CAACTAAAAA	TGGGTAAATC	CCTGGATTa	AATCTACTTC	60
TAGTCcCATT	TATaTgGAAY	aCCTTTAAnt	TTTAATTGtA	CCACCACCGA	TTGaAATaCC	120
GATAATTTcN	AATGTAGCGA	CCATCATTAC	GAGATGATTT	GATATAAGCA	CAGTTTGGAT	180
GTTGACCAAT	ACTATCGCCT	TCTTCTTCGA	TGATATCTAT	TTTAATACCA	TCATCAGCTG	240
CAATTTCTAA	TGAAGATTTA	ATTCCGGTTAT	CAAATGTTGA	ATATCCCATT	GCTCCACCCA	300
CAATAGCGAC	ATCTGTACCA	TGTCCTTGGT	GTGTTTGAGC	AAATGATTCA	TAATAAGTA	360
TTTCAATATT	TTTAGGAATA	TCTCCCAATA	TTGCGCGTGC	TGAATTCCCA	ATCTTTACTG	420
CACCAGCCGT	ATGAGAACTT	GAAGGGCCCA	TCATAACTGG	TCCGATAATA	TCGAAAGCAC	480
TTTGATAATC	ATAGCTCTTT	GCCATAATTA	AACACTCTCC	TTAATATGAT	TCTTTTTTGT	540
CGGCATTTTA	AAGTTGATAT	TCATTAAATT	AAACTTATTA	ATTAGTGTTT	CAATAATATA	600
GGCTAAGACA	ATGCTGACAA	TAATCACTGT	TGCGATTGTT	ACAATTGATG	TCACTGCATT	660
ATTAAAGCCA	AACAATACGA	TGGCGCCTGC	AATTGGTGTT	GCCATACCTT	TGACACCTAT	720
TACTAGTCCG	CTAAATGTCA	CGATACATGC	GTTGACGAC	CCAATCAGTG	CATTTGTACC	780
ATATAGTTGT	ACTGGATATT	GCGCTATTAA	ATCAATTTGC	GTCAATGGCT	CAATACAAAC	840
TGCAAATGCT	TTTGACGGTC	CACCAATGTT	TAATTTTCGG	AATAAAATAA	GGTTAACAAA	900
TGAGCTACCT	GTACATGTTA	GTGCTCCAAT	AGCCATAGGA	ACACCTGTCA	GTCCTAATAA	960
ACTTGTTAAT	ACCATTGAAC	TTAGCGGTGT	CATACCTGTA	ACAGGAATCA	CTAGTCCTAA	1020
AATGACCGCT	AATGCATATG	GATTGTTATC	ACCTACCGCA	GTGACAGCAC	TACCTATTTG	1080

TTTTAATGTT GCTAGCACAC CAGGTGTAAT GATTGATGCA AGTCCGAAAG CAATTGCTGG	1140
TGCAAATAAG ATCACCACAA TTAAGTCCAA GCCTTCTGGA ACTTTCTTTT CAATCCATTT	1200
AATTAATAAA GcTACGCCAT AAGCTGCGAT GAATGCTGGT AATAATTTAA AGTCATGTAA	1260
TACTAAACCA ACAATGACCG CAAATACTGG TGCAACGCCT AAGTTTAAGC ACGTTAGAAT	1320
ACCTACTGcG ATACCGCTTA AACTTCCTGC TAAATCCCCA ATATtTGTA GAAATTTAAT	1380
ATCAAATACG CCACCAATAG CATAACTTAA GAATGCTTGT GGTAGAAATG TCGCACAAAGC	1440
TGCACCGGAT AATGCTTGTA GTCCTTGTTT ACCGTACGGT GCATACTTTA AAAATAGCGT	1500
CATGATCACT AAAACCAAGA CTAATGTGCC TACACCTAAC AGAATATCCA TTTCCCAAAA	1560
ACCTCTCTCT ATGTTTATTT TATTTTCAGA CCATAAACAT CGTACACCCT TAAGAAAACG	1620
TTTTCAACTT TTATCTGTTA TCAAATCaAA TATTTAAGTG AAATATTTCA TATTTGTGAA	1680
AGATTTTTTA AATGGATTGT TTCAAAACT ACTTATGTTG TCGTTAATAT TTTACTAATTA	1740
ACTTTTTACT CTATATTTCA AACAGTtTG TGACAGTTTT TTGATAACTT TTTTACATCT	1800
GAAAGTAAGT AATATTTCTA AAAACTTTTA ATATTTATAC ACTTTATCTT TCGAGCTATT	1860
TATTTTTTGT TTTTGTGCTG TGTTTATAAA ACCGCACACT ATATTCAAAA ATAAC TTATT	1920
ACACATATAT TTGCAATAAG ATAATTAAAG TAGGATATTA TTTTtagTTT TcGATAGGA	1980
ATGATGATAG TCTATAGGTT GAATCTTTAC TTTTTTTTAA AGCTAAATTT ACATCAACTT	2040
AACAATGGTT GGTTATACTG AAGATGAAAA TATTTAGTAT AACTTAGTGG AGGCGATAAA	2100
GGTGCAATTG AGTCATTCCG TTAAAGTTGC AATTTCTATC TATTTAGCAC TTATCTTTAT	2160
AACGTTCACT TCTTATTTAG TCATTATTTT ATATACGAGT ATGACTGGAC ATGATGTATC	2220
ACATTTTCGTG TTAGATAGTC AGCATTCTCA TCATGGATCT CTTACGCAAA AACATTTGAG	2280
TCTTCCTGAA ATCTCATTTA AATAGTTTAT CCTCTGTGTT TCAACATTCA TTTCCCATAT	2340
CGATTCATTT ATCTATCATC TAGACCACTA CATtTAGAT GATTTTTTTA TTTTCTCATT	2400
TCACTCTTTC TTAAGAGTCG ATATAATGAA TTAAATCATT ATCATACACC GACATATTTT	2460
ATGTTGTTGG TGTTAAGTTT aAAGGGGTGA GATACTTGGC GAATaATCaT TCAGCTTT	2518

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

ATACTACTGG ACCGTcNACC AATTGACAAA ACCTGAAAAC TGGATTTTTA TTGCAGATT	60
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ACATCGAACC TGGAAGAACA ATCCCCAGGA GTTGATGATA TTCGAGATAT GGCATACAAT	120
CAAGGTAGTT TAGATAAGAC AATTTATGAA ATTTCTAAAC GCACAGTACT ATTTTAAATA	180
CAGAAAGATA TTACGGTATA TAATAAGACG ATTGACTGTT TAAATTATTA TAACATAGT	240
GACGAAAGAA TAAAGGATGA TTAAATGAAT TCACAAGAAT TATTAGCAAT TGCTGTGGAT	300
GCAATTGACA ATACCCCAGG CGAAGATACG ATTTCTTTAG AAATGAAAGG TATCAGCGAT	360
ATGACAGATT ATTTTGTGT AACGCACGGA AATAATGAAC GACAAGTTCA AGCGATTGCT	420
AGAGCGGTGA AAGAAGTAGC CAATGAACAA AATATAGAG TAAAACGTAT GGAAGGATAC	480
AATGAAGCGC GTTGGATATT AATTGACTTA GCTGATGTTG TGGTACATGT TTTCCATAAA	540
GACGAAAGAA ATTATTATAA TATTGAAAAG TTATATCAAG ATGCACCATT AGAATCATAT	600
AGTCAGGTTG CGTATTAATT ATGTCGCAAT ATGCAGAAAT GAGCCTAGTG TACGATCAAT	660
TGACTCAAGA TCAACCATAT GAAAAATGGT TTGAAATTGT AAAAAATCAC TGCAAAGATG	720
AATCAAATAT TTTAGATATT GGATGCGGTA CTGGTAGTTa ACAGTTCAAT TAGAAGCTTT	780
AGGTAATGTT	790

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

ATAGATGAAG GTGCAATAT TGAAaTAGGT TATTTACCTG GACGCTTGAA ATGGTTAGTT	60
GCTGATTTAT TAACTAAACA AGGATTAAAA GTAGTTAACG ACGATATGAC AGGAAGAACG	120
TTAAAAGATC GTAAATTATT AACAGGTGAC AGTCCTTTAG CTTCAAATGA GTTAGGAAAA	180
TTAGCAGTTA ATGAAATGTT AAATGCAATA CAAAATAAATAATTAAATAT TAATTAGAGG	240
AGCCTCATAT GTAAATGTAT GAGGGCTCTT TTTTTGGCA AAATTTAAGT GATACTTGTA	300
AAATAGAACC TATTATGAGT ATGATTTAAG AAAACGCTTG CAAAATAAT AACCGCAACT	360
AGCGATATGG AGGAAACATG ATGTCTTATA GCATTGGAAT TGATTATGGA ACTGCTTCAG	420
GCCGTGTGTT TTTAATTAAT ACAACTAACG GTCAAGTAGT ATCAAAATTT GTGAAACCAT	480
ATACACATGG TGTCATTGAG AGTGAATTAA ATGGTTTGAA AATACCACAT ACATATGCAC	540
TTCAAAATAG TAATGATTAT tTAGAAATTA TGGAAGAAGG AATATCATAT ATAGTACGTG	600
AATCAAAAAT AGATCCAGAC AATATAGTAG GTATTGGTAT AGACTTTACT TCATCTACTA	660

TTATTTTAC TGACGAAAAC CTTAACCCGG TACATAACTT AAAACAATTT AAAACAATC	720
CACATGCGTA TGTGAAACTT TGGAAACATC ATGGTGCATA TAAAGAGGCA GAGAAATTAT	780
ATCAAACCTGC TATTGAAAAT AATAATAAGT GGTTAGGCCA TTATGGAÆT AATGTTAGTA	840
GTGAATGGAT GATTCCCAA ATAATGGAGG TCATGAATCG AGCACCAGAA ATTATGGAAA	900
AAACGGCTTA TATTATGGAA GCGGGCGATT GGATTGTAAA TAAATTAAct AATAAAAATG	960
TACGCTCGAA TTGTGGATTA GGTTTCAAAG CATTTTGGGA AGAAGAAACA GGGTTTCATT	1020
ATGATTTATT TGATAAAATA GACCCCAAAT TATCAAAAGT AATTCAAGAT AAAGTATCTG	1080
CACCGGTTGT TAATATTGGT GAAGCAGTAG GGAAACTGGA TGATAAAATG GCACAGAAAT	1140
TAGGATTATC AAAAGAACT ATGGTAAGTC CTTTTATTAT TGATGCCCAT GCTAGTTTAT	1200
TAGGTATTGG GTCTGAAAAA GATAAAGAAA TGAActATGGT GATGGGAACA AGCACATGCC	1260
ATCTTATGTT AAATGAAAAG CAACATCAAG TGCCAGGTAT ATCAGGTTCT GTAAAAGGAG	1320
CAATTATTCC AGAATTATTT GCTTATGAAG CGGGGCAATC AGCAGTAGGT GATTTGTTTG	1380
AGTATGTCGC TAAGCAAGCA CCAAAGTCAT ATGTAGATGA AGCAGAAAAT AGAAATGA	1440
CTGTATTTGA ATTAATGAAT GAAAAGATAA AACATCAAAT GCCAGGTGAA AGTGGGCTCA	1500
TTGCTCTTGA TTGGCATAAT GGAAATCGAA GTGTATTAAG TGATAGCAAT TTAACAGGTT	1560
GTATCTTTGG ATTAActTTA CAAActAAGC ATGAGGaTAT TTATAGAGCm TATTTaGaAG	1620
CTACaGCATT TGGTACtAAG ATGATTATGC mACAGTATCA AGATTGGCAT ATGGaAGTAG	1680
aAAAGGtATT TGCatGTGGc gGTAtACcLA AAAAGAATGC TGTTATGATG GATATCTATG	1740
CGAATGTACT GAATAAAAAA CTAATTGTTA TGGATAGTGA GTATGCACCA GCAATAGGCG	1800
CAGCAATATT AGGTGCAGTC AGT	1823

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

ACGATCATCT GCATCAGCGA ATTCCGATGc AaTTcATATG tCCtAATAAC AAAAGAATAG	60
GTTTTaAAAAG ATATGCATAC CGTAATGaTA GATATAGTTT TAAACGTGAC TTCAAGCTAT	120
ATGaATGTGA TGACTGTTCA TCATGTTCTT TGAGACATCA ATGCATGAAG CCAAATTGA	180
AATCCAATAA GAAAATTATG AAGAATTATA ATTGGGAATA CTTTAAAGCC CAAATTAATC	240
AAAAGCTTTC TGAACCAGAA ACGAAAAAAT CTATAGTCAA AGAAAAATTG ATGTAGAGCC	300

TGTTTTTGGG	TTTATGAAGG	CTATTTTGGG	TtTCACTCGA	ATGTCAGTTC	GGGAATAAAT	360
AAAGTTAAAC	GAGAGCTAGG	TTTTGTATTA	ATGGCACTTA	ATATAAGGAA	AATAgcaGCT	420
CAACGAGCTG	TACATTATAA	AATACATATC	AAAAAAGCTG	ATTTCTATCA	AATAAATAAT	480
AGAAATCAGC	TTTTTTACAT	TGCCTAAGAA	CTTTAAGGAA	CTTAATGTCC	CAAGCTCTTT	540
TTTGTTATAT	CTAATTCGTA	ATTTATGATT	GTTTATTCGG	TCCTTTGATG	TTCACTAAAT	600
GTGACTTTAA	ATCTTGTTCT	AATTGTTGTA	ATTCTTTTTT	AGCTAATTGT	CGTTCTTCGC	660
GACCGTGTTG	TTGAATAATT	AATGTTTCTT	CAATTGTCTC	AATAATGTTA	CGCTGTGTAC	720
GTTTCAATGT	ATCAAGATCA	ACAATGCCAC	GCTCATTTTC	TGTTGCAGTT	TCAATCGCAT	780
TTTGTTTCAA	CATTTGAGCA	TTTGCTGTTA	ATAAATCATT	AGTTGTATCA	GTGACAGCTC	840
GTTGTGCAGC	AACTGCATTA	CGCTGTCTCA	TTAATGTAAG	CGCAATGGCC	ATTTGATTTT	900
TCCATAGTGG	AATACTTGTC	AAAATTGAAC	TTTGTATCTT	CTCGGCAAGT	GCTTGATTAA	960
CATTTTGAAT	CATACGAATT	TGTGGCGCAG	TTTGCAAAGC	TATTTGTCTT	GAAAGCTGTA	1020
AGTCATATAT	GCGTTTATCT	AGTCTATCTA	TAAATTGCTG	CATATCTGCA	ACTTGTTGAA	1080
TATCCATTTG	ATTAGTGGAt	TgtGCGCTTG	CTGTTGCAAT	TGTGGTAGCT	TTTCATTTTC	1140
TAATTGCAAC	TTTTTTTGcT	GTGCAGCAAT	GATATGCAAT	GATAAGCAT	CAAAGTATTG	1200
TTTGTTTTTA	TCATATAGCG	TATCTAATAA	TTCAATATCT	CTTGTTAAAT	GTGTTTGATG	1260
TTTCTGCAGT	TGAATCGTTA	TGCGATCGAC	TTGAGCACTA	ACTGATTGCA	TTCTTGAAAA	1320
GATTTTCATTG	ATAGACGACT	TTGCTCTGCT	AAAAATTCTT	TTTAACATAG	ATGGTTTATC	1380
AGTATTTAAC	TCATTTGGAT	TAAGTACTT	TAGTTTTGAC	ATTAGATCTG	ACAAAGTATC	1440
TCCAATAGGA	CCAACATCTT	TACTTTGTAC	TTCATCCAAC	ATTTGATGTG	AAAATTGAGA	1500
CATTTGTTTC	TGkAAATCAG	AACCAAACGC	TAATAAACCT	TCATTGTCTA	AAGGGTTAAT	1560
TTGTTTACTG	ATTGTGTCTA	CCTGTTTTT	TTGTTCAATT			1600

(2) INFORMATION FOR SEQ ID NO: 373: -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

ATGTTGATAA	TGGTAGCTTC	TACAAGAATA	AAGACCAACA	AGTTGGTGCA	ACAATTCTTG	60
aTAGTAAAC	TGGTGTTTA	GTTGCTATAT	CTGGTGGACG	TGATTTCAAA	GACGTCGTTA	120

ACAGAAACCA AGCAACAGAT CCTCACCTA CTGGTTCATC TTTAAAACCTTTCTTAGCGT	180
ATGGACCTGC CATTGAAAAT ATGAAATGGG CAACAAACCA TGCGATTCAA GATGAATCTT	240
CATATCAAGT TGATGGTTCT ACATTTAGAA ACTATGATAC GAAGAGTCAC GGTACTGTAT	300
CTATTTATGA TGCTTTACGA CAAAGTTTCA ATATCCCAGC TTTAAAAGCT TGGCAATCAG	360
TTAAGCAAAA TGCTGGTAAT GATGCACCTA AGAAATTCGC TGCCAAACTT GGCTTAAACT	420
ACGAAGGCGA TATTGGTCCA TCTGAAGTAC TTGGTGGTTC TGCTTCAGAA TTCTCACCAA	480
CACAATTAGC ATCAGCATTT GCTGCAATCG CTAACGGTGG TACTTATAAC AACGCGCATT	540
CAATTCAAAA AGTAGTTACT CGTGATGGTG ACA ACAATCGA ATACGATCAT ACTAGCCATA	600
AAGCGATGAG TGATTACACT GCATACATGT TAGCTGAGAT GCTAAAAGGT ACATTTAAAC	660
CATATGGTTC TGCATATGGC CATGGTGTAT CTGGAGTAAA TATGGGTGCT AAGACAGGTA	720
CTGGTACTTA CGGTGCTGAA ACTTATTCAC AATATAATTT ACCTGATAAT GCAGCGAAG	780
ACGTGTGGAT TAACGGCTTT ACACCTCAAT ACACTATGTC AGTGTGGATG GGCTTCAGTA	840
AAGTTAAACA ATATGGTGAA AACTCATTTG TrGGACATAG CCAACAAGAA TATCCACAGT	900
TCTTATATGA AAATGTGATG TCAAAAATTT CATCTAGAGA TGGCGAAGAC TTTAAACGTC	960
CTAGCTCAGT AAGTGGTAGT ATCCCATCAA TCAATGTTTC TGGTAGTCAA GATAACAACA	1020
CTACAAATCG TAGTACACAC GGTGGTAGTG ACACATCAGC AAACAGCAGT GGTACTGCAC	1080
AATCAAATAA CAATACTAGA TCTCAACAAT CTAGAAACAG CGGTGGATTA ACAGGTATAT	1140
TCAACTAATC CACTCAACAT AAAATCCTCA GTTATACCA ATTTATGGTG TAGCCGAGGA	1200
TTTTnTTAGG TTCTTCATCT TTTATGG	1227

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CCATATGGtG CAACATTCTT CGTATTTAGT GATTATTTAA AACCAGCGTT ACGTTTATCA	60
TCAATTATGG GATTAAATgC aACGTTTCATC TTCACACATG AyTCaATTGC AGTAGGTGAA	120
GATGGTCCTA CTCATGAACC AATTGAGCAA TTAGCTGGAT TAAGAGCCAT TCCAAATATG	180
AATGTTATCC GTCCTGCTGA TGGTAATGAA ACAAGAGTAG CATGGGAAGT TGCCTTAGAA	240
TCTGAATCTA CACCTACTTC ATTAGTATTG ACACGTCAAA ACTTACCGGT ATTAGATGTA	300
CCAGAAGATG TAGTTGAAGA AGGCGTTCTGA AAAGGTGCCT ATACAGTTTA TGGCTCTGAA	360

GAGACACCAG AATTCCTATT ATTAGCTTCA GGTTCAGAAG TTAGTCTTGC AGTTGAAGCT	420
GCTAAAGATC TTGAAAAACA AGGTAAATCA GTACGTGTTG TTTCAATGCC TAACTGGAAT	480
GCATTGAAC AACAATCTGA AGAATATAAA GAATCAGTTA TCCATCAAG CGTAACAAAA	540
CGTGTTGCGA TTGAAATGGC TTCACCGCTT GGATGGCATA AATATGTAGG TACTGCAGGT	600
AAAGTTATTG CTATTGACGG CTTTGGCGCA AGTGCACCTG GCGATTTAGT AGTTGAAAAA	660
TATGGATTTA CAAAAGAAAA TATCTTAAAC CAAGTTATGA GCTTATAAGA ATAATTTATA	720
AAGCGAGTAT GTTTAGAAGT CTAGGATGCA TAATCTTAGG CTTCTTTTAA AGTGTTGAAA	780
TTTAGAGTAT AGCACTTAAA CTACATCATA AGTGATAAGT TATGAAAGTA TACTATTTCA	840
GATTAATCTT TAAAAGCTCT GTTATAACAG CATGATTTTT GATATTATTT TTAGTATCGA	900
TATTAATAA CTTGAATAAA CTAGTTCTTG AAATAATGTG ATGAATTTAG TAAAATTCAG	960
TAGGATAAAG AAAGCGGGTG AAACAATGGC AACTTGGTTA GCAATTATTT TTATAGTAGC	1020
TGCATTAATT TTAGGTTTAA TTGGAGGTTT CCTTTTAGCT AGAAAATATA TGATGGACTA	1080
CTTGAAGAAA AACCACCAA TCAACGAAGA AATGCTTCGT ATGATGATG TGCAAATGGG	1140
TCAAAAACCT TCTCAGAAGA AAATTAATCA AATGATGACG ATGATGAATA AAAATATGGA	1200
TCAAAATATG AAGAGTGCGA AAAAGTAAAT TCGCAATTGA TAGAGGCTAT TTTCCAGATA	1260
TGGAAATGGC CTCTTTTTAT AATCAAATTA ATAAGAATAA ATATGTTTAT TAAAATTAAA	1320
GTTAACAAAA TGACGAATAG ACTGAGAAAT GCTATAATTC ATTTTGTATG ATTTACAGAG	1380
AGTTTATTTA ACGAGAAGGT GTCyGCGTGC TCTATTTAAT ATTTTCAATC ATTGTAGCTT	1440
TATTTATGGG AACTATAGTT ATAGTTATTC GTATGAAAGC TCAAAATTAT CCGGTAAÅkG	1500
AGAAAAAAAT AGTTTTGCCa CCgTTTTTTTA tGGCgACCGG TGCATTGATG TACGTCGTTC	1560
CaTATTTTAG GCTAACAGGA TCGGAAATGC TAGAAGCCTT TATAATTGGT TTGCTTTTTT	1620
CtACAGTTCT AATTTGGACT TCTCGATTTG AAGTCAAAGG TACAGAAATT TATATGAAAC	1680
GATCTAAAGC ATTTCCAGTT ATTTTGATTT CATTACTTAT CATTTCGTACT GTGATGAAA	1740
TATTCATTAG TAATGAAATA GATCCTGGAG AATTAGGCGG CATGTTCTTT TTATTAGCAT	1800
TCTGTATGAT TGTTCTTTGG AGAGCAGCAA TGCTATATAA ATACAAAAAA CTAAAGAAAA	1860
CATTAATCAA TTAATTACTT TTaAAACCAC TTGTGATCGA CTTCTAAATC AGTCAATGAG	1920
TGGGTTTAAT nTTACTTGGA AAAGGnGGAA AGG	1953

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

ACATTTGATC	AA ⁿ TTATCGA	CATTAAAGAT	GAATTCAnTT	GATCGTnTCA	ATGATTATCC	60
TGTTGAAGTA	GCACGTTTGC	TTGATATAGT	GGAmATaAAA	GTACACGCAT	TACATTCAGG	120
TATC ^c ACGTT	GATTAAAGAT	AAAGGGAAAA	TA ⁿ TGATAT	TCATTTATCT	GTAAAAGCCA	180
CTGAAAATAT	TGATGGCGAA	GTGCTGTTCA	AAGCAACACA	ACCTTTAGGT	AGAACAATGA	240
AGGTTGGTGT	TCAAAATAAT	GCAATG ^r CAA	TTACTTTAAC	GAAACAAAAT	CAATGGCTTG	300
ATAGTTTGAA	GTTTTTAGTT	AAGTGCATTG	AAGAAAGTAT	GAGAATCAGT	GATGAAGCA	360
AAAGAAGCAT	TTAATGGCGT	TGTCGTGTTA	ACTGCTGCAT	TAATTGTCAT	TAAAATTCTG	420
AGTGCTGTAT	ATCGAATTCC	ATATCAAAAT	ATATTAGGCG	ATACAGGTTT	GTATGCATAT	480
CAACAAGTGT	ATCCAATTGT	AGCATTAGGA	ATGATATTAT	CGATGAATGC	CATTCCTAGT	540
GCAATTACAC	AAAA ^t TATAGG	GAAGTATCAT	AGTGACGAAG	CATATGCAAA	AGCAGTCGCT	600
TATATACAAT	TAGTTGGTAT	ATTATTATTT	ATTGCTATTT	TTGTGTTTGC	GAACAATATT	660
GCACATATGA	TGGGTGATGG	CCATTTAACA	CCAATGATTG	AAGCTGCAAG	TTTAAGCTTT	720
ATATTTATAG	GTATGCTTGG	CGTGTTAAGA	GGTTATTATCA	AATCTGCAAA	TAATATGACA	780
GTTCCGGCTA	TTTCCCAGGT	TATAGAACAA	GTTATACGAG	TAGGTATTAT	CATTGTTACT	840
ATTGTTATTT	TTGTAGACAG	AGGTTGGACG	ATATATGAAG	CGGGAACAAT	TGCTATTTTA	900
GCATCAACGA	TAGGTTTTTT	AGGTTCTTCA	ATTTATTTAG	TAGCGCACCG	ACCTTTTAAG	960
TTTAAATGG	TAAATAACAC	TGCAAAGATC	GTTTGGAAC	AGTTCGCACT	TTCGGTTTTG	1020
ATTTTCGCTA	TCAGTCAATT	AATCGTAATT	TTATGGCAAG	TGATTGATAG	TGTTACTATT	1080
ATTAAGTCAC	TTCAAGCGAT	ACGCGTGCCA	TTCGATGTTG	CCATAACTGA	AAAAGGAGTC	1140
TATGACCGTG	GTGCATCATT	T ⁿ TCAGATG	GGATTGATTG	TA ⁿ CTACAAC	ATTTAGTTTT	1200
GCGCTCATTC	CTCTGTAAAG	TGACGCAATC	AAAATGAATA	ATCAGGTACT	TATGAATCGT	1260
TATGCAAATG	CGTCATTAAA	GATTACGATT	TTAATAAGTA	CAGCAGCGGG	AATAGGATTA	1320
ATTAATTTAT	TGCCTTTAAT	GAACGGTGTTG	TTTTTTAAGA	CGAATGATT	AACCTTAACG	1380
TTAAGTGTTT	ATATGATTAC	GGTCATTTGT	GTATCGTTAA	TTATGATGGA	TATGGCATT	1440
TTACAAGCGC	AACATGCTGT	GAGACCTATT	TTGTTGGTA	TGACGGCAGG	ATTGGTTATT	1500
AAATTTATAC	TTAATATCAT	TTTGATTTCGT	TTAAGTGGCA	TTATTGGTGC	GAGCATTAGT	1560
ACTGTTGTAT	CATTAATTAT	ATTCGGTACG	ATTATCCATA	TTGCTGTCAC	GAGAAAATAC	1620
CACTTATATG	CGATGAGACG	ATTTTTTATC	AATGTTGTTT	TAGGTATGGT	ATTTATGTCG	1680

ATTGTTGTTC AATGCGTGTT AAACATAGTG ACAACACACG GTAGAATCAC TGGACTCATT	1740
GAATTATTAT GTGCAGCAGT ATTAGGTATC ATTGCATTGT TTTTCTATAT TTTTAGATTT	1800
AATGTTTTGA CATATAAAGA GTTAACTTAT TTACCATTGT GTTCAAAGTT GTATCAAATT	1860
AAGAAAGGAA GACGTTGATG GCACATACCA TTACGATTGT TGGCTTAGGA AACTATGGCA	1920
TTGATGATTT GCCGCTAGGG ATATATAAAT TTTTAAAGAC ACAAGATAAA GTTTAGCAA	1980
GAACGTTAGA TCATCCAGTT ATAGAATCAT TGCAAGATGA ATTAACATTT CAGAGTTTTG	2040
ACCATGTTTA TGAAGCACAT AACCAATTTG AAGATGTCTA TATTGATATT GTGGCGCAAT	2100
TGGTTGAAGC TGCTAATGAA AAAGATATTG TCTATGCGGT TCCGGGTCAT CCTAGAGTTG	2160
CTGAGACAAC TACAGTGAAA TTACTGGCTT TAGCAAAGGA CAATACTGAT ATAGATGTGA	2220
AAGTTTTAGG TGGGAAAAGC TTTATTGATG ATGTGTTTGA AGCAGTTAAT GTAGATCCAA	2280
ATGATGGCTT CACACTGTTA GATGCGACAT CATTACAAGA AGTAACACTT AATGTTAGAA	2340
CGCATACATT GATTACGCAA GTTTATAGTG CAATGGTGC TGCTAATTTG AAAATCACTT	2400
TAATGGAACG ATATCCTGAT GATTACCCTG TTCAAATTGT CACTGGTGCA CGAAGCGATG	2460
GTGCGGATAA CGTTGTGACA TGCCCATTAT ATGAATTGGA TCATGATGAA AATGCATTCA	2520
ATAATTTGAC GAGTGTATTC GTACCAAAAA TCATAACATC GACATATTTG TATCATGACT	2580
TTGATTTTGC AACGGAAGTG ATTGATACTT TAGTTGATGA AGATAAAGGT TGTCCATGGG	2640
ATAAAGTGCA AACGCaTGmA AcgCTAAAGC GTTATTTACT TGAAGAAACA TTTGAATTGT	2700
TCGAAGCTAT TGACAATGAA GATGATTGGC ATATGATTGA AGAACTAGGA GATATTTTAT	2760
TACAAGTGTT ATTGCATACT AGTATTGGTA AAAAAGAAGG GTATATCGAC ATTAAAGAAG	2820
TGATTACAAG TCTTAATGCT AAAATGATTC GTAGACACCC ACACATATTT GGTGATGCCA	2880
ATGCTGAAAC TATCGATGAC TTAAAAGAAA TTTGGTCTAA GGCGAAAGAT GCTGAAGGTA	2940
AACAGCCAAG AGTTAAATTT GAAAAAGTAT TTGCAGAGCA TTTTTAAAT TTATATGAGA	3000
AGACGAAGGA TAAGTCATTT GATGAGGCCG CGTTAAAGCA GTGGCTAGAA AAAGGGGAGA	3060
GTAATACATG AGATTAGATA AATATTTAAA AGTATCACGG TTAATAAAGC GACGTACGCT	3120
AGCAAAAGAA GTAAGTGATC AAGGTAGAAT TACAATAAAT GGTAATGTTG CTAAAGCTGG	3180
ATCGGATGTT AAAGTTGAAG ATGTGCTGAC GATTCGCTTT GGTCAAAAAT TAGTAACAGT	3240
TAAAGTAACT GCATTAAATG AACATGCATC TAAAGATAAC GCGAAGGGTA TGTATGAAAT	3300
CATTGAAGAG CGTCGACTTG AAGAAGCGTA AATTGGAGGT GACAAGCAAT GAAAAATAAA	3360
GTAGAACATA TAGAAAATCA GTACAGTCG CAAGAGAACA AGAAAAAACA ACGTCAAAAA	3420
ATGAAAATGC GTGTTGTTCg TAGGCGTATT ACAGTATTTG cGGGCGTATT aCTTGCGATA	3480

ATTGTTGTTT TATCaATCTT GCTTGTGTC CAAAAACATC GCAATGATAT TGATGCACAG	3540
GAGCGAAAAG CGAAAGAAGC ACAGTTTCAA AAGCAACAAA ATGAAGAAAT GCGTTAAAA	3600
GAAAAGTTGA ATAATCTGAA TGACAAAGAT TACATTGAAA AAATTGCGCG TGATGATTAT	3660
TACTTAAGCA ACAAAGGTGA AGTGATTTTT AGGTTGCCAG AAGACAAAGA TTCGTCTAGC	3720
TCAAAATCTT CGAAAAAATA AATCCAAATT GATTCAAAAT TATCCGAGTA TAGACATTGT	3780
GAAAAAA	3787

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

TAAACCATTT CAAACTGAGG AACGCnAAGA CGGsACgTTT CCAGATTTAG AAGTATTTAA	60
AAATGAATGT GATTTAAGCT ATGACATAAC GTCACCTTAT ACTTTTAAGC AACCTGTATC	120
ACCACACCTT GCATTTAAAA TGACAGATa AATTTTTCTA AATAAGCAGC GTGTATTAGA	180
TAAGGTAAAA GTTTTAGATA AGGAATTTGA TTTTATCTTA ATTGAGGGTG CTGGGGGAAT	240
TGCCGTACCA ATATATGAAG GTACAGATGA TTTCTACATG ACTAAAGATC TAATCAATGA	300
TTGTGCAGAT TGTGTCATCA GTGTGTTGCC ATCAAATTA GGTGCTATTA GCGAGCCAT	360
TGTTCAACCA GATTATGTTA ATCAGAATGT ATCGGCGAGT AATTTTTTAA TAATGAATCG	420
CTATACAGAC AGCTATATTG AAAAAGACAA TCAAATGACG ATTGGAAAAT TAACAAATAA	480
AACAGTCTAT ACATTTGAAG AACATGCCAC GTATGAAAAT TTCTCAGAAG CATTTTTTAA	540
ACAATTAATA GGAGTTAAAA ATGAATTACA CACAACAAC TAAACAAAAA GACTCAGAAT	600
ATGTTTGGCA TCCATTTACA CAAATGGGTG TATATAGCAA AGAAGAAGCA ATCATCATTG	660
AAAAAGGAAA GGGTAGTTAC CTTTACGATA CGAATGGCaA TAAATATTTA GATGGTTATG	720
CATCGTTGTG GGTCAATGTG CATGGTCATA ATAACaATA CTTnAATAAG GTAATTAAAA	780
AGCAACTCAA TAAATTGCC CATTCTACGC TGCTAGGATC ATCAAATATT CCGTCAATAG	840
AACTTGCGGA AAAATTAATC GAAATCACGC CAAGTAATCT AAGAAAAGTA TTTTATTCTG	900
ATACAGGCAG TCGTCTGTT GAAATCGCAA TAAAGATGGC ATATCAGTAT TGGAAAAATA	960
TTGATAGAGA AAAATATGCC AAGAAAAACA AGTTTATAAC GCTAAATCAC GGTTATCATG	1020
GGGATACGAT TGGTGCAGTA AGTGTTGGTG GTATCAAGAC CTTTCATAAA ATATTTAAAG	1080
ACTTAATATT TGAGAATATT CAAGTAGAAA GCCCATCTTT CTATCGCAGT AATTACGATA	1140

CTGAAAATGA AATGATGACA GCTATTTTAA CGAATATAGA GCAAATTCTA ATTGAAAGAA	1200
ATGATGAAAT CGCAGGGTTT ATATTGGAAC CGTTGATTCA AGGTGCGACA GGCTTGTTTG	1260
TTCATCCTAA AGGCTTTTTG AAAGAAGTCG AGAAATTGTG CAAAAAATAC GATGTCTTAT	1320
TAATTTGTGA TGAGGTAGCA GTTGGTTTTG GGAGAACTGG AAATGTTT GCATGCAATC	1380
ATGAAGATGT TCAACCGGAT ATTATGTGTT TAGGTAAGGC GATTACTGGT GGCTACTTAC	1440
CACTTGCAGC TACATTGACA TCTAAAAAAA TATACAATGC ATTTTAAAGT GATTTCGCATG	1500
GTGTGAATAC CTTTTTCCAT GGTCaTACAT ACaCCGAAA TCAAAATcGTT TGTaCGGTTG	1560
cATTaGaAAA TATaAGaCTT TATGaAAAAC GTaAGTtnAT TGTgCACATa TTGaAACGaC	1620
ATCATCAACA CTTGAGAAAC AGTT	1644

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

ATGATTTTtA aAAATCATTa AGTTAAGGTr GATACACATC TTGTCATATG ATCAAATGGT	60
TTCGCCAAAA ATCAATAATC AGACAACAAA ATGTGCGAAC TCGATATTTT ACACGACTCT	120
CTTTACCAAT TCTGCCCCGA ATTACACTTA AAACGACTCA ACAGCTTAAC GTTGGCTTGC	180
CACGcmTTAC TTGACTGTAA AACTCTCACT CTTACCGAAC TTGGCCGTAA CCTGCCAACC	240
AAAGCGAGAA CAAAACATAA CATCAAACGA ATCGACCGAT TGTTAGGAA TCGTCACCTC	300
CACAAAGAGC GACTCGCTGT ATACCGTTGG CATGCTAGCT TTATCTGTTC GGGCAATACG	360
aTGCCCATTTG TACTTGTTGA CTGGTCTGat ATCcGTGAGC AAAAACGGCT TATGGTnTTG	420
CGAGCTTCAG T	431

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2006 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

TTTnTATAAC GTATTATAAA TCGTTAAAAA TTTTGTTGT GTTTGCGTCA CGTAGACAAC	60
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CTCCATAAAG	T TACTTAATC	ACTCTCATCA	TACAATAATT	TTTACTCAAA	TTGGAAnAAT	120
TATAAAAATT	AAATATAGAT	AGGCTTTGAA	AATTAGTTTT	ATACAAGGTT	AGTAGCTGTA	180
ACTGTAAAAT	GTTCTTAATA	TTGTAAAAT	GTAATGCTTG	AAAGCGCTTT	TAAAaAATAT	240
TATTATATAC	ATGGTTAGAC	AAATAGACAA	ATCACTATAC	AAATATTGGG	AGGAATATTT	300
TATGAAATCA	ACACCACACA	TTAAACCAAT	GAATGACGTC	GAAATTGCAG	AAACGGTTCT	360
ATTGCCAGGA	GATCCGTAA	GAGCTAAGTT	CATTGCAGAA	ACTTATTGGAT	GATGTGGA	420
ACAGTTCAAT	ACAGTGCGAA	ACATGTTTGG	TTTTACCGGA	ACATATAAAG	GTAAAAAAGT	480
TTCTGTCATG	GGTTCAGGTA	TGkGTATGCC	ATCTATTGGC	ATTTACTCTT	ATGAATTAAT	540
TCATACATTT	GGTTGTAAAA	AATTAATTCTG	CGTTGGCTCT	TGTGGCGCGA	TGCAAGAAAA	600
CATTGATTTA	TATGATGTGA	TTaTTkCACA	AGGTGCCTCT	ACTGATTCAA	ATTACGTTCA	660
ACAATATCAA	TTACCAGGTC	ATTTTGCGCC	AATTGCTTCT	TATCAATTAT	TAGAAAAAGC	720
AGTTGAAACA	GCACGTGACA	AAGGTGTACG	TCATCATGTA	GGTAATGTGT	TATCAAGTGA	780
TATTTTCTAT	AACGCGGATA	CAACAGCGAG	GAACGTTGG	ATGCGTATGG	GTATTTTAGG	840
TGTAGAAATG	GAATCaGCTG	CaTTATACAT	GaATGCAaTT	TACGCTGGTG	TCGAAGCATT	900
AGGTGTGTTT	ACAGTGAGCG	ATCATTTAAT	TCATGAAACG	TCAACAACaC	CTGAGGAAAG	960
GGAACGTGCA	TTTaCAGATA	TGATTGAAAT	TGCACTGTCA	TTGGTGTAGA	TGATTATAA	1020
TGTTGAATAT	TCTAAAATAA	AGAAAGCAGT	ACCTATTTTA	TTATTCTTAT	TTGTATTTCAG	1080
TTTGGTTATA	GACAACTCAT	TTAAATTGAT	TTCTGTAGCC	ATTGCTGATG	ACTTAAACAT	1140
ATCTGTAACG	ACAGTAAGTT	GGCAAGCGAC	ATTAGCCGGT	TTAGTAATTG	GTATTGGCGC	1200
TGTAGTATAC	GCTTCATTAT	CTGATGCCAT	TAGTATACGC	ACACTATTTA	TTTATGGCGT	1260
GATATTAATC	ATTATCGGAT	CAATTATTGG	TTACATTTTC	CAACATCAAT	TCCCATTACT	1320
TTTAGTTGGA	CGTATTATTC	AAACTGCCGG	TTTAGCTGCT	GCAGAGACAT	TATATGTGAT	1380
ATATGTTGCA	AAGTATCTTT	CTAAAGAGGA	CCAGAAGAT	TACCTTGGCT	TAAGTACGAG	1440
CAGTTATTCC	TTGTCATTAG	TTATCGGTAC	ATTATCAGGT	GGATTTATTT	CTACGTATTT	1500
ACACTGGACA	AATATGTTTT	TAATTGCATT	AATCGTAGTA	TTTACGTTGC	CATTCCTATT	1560
TAAATTATTA	CCAAAAGAAA	ATAATACGAA	TAAAGCTCAT	TTAGATTTTG	TTGGCTTAAT	1620
TCTAGTGGCA	ACTATTGCTA	CAACAGTCAT	GCTGTTTATT	ACGAACTTTA	ATTGGTTATA	1680
TATGATTGGT	GCCTTAATTG	CGATTATCGT	TTTTGCGCTA	TATATTAAAA	ATGCGCAACG	1740
TCCATTAGTA	AATAAATCAT	TTTTCCAAAA	TAAACGTTAT	GCTTCATTTT	TATTTATAGT	1800
ATTTGTAATG	TATGCTATCC	AATTGGGTTA	TATTTTACG	TTCCCATTCA	TAATGGAGCA	1860
AATTTATCAT	CTGCAACTAG	ACACAACATC	ACTGTTATTA	GTACCGGGgT	TaTATAGTAG	1920

CAGTCATTGT TGGtGgCACT AAGTGGgTtA AAATCGGgCG rAATATCTGG AATTCCAAAA 1980
 CCAAGCGGAT TATCACAGCC AATTAA 2006

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

TGGGGAAAAA AAGACCCAGC AGTATTAGAA GAATCGTTAA ATATTTCTAT TGAAGAAATG	60
AATCGTATCA TAAAATTAGT CGAAGAATTA CTTGAATTGA CTAAAGGAGA TGTAATGAC	120
ATTTCTTCTG AAGCACAGAC CGTGCATATT AATGATGAAA TTCGCTCGCG AATACACTCA	180
TTAAAACAAT TGCATCCTGA TTATCAATTT GATACGGATC TGACATCTAA AAATCTAGAA	240
ATTAAAATGA AACCTCATCA ATTCGAACAA TTATTTTAA TCTTTATTGA TAATGCAATC	300
AAATATGATG TGAAGAATAA GAAAATTAAA GTTAAGACAA GGTTAAAAAA TAAGCAAAAA	360
ATAATTGAAA TTACAGATCA TGAATTGGT ATTCCAGAGG AAGATCAAGA TTTCATTTTT	420
GATCGCTTTT ATCgAGTGGA TAAATCTCGT TCAAGAAGTC AAGGCGGTAA TGGACTCGGA	480
TTATCTATTG CTCAAAAAT CATTCAATTA AACGGAGGAT CGATTAAAAT TAAAAGTGAA	540
ATTAACAAAG GAACAACGTT TAAAATCATA TTTTAATCAT GACTGAGAG TCAATCAAAG	600
TCATAGGATC AATTTTTTAA GTACACATTA GCTGTGACTA ATGTATAAGA ACAACTATAA	660
AACAAATAAA CAGTGTTTCT TTATCATTTT TGTGTACTC CCAAAATTTA CAATAAATA	720
CATCTATAAA CCTAGAAGAA TCAACGCTTT TGTGATTCT TCTTTTAGC AGATAAATAG	780
GTAAATCTAC TTAAACAAAT AACTAAATAG TGATATTATT ACATTGTAAG CGTTTCAACA	840
TTTTTGTGGA GGGTGTA AAA TGAATAACGA AAGAAAAGAA GTTTCAGAGG CTCCTGTAAA	900
CTTCGGTGCG AATTTAGGTC TAATGTTAGA TCTATATGAT GACTTTTTTAC AAGATCCATC	960
ATCTGTACCA GAAGATTTAC AAGTCTTATT CAGCACAATT AAGAATGATG ACTCAATTGT	1020
ACCAGCTTTA AAAAGTACAA GTAGTCAAAA TAGCGACGGC ACAATTAAGC GTGTCATGCG	1080
TTTAATTGAT AATATTCGCC AATACGGGCA TCTTAAAGCC GATATTTATC CTGTAAATCC	1140
TCCAAAAAGG AAACATGTAC CTAAATTAGA GATTGAAGAC TTTGATTAG ATCAAGAC	1200
TTTGGAAGGT ATATCAGCAG GAATTGTTT AGATCACTTT GCCGACATTT ATGATAATGC	1260
TTATGAAGCA ATTTTAAGAA TGGAAAAACG TTACAAAGGA CCAATTGCAT TTGAGTATAC	1320

ACATATTAAT AACAAATACCG AACGTGGTTG GTTAAAAAGA AGAATTGAAA CGCCATATAA	1380
AGTAACGTTA AATAATAACG AAAAAAGGGC ACTATTCAAA CAATTAGCGT ATGTTGAAGG	1440
GTTTGAAAAA TATCTTCATA AAAACTTCGT TGGTGCAAAG CGTTTTTCAA TTGAAGGGGT	1500
AGACGCACTT GTACCGATGT TACAACGTAC TATTACGATT GCTGCGAAAAG AAGGTATTAA	1560
AAATATACAA ATAGGCATGG CTCACCGTGG ACGTTTAAC GTTTTAACGC ATGTCTTAGA	1620
AAAACCGTAC GAAATGATGA TTTCAGAATT TATGCATACA GATCCAATGA AATTCTTACC	1680
TGAAGATGGT AGCTTGCACT TAACTGCTGG ATGGACTGGT GATGTGAAAT ATCACCTTGG	1740
TGGCATTAAA ACTACTGATT CATACGGTAC AATGCAGCGT ATTGCACTGG CTAACAATCC	1800
AAGTCACTTG GAAATTGTTG CACCTGTTGT TGAGGGGCGT ACGAGAGCAG CACAAGATGA	1860
TACACAACGA GCTGGGGCTC CGACGACTGA TCATCATAAA GCAATGCCAA TTATTATACA	1920
TGGCGATGCT GCTTATCCTG GTCAAGGAAT TAACTTCGAA ACAATGAACT TAGGAAACTT	1980
GAAAGGCTAT TCTACGGGTG GTTCATTGCA TATTATTACT AACAAATAGAA TTGGATTTAC	2040
TACAGAACCA ATTGATGCAC GTTCAACAAC TTATTCTACA GATGTGGCCA AAGGTTATGA	2100
TGTGCCAATA TTCCATGTCA ATGCAGATGA CGTTGAAGCT ACTATTGAAG CAATTGATAT	2160
TGCAATGGAA TTTAGAAAAG AGTTTCATAA AGACGTCGTT ATTGATTAG TAGGTTATCG	2220
TCGTTTCGGA CATAACGAAA TGGATGAACC ATCAATTACT AATCCAGTTC CTTATCAGAA	2280
TATTCGCAAA CATGACTCTG TTGAATATGT GTTTGGTAAA AAGCTTGTTA ATGAAGGTGT	2340
CATTTTCAGAA GATGAAATGC ATTCATTTAT AGAACAAGTC CAAAAGGAAC TAAGACAAGC	2400
TCATGATAAA ATTAATAAAG CTGATAAAAT GGATAATCCA GATATGGAAA AGCCTGCAGA	2460
TCTTGCAATTA CCGTTACAAG CAGACGAACA ATCATTTACT TTTGATCACT TGAAAGAAAT	2520
AAATGATGCA TTGTTAACAT ATCCGGATGG CTTTAACATT TTGAAAAAGT TAAACAAAGT	2580
TCTTGAGAAG CGTCATGAGC CGTTTAATAA AGAAGATGGT TTAGTTGATT GGGCACAAGC	2640
AGAACAACCTT GCATTTGCGA CAATTTTACA AGATGGTACA CCGATTGCTT TAACTGGTCA	2700
AGATAGTGAA CGTGGTACAT TCAGTCATAG GCATGCCGTG TTACATGATG AGCAAACAGG	2760
TGAAACATAT ACACCTTTAC ATCATGTTCC TGATCAAAAA GCGACATTTG AATTACACAA	2820
TTCTCCGCTT TCAGAAGCAG CAGTAGTTGG TTTTGAATAC GGCTATAATG TGAAAAACAA	2880
AAAAAGCTTC AATATTTGGG AAGCACAATA TGGTGATTTT GCAAATATGT CACAAATGAT	2940
TTTTGACAAC TTCTTATTCA GTTCTCGCTC AAAATGGGGA GAACGTTTCA GATTAACATT	3000
ATTCTTACCT CATGCATATG AGGGTCAAGG GCCTGAACAT TCATCAGCAA GATTAGAGCG	3060
ATTTTTACAA TTAGCTGCTG AAAATAATTG CACAGTTGTC AACTTATCTA GTTCAAGTAA	3120
TTATTTCCAC TTATTGCGTG CACAAGCGGC TAGTTTAGAT TCTGAACAAA TGCGACCATT	3180

GGTTGTTATG TCACCAAAAA GCTTACTGAG AAA'AAAACA GTTGCAAAAC CAATTGATGA	3240
ATTTACTTCT GGTGGATTTG AGCCAATTTT GACAGAATCA TATCAAGCGG ATAAGGTTAC	3300
AAAAGTTATT TTGGCAACTG GTAAAAATGTT CATTGATTTA AAAGAAGCAT TAGCTAAAAA	3360
TCCAGACGAA TCAGTATTAC TCGTTGCGAT TGAAAGATTG TATCCATTCC CAGAGGAAGA	3420
GATTGAAGCA TTAGTAGCAC AATTGCCAAA CCTTGAAGAA GTGTCATGGG TACAAGAAGA	3480
ACCTAAAAAT CAAGGTGCAT GGTTATATGT CTATCCATAT GTTAAAGTGC TAGTTGCAGA	3540
TAAATATGAT TTAAGTTATC ATGGCAGAAT TCAAAGGGCT GCTCCAGCTG AAGGCGATGG	3600
AGAAATTCAT AAAGTTGTTT AAAATAAAAT TATAGAAAAT GCATTAAAAA ATAAGTAGGG	3660
GGAAATAAGT CATGCCAGAG GTTAAAGTTC CAGAATTAGC AGAATCTATT ACAGAAGGTA	3720
CCATTGCAGA ATGGTTGAAA AACGTAGGGG ATAGCGTAGA AAAAGGTGAA GCTATTCTTG	3780
AATTAGAAAC TGATAAAGTT AATGTCGAAG TTGTATCTGA BAAGCAGGT GTATTATCTG	3840
AACAAGTTGC AAGTGAAGGC GACACTGTAG AAGTTGGACA rGCAATTGCT ATCATCGGCG	3900
AAGGTAGTGG CAATGCTTCT AAAGAAAATA GTAACGACAA TACTCCACAA CAAAATGAAG	3960
AAACAAATAA TAAAAAGAA GAAACAACAA ATAATTCGGT AGATAAAGCT GAAGTAAATC	4020
AAGCAAATGA TGACAATCAG CAACGTATTA ATGctACGCC TTCTGCGCGT CGATATGCTC	4080
GTGAAAATGG TGTGAATCTT GCTGAAGTAA GTCCGAAAAC AAATGATGTG GTTCGTAAAG	4140
AAGATATTGA TAAGAAACAA CAGGCACCGG CATCAACACA AACAAACAAA CAAGCATCTG	4200
CAAAAGAAGA GAAAAAATAC AATCAATATC CTACAAAACC AGTGATTCTG GAAAAAATGT	4260
CACGTAGAAA GAAAACAGCT GCCAAAAAAT TATTAGAGGT ATCTAATAAT ACAGCTATGT	4320
TAACAACATT TAACGAAtTG AcATGACAAA TGTTATGGAA TTGCGTAAAC GTAAGAAAGA	4380
ACAATTTATG AAAGATCATG ATGGTACTAA ATTAGGATTT ATGTCATTt TACTAAAGC	4440
TTCTGTAGCA GCTTTGAAAA AGTATCCAGA AGTTAATGCA GAAATCGACG GCGACGACAT	4500
GATTACGAAA CAATATTATG ATATTGGTGT AGCTGTTTCT ACAGATGATG GATTATTAGT	4560
ACCATTTGTA AGAGATTGTG ATAAAAAGAA TTTTGCAGAA ATCGAAGCAG AAATTGcTAA	4620
TTTAGCAGTT AAAGCaCGAG AGAAAAAACT TGGCTTAGAT GATATGGTTA ATGGTTCATT	4680
TACGATTACA AATGGCGGTA TTTTGGATC AATGATGAGT ACGCCAATTA TCAATGGTAA	4740
TCAAGCTGCA ATCTTAGGCA TGCATTCAAT TATTACAAGA CCAATTGCGA TTGATCAAGA	4800
TACAATCGAA AATCGTCCAA TGATGTATAT TGCATTAAGC TATGATCATA GAATTATT	4858

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2222 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

ATCAGTCACA CGGTAGGCAT ATAAAATGAG TCGTTTCTAC AACATTTTTA AACAGTTCAT	60
TCAATATTAT TTTTATCTAA TAATnATATT GGGAGGATTA TACCTTTATA CACACCATGC	120
ATTTATCTTA GGATTAATCA TTGGTGTTAC TGGTTCTGCA ATCAACACAT GA TTTTTTGA	180
ATGCTATTTA GCTAAAGCTA AAAGACCAGA CACTATGCAT ATTTCAACTG GAAATATGTG	240
GCGATACTTA GTTGCAATTA TTGCCTGTAT GATTTGGTAC CTTAATAAAG CGCATGTAAG	300
TATCATCGGT ATAATTATTG GTTTAATGAT TTCATATGTT GTAGTTATCA TACGTCCTTT	360
ACTAAAGGTG AGCAAATAAA TTAAGAAAGA GGTGAGATTA TGGATCACAA ATCCCCGCTC	420
GTGAGTTGGA ATTTATTCGG TTTTGaTATC GTTTTCAATT TATCAAGTAT ATTGATGATA	480
CTTGTTACGG cGTTTCTTGT TTTTCTACTT GcTATCATTT GTACGCGTAA TTTGAAAAAA	540
AGACCAACTG GCAAACAAAA TTTCGTTGAA TGaTTTTTTG ATTTCTGTGAG GGAATCATT	600
GAAGGTAACA TGGCTTGGA AAAAGGTGGT CAATTCCACT TCTTAGCAGT AACGCTGaTT	660
CTGTACATTT TTATAGCTAA TATGTTAGGT CTTCCGTTTT CTATAGTAAC GAAAGATCAC	720
ACATTGTGGT GGAAATCACC GACAGCnGAT GCAACAGTGA CTTTAACGTT GTCTACAAG	780
ATAATACTGT TAACTCACTT TTATGGAATT AAAATGCGTG GTACGAAACA ATATCTTAA	840
GGTTATGTAC AGCCGTTTTG GCCATTGGCA ATTATTAATG TTTTGAAGA GTTCACTTCA	900
ACATTAACGC TTGGTCTGCG TTTGTACGGT AACATATTTG CAGGTGAGAT ACTATTAACA	960
TTACTTGCTG GCTTATTCCT TAACGAACCA GCATGGGGTT GGATTATTAG TATCCCAGGA	1020
TTAATTGTTT GGCAAGCATT TTCAATATTT GTAGGAACAA TCCAAGCATA TATCTTTATT	1080
ATGCTTTTGA TGGTTTATAT GTCACATAAA GTGGCAGATG AACACTAAAA ATTTCAATAA	1140
TTATATACAA TCACAGGAGG AAATTAAATT ATGAATTTAATCGCAGCAGC AATCGCAATT	1200
GGTTTATCAG CATTAGGAGC AGGTATCGGT AACGGTTTAA TCGTTTCAAG AACAGTTGAA	1260
GGTGTAGCAC GTCAACCAGA AGCACGTGGT CAATTAATGG GTATCATGTT CATTGGTGTA	1320
GGTTTAGTTG AGGCATTACC TATCATCGGT GTAGTAATTG CATTATGAC ATTTGCTGGA	1380
TAATTAACAG ATAAAAGAGG TCGGGACAAA GCGCATAGGA CATAATTCAT GATGCATATA	1440
TAGTAATATC TTTGAACTTT ATTAATAGT TGAGATATGA ACGCACCATG CCTATCGCAT	1500
AAATTCAGTA GGTCTAACC TCGTCGTTTT TTTCTATATA AACTAGCGA TTATTTTAAT	1560
GAAAGGAGTG TCATGAACCC GTGACTGAAA CAGCTAACTT ATTCGTTCTT GGTGCAGCTG	1620

GAGGCGTTGA GTGGGGTACT GTGATTGTAC AGGTCCTAAC TTTCATCGTG TTAcTTGCGT	1680
TACTTAAAAA GTTCGCATGG GGTCCATTGA AAGATGTAAT GGATAAACGT GAAAGAGATA	1740
TTAACAGAGA TATCGATGAC GCAGAACAAG CTAAGTTAAA TGCACAGAA CTTGAAGAAG	1800
AAAATAAACA AAAACTTAAA GAAACACAAG AAGAAGTTCA AAAGATTTTA GAAGATGCTA	1860
AGGTTCAAGC ACGTCAACAG CAAGAACAAA TTATTCaTGA AGCAAACGTA CGTGCAAACG	1920
GTATGATTGA AACAGCACAA AGTGAAATCA ATAGCCAAAA AGAACGTGCC ATTGCAGATA	1980
TTAATAATCa AGTATCTGAA CTATCAGTGT TAATTGCTTC TAAAGTTCTT AGAAAAGAAA	2040
TTTCTGAACA AGACCAAAAA GCATTGGTTG ACAAGTATCT AAAAGAGGCA GGCGATAAAT	2100
AATGGTAAAA GTAGCTAACA AGTATgcTAA AGCATTATTT GACGTGTCAT TAGATACAAA	2160
TAATTTAGAG ACTATTAATG AAGAATTAAC AGTTATAAAT GAAGCAGTAA AAGATAAAAT	2220
TG	2222

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

TAACAATTCC TaTATTCATG TTTAATACGA AACACTACAT TTACATTGTA ATTCACTATC	60
TTTTGAAGTA ATAAAGTGAT TTGTTCAATC GATAGCTCAT TGCTTGTGTCGATTGTAACA	120
ATTATATGCA AGTTTTCAGG ATTAACACCT AATCTTTGAA TGATTTGTTT AATAGTATAA	180
TAATCCATCC AATAAAAATT ACTTCCTTTA ATATAAATGT TTTTAGGTTG ATACATTTGA	240
CTCCTTTTTG TAGGCTCAAA AGGTATATCA ATCTCGCGCA TACTTGAAGA ACTTTGATTA	300
GTATCATCAA ATAATTCAAT TATATTTTTA TCAATTTCAA CTAATTGGGA ATGGTTAATT	360
GAATGAGATG TTGGACTATA TCTTTTTCTA ATTAATTTAG GAGTGTTACC ATACGTTTCT	420
TTAAAGAGGT GTATAAACG AGAATAATGA TTAAACCAT GACTACTTGC GATTTCTTCA	480
ATAGGCTTCT TAGrAGTTAA AATATCAATT AaCAATGCT CCAGTCTAAT ATGATTTAAA	540
TATTGAATAA AATTACTATA AGGTGTCGCT TTAAACATGT CACTTAAAGC TTTGTTTGTA	600
ATACTAACTT GATTAATGAC ATCTTTCCTA TTTATCTTTT TATGGTGGTT GTTTGTTAAA	660
TAATCGTGCA CTTCTTCGGC TACTAAATGA CGACTACCAT CGTATGTATT TAATGACAT	720
AATTCAACAC ACATGTAATT AATAATCTTA TCATTAGCAT TATAAGACTG TTGTTTAATT	780

TTGCTGTAGA TTAAATACTT AATCAAGATT CTAAAAGTGC TAGCAACCTC ATTTGTTAAT	840
ATCTTGCCAC GCATCATATA GTTTGCATTC ATAAACTTCA AAAATGTCTT TGCACTTACT	900
TCAACAACAC AACATACACT ATCATCATTA CCATCAATTT GATACAAATC ATTC AACATA	960
ATAATGGTGA CATCATTTCT TTTTACATCA TATTGTTGTA GATTGATTGA AACTACACCT	1020
GTACCTTGTA GCCAATATAT AATTTTtAAG TTCGCTTCCT TCACACTACT CATTTTCATA	1080
CTTTTATAAA TATGTAGTGA ATAATAwCtG tCACnTACATCccACAaTAC aATATnATGG	1140
ATT	1143

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

GGACCACCTT TTTTACCTGT ACGACTAAAG CCAACTGTTT TAAAGGCACC AACAGCATGC	60
CACACTTGAA TAATTTCTTG TGATGGTCTA AAGCGAACCG TATAAATTAA TGGATGGAAA	120
TCATCAACAA AAATATAATC GGCCTTACCA AGTAAATATG GCAATCTAAA CTTGTCTCTC	180
CATTTGCGTC TATCCGTAAT ATTCTCCTTA AATACCGTTT TAATATCATA ATCAAAATCT	240
ACTTTTTTGGC GTAGTAACTC ATCATATACA TACTTGAAAT TCCCTGATAA ATTCGGACGC	300
GAATCTGATG TGAATAATAT TGTTTTGCTT CTTTAAATAT GTAGTAACTT TGTAATATTA	360
AAAATAGCTT TAAATAAGAA ACTTCTACTT TCAAATGAAG CTTTATGaCC TTGTTTtATGA	420
AGCCAGTG TG cACTTgTCGC AATGaCCCCCT GaTTTCyCyT GagGtAAGGk GaTTTCmATA	480
TCAAATACAA ATTCGTTAAC GTCACT	506

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

AGCATCTGCA AtGAGTcTCT AATACAACGA TACGTTTTGC ATCTTTAGGT ACTTTTACTG	60
TACCATTTTC ATCTTTTACC GAAATAGTAT CTTTAGTTGA TGATTCTTTT TTA CTGTAAT	120
TATCCGTATT ACCACAAGCT GCAACTAAAA GTAAGGCAAC TATTAATCCC AATATACTAA	180

AAGTTTTTAG ACCTCTCATC GTTCCACTCC TTAATATGTA TAACTTCATT TATTATTTTA	240
TTGATAACAA TTATCATTGT CAAGTAGCGT TCAATCTTTT TTATATTTCT AAAATGTATG	300
ACTATATATT TCCTCTAATA ATTATGACTA CAATTAGCAC ATTCCTTAG ACAAATACT	360
GATAATGTAT CATTGCTATA TCATCTTTGC ATTAATACAA TTGACACCAT TTAGCATGAC	420
C	421

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

TGCACTTGAT ACTTTAGCAC ATGAAATTGC TAATCGATTA GTTGCAAATG ACAAGAATGA	60
AGCAACTTTG GAAATGACTA ATAAAATGGC AACGATTTCGT TTACAGAAC CTACGCTGAT	120
TGCATTAGCA GGGGGTAATG TCAAAGCTTA CACTGAGCAT ATGACTATAT CTCCATATAA	180
ATTGTATTTG TTAGATAAAG GCGATGTTTT AAAGTTTAGA GAAACAAGTT ATACATCGCG	240
AGTGTATTTA GCTGTGGAG GCGGATTTGA ATTAGATGCA TGGTTAGGAT CTAACCTAAC	300
CGACTTTAAT GTAAAAATTG GTGGTTTTAA AGGTAGAACA TTACAAGATG GCGATGAAAT	360
AAAGCTTAAG AGAGATTATA CAGCTCGTCA TCATAAGTTA TTTGAAAACC TTGCTCACAC	420
GAAACAAACA GATTGGGGTA TTGATGGATA CGCCTTGTC TTTAATTATA TGTCTGATGT	480
ATTTTCATGTC GTTAAAAATA AAGGTACGGA AGATTTTAAA GAAGATGCCA TTCAAAGATT	540
TGTGAAACAT GATTATAAAG TAACGAGCAA AGCAAATCGC ATGGGGATGA TGCTTGAAGG	600
TGAAAAAATC AAAGCTTTTT ATGAAGATAT GCCACCGTAT CAGACTGTCA AAAAAGGAAC	660
GATACAAATT AAGCGTGATG GCACACCTAT TATCCTATTA AATGATCATTATACGCTAGG	720
TAGCTACCCG CAAATCGGTA CAATCGCAAG TTATCATTTA ACGAAATTAG CACAAAAACC	780
GCAAGGATCA CGTTTGAAAT TTCAATTTAT AGATATTTTA ACGGCTGAAA AGAACCTTGT	840
TAAgTATAGT AACTGGTTAA AC	862

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

AAATGAGTTG ATGATGGCTC CTATTCCATC TATCTCTAGG TATGACAGAA sATAAACGGT	60
CTTCTACCTG TCTsACATTA TCTTTCCAAC GATTAATACC TAAGCGTTTA GAAACACGTT	120
CTACATGCGT ATCAACAGCT AATGAAGGTT CATCAAATGC TACACTCATG ActACATTAG	180
CAGTTTTACG TCCTACACCT GCTAAACTT CTAATTCCTT ATGTGTTTGT GGTATTTCTC	240
CATTAAATTG ATCAATCAAA GATTGACAAA GTTTCTTAAT ATTCTTAGCT TTGTTACGAT	300
ACAGACCGAT AGAACGAATA TCATTCATAA GTTCTTCATC ACTGACTGCC AAATAATCTT	360
CAGGCGTTTT GTATTTTTTA AACAGCTCAG TTGTTACTCT ATTTACTAGA ACECTGTAC	420
ATTGCGCTGA CAATAATACA GCAATAGTTA ATTGGAACGG ATTATCATGT TTTAATTCAC	480
ATTCTGCATC CGGAAACATA TTTGCTATAA CATCAATCAT TTCTAATGCT TTTTCTTAC	540
TTACCATCAA GGTTCTCCCC GTTTAACCAA TCAAATTTAG GTACCGTTTT AACTGTGTGC	600
GTCATTTTCG GTTTATTGAA TTTTCTCTT ATTTTCTAG AATCGTCAAT TGTTTTGACA	660
TTGTTTTTCT TCCAATTAAG TAAAATACGA TCTATATATT TAAAGCTAAG TTTATTCAAA	720
CTATTCGCCT CGTCTAATGC CGCTTGATA ATTGCAGTAT CGTGTTTATC AACATCAATC	780
CATTGATTTA ACGTTTCTAT TTCATATGGA GATAEGGCC TTGCAAATGT ATCCTCTAAA	840
ACTCTAAATA ATTGTTTAAA TTTTCTTTA CTATTTAGCT CTTTCGTTTC CATACTTTGT	900
TGCTTCAATA TATGACTTAA TTTTTCGAAA AAAGGATCTA GATTCATATA TTCGGkAAAT	960
CTACCTTCyT CATCyTTTTG aACTkgtAAT tCTAGCAATT CACGTgTATC AAATTTTGGA	1020
TACCATT	1027

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

AAGGnTTGGA GGGAATTAAT nGATGGCAAA TCCCAGaTAA AGTACACaAC GCATGGAATG	60
TGATGCATTT AATATTTCCA GTAGTTAGTA CGACGTTTGC AAGCTTTAAA TCTATGTATG	120
GGGGCATACC AAAAGATTTC ATAGACTACT TATTTATTGA TGAAGCAGGA CAAGCAATAC	180
CTCAAGCAGC TGTGGGAGCA TTATATCGTT CAAAAAAGT TGTAGCTGTA GGTGATCCGA	240
TTCAAATAGA ACCGGTTGTG ACTTTAGAAA GTCATTTAAT TGATAACATT CGTAAAAATT	300

ATCATGTTCC GGAATATCTA GTTCTCTAAAG AAGCTTCCT GCAGTCTGTT GCAGACAACG	360
CCAATCAATA TGGTTTTTGG AAATCTGATG CTAAGTATAG TAATCAAAAA ACCTGGATAG	420
GCATACCTTT ATGGGTGCAC AGACGATGTT TAAAACCTAT GTTCACGATa GCTAaCCAAa	480
TCGCTTATAa TAaTAAaTG GTGTTGCCAa GTAaTATTAC AAAaGTAGGT AAAaCAGGTT	540
GGTATGACGT TAAAGGAAaC GCAGTTCAAA AACAATTTGT GAAAGAGCAT GGTGAAAAaG	600
TAGTGGGATT ATTAGCTGAT GATTGGATTG AAGCAATTAA GGAAGGTAAA AATGAACCGA	660
GCTCATTTGT AATATCGCCT TTTTCAGCAG TACAGCAACA GATTAAACGT ATGTTAAAGC	720
AACAACCTACC GACTAGAATT GATATTGAAC GTACAAAAAT TAATCAATGG GTCGATAAAT	780
CCATTGGTAC TGTTCACTACT TTTCAAGGTA AAGAGGCTCA GAAGGTGTAT TTTGTAATAG	840
GTAAGTATAA TACCCAAGAT GGTGCTGTGA ACTGGTCATG CGAAAAACCA AACTTGTTAA	900
ACGTTGCAGT GACAAGAGCT AAGAAAGAGT TTAaTGAATT GGCGAATGC AAAGAATACA	960
GATGAaACCA TTTTATGAGA CGATTTTTTAn AGnAAGAAAT GTAAAA	1006

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

CGTTTCATCA AGTnATCGAT CCTAATTTAC AAAATATTCC GGTTAGACTT GAAGAAGGGC	60
GTAAAATAAG AAAAGCCTTT AAACCAACTT CAAAAGATAG CGTTATATTA TCAGCAGATT	102
ATTCTCAAAT TGAATTGCGT GTATTAGCAC ACATTACACA AGATGAGAGT ATGAAAGAAG	180
CATTTATCAA CGGCGATGAT ATTCATACAG CAACTGCTAT GAAAGTATTT GGTGTAGAAG	240
CTGATCAAGT CGATAGTTTA ATGCGTCGTC AAGCAAAAGC AGTTAACTTT GGAATTGTTT	300
ATGGGATAAG TGATTATGGT TTAGTCAAA GTTTAGGTAT TACTCGTAAA AAAGCAAAAG	360
CATTCATTGA TGATTATTTA GCTAGTTTCC CAGGTGTAAA ACAATATATG TCTGATATTG	420
TAAAAGATGC CAAAGCTTTA GGTTACGTGG AACATTGCT ACATCGTCGA CGCTATATTC	480
CTGATATTAC GAGTCGTAAC TTTAATTTAC GCGGCTTTGC TGAACGTAT GCTATGAATA	540
CGCCAATACA GGGCAGTGCT GCAGATATCA TTAACTGGC AATGGTTAAA TTTGCTCAAA	600
AAATGAAAGA GACAACATAT CAAGCTAAAC TATTATTACA AGTACACGAT GAATTAATTT	660
TT	662

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

TCATCCAAAT TTTGGAAATT CCACATTTTA CATATCGTAA TTTTTTAGGA AACTAGTGAA	60
TATAACAAAT CCCTCCTCTC ATTTTAAAA TAGATATATC ACTTCCCCAC TTTTACTTAA	120
CTAAACTGCA ACGGTTCCCTA ATACCAAAAT CCTGCCCTCT ATTTTATCA ATTCAAGCAT	180
ACTTATTGAA AAATGTTAAC GTTTTCTGA TAATCATTGT AAGCGCATTT ATTTTATAAA	240
CTAACGTTTG AAATATACTA CAGGAGTGAC ACGTAATGAC TCAAATTACT GAAAAAGAAT	300
TAAAAAGAA GTATTTAGAT TTACTATCCC AAAATTTTGA TACTCCAGAA AAAGTTGCAA	360
CTGAAATTAT CAATTTAGAA TCAATTTTAG AATTACCTAA AGGTACGGAA CATTTCGTCA	420
GCGATTTACA TGGTGAATAT GAAGCTTTC AACACGTATT ACGCAACGGT TCTGGGAACG	480
TGCGAGCGAA AATCAATGAT ATTTTCAAAG AGAGACTTTC AACTAAGGAG CTTAATGACT	540
TAACTGCTCT TGTCTACTAT CCAGAAGrCm AATTtAAAAT TgATTAAAAG TGATTTCCAA	600
AATTgCGGtC mActTAATGt CyGGtATATC ACaACmATCG aACATTTAAT TGAGTTAATT	660
AAATATTGT	669

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CACATGGCTG TTAGAGATAT GAATGGCCAT GCGTTACCTT TAACAAAAGA TGGCAATTTT	60
TATCAAACGA ATGTAGATGC AAATGGTGTT AATCATGGTG GTAGTGAAAT GGTGCAAAAT	120
AAAACAGGTC ATATGAGTCA ACAArGCCAT ATGAATCAGA ACACACATGA ACCAACAGCC	180
ACACATGCAA CAAGGTCATA TGCAATCATC AAACCATCAA ATGATGAGTC CAAAAGCAAA	240
TATGCATTCA TCAAATCATC AAATGAACCA AAGTAACAAA AAAGTTTTAC CAGGCTGG	300
TGAAAGTATG ACATCAAGTA TTCTTACTGC AAGTATTGCC GCACTACTAT TAGTATCTGG	360
GTTATTCTTA GCATTTAGAC GACGTTCAAC AAATAAATAA ACATAATACG ATTAATAATA	420

GAAAAATCGT GTGATTATCT GaGGGAGCCT AGGACATAAA TCAATGTCCT AGGcTcNCTA	480
AtGTTATATT GGCAGTAGTT GACTGAATGA AATTGCGCTT GTAACAAGCT TTTCCATTTC	540
TTACCAACTC CCTAAATAGT CATCAAAAAA TTTCTTATAT TTTAATAATT TTTAATAATC	600
CGATTGTCTT ATACGTGTCA GTGTTAATTC AGATATTTCC TGTGGAATAT ACCACTTATT	660
AATCATAATT GGATAAGGTG tTTGTGCGTA CAGTGTTCa ATAATCAGCC AACAATGTGT	720
ATCACCaTCA AACACGTGAC TATGATTTTtk GAAGTGGGGC GCTTTGGTAA TAGACATTTT	780
TAAATCTGAT TGATATGCAT TGCTATAAAT CGTTTGCTCA ACGAATGTCT TCATGTCGTC	840
TTCGTTTTGT GTATTCACCT TAAATGTGTC AATGACATTT AACGGTATAA AGGTAAAGCA	900
AAATGCATCA GCTTGCTTAG AATGATTGTC CTTTTTTTGA TAATAGCGTT CCATTGCAAT	960
GACGGCAGAA GGATGGTTTG CAAACAAATG ATTTGTATAT TCACTTTCTA AATCAACACG	1020
ATAATTAATT GATGACATAG ATACGCGAGC TAGCAATATT TGATCAAGTG GATGCTTAAA	1080
TTGATCCATA CTTGAAGCGT GTTGGGCATT TGTTTGTGGA ATAACAAAGT GTCCCTTCCC	1140
TCTTGTACTC TCTACGATGC CATCTTCGGC TAACAATTTt ATAGCTTGGC GCAAAGTCAT	1200
ACGACTGGAC ATCAAAGCGC GCACAAAGTT CCTTTTCAGT AGGTAATGC	1249

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

AATGATGATT CATTCAAAGA AATTAACGCT CGGTATATGCTTGGTATTAC TCATTATATT	60
GATTGTAGGT TATGTCATTA TGACAAAAAC AAATGGTCGA AACGCCCCAA TTAAGACAC	120
ATTTAATCAA ACATTAAAAT TATATCCAAC CAAAATCTC GATGATTTTT ACGATAAAGA	180
AGGCTTTTCGA GATCAAGAAT TTAAAAAGGG TGATAAAGGT ACTTGGATAG TTAATTCTGA	240
AATGGTAATC GAGCCAAAAG GTAAGGATAT GGAAACGAGA GGAATGGTGC TCTATATCAA	300
TCGCAATACT AGAACCACAA AAGGGTATTA TTTTATAAGT GAAATGACAG ATGACAGTAA	360
CGGCAGACCA AAGGATGATG AAAAAAGGTA TCCGGtAAAA ATGGAACATA ATAAAATCAT	420
ACCAACGAAG CCACTACCGA ATGACAAGTT AAAAAAGAG ATTGAAACT TTAAGTTCTT	480
TGTACAATAT GGCAACTTTA AAGATATTAA TGATTATAAA GATGGTGATA TTTCATATAA	540
TCCTAATGTA CCAAGTTATT CGGCAAAATA TCAATTGAAT AATGATGATT ATAATGTCCA	600

ACAGTTaAGa AAAAGATATG ATATTCCAAC CAAACAAGCG CCGAAATAT TATTGAAAGG	660
CGATGGAGAT TTAAAAGGTT CATCCGTAGT TcTAGAAGTC TTGAATTTAC CTTTGTGCGAA	720
AATAAAGAAG AAAACATTTA TTTTACAGAT TCTGTACAAT ATACTCCAAG TGAGGATACA	780
AGGTATGAGT CAAACTGAAT ATCAAATAAA ACCTGGTAAT ATAACAAGTA ACTCTGAAGA	840
AACAAGTTCG ATATCTAAAG TGAGCTGTGA AATATAGGTA GCCATTTCAA AAAATTTAAA	900
GGTGAATTTG ATAATGTAGC TCAAGGAGAT TGGGTAAAA AGGCGAAGAA TGAAGTGGAT	960
GATATTAGTA AGAAATTAAA AAATATTCAA AGAACGGAAG TTTAATAGCT TATATGATTC	1020
TTGGAGCTAA GACAGCATGC GTTCATTCAT GCCATTATTA ATATAAGCAC CGCAACAAAA	1080
AAGCTTCTAA TGTGATACAG GAACCTCATA TTCCGTATCA TGTTAGAAGC TTTTAATGTC	1140
TAAAGAACAT CTACATTTTA TCATATTTTC TGAAGTATTA AACTTTTATA TAATTAAATA	1200
TTTCTTAATT TTCCAAAATA GTGATAAATT TGTGAAATAC ATCACAAATC CCTTATTTA	1260
TTTGGAATT CATGTAATAT TAGACTTGTA AGAAGTTAAT AAATAGAGAG AGACGAGAGA	1320
GTTTATATAA ATACTATATA AACATTGGAG TGATGATTAT GAGAAAAGAG ATTGAAGCGC	1380
TTATTTTCTC AGACGTAAtA GCTATGATAT TTACGTGAAC ACTGGTGTAA ATCAAGGATT	1440
AATTGGTGAC ATCAAAGATG GTTACCTAAC TATTGATTCT ATGCCTTACA TTGATGCTGA	1500
GCGTTTGTAT CACTTTGCTA TGGAACGTAA ATCGTTAGTC ACTAACTAGT TCTTATTGCC	1560
AATGATTACT ACCCCTAGTC GCGGCAATT GAAGTGTGAT TGATGTAACT TGCCCTCGTT	1620
GGTGAGCAAT TGAGGGCAGA CCCCTTTAAT TAAGTAAACC CTAACCTCCC ACAAATCTGG	1680
AACGATACTA AAAGCCACGT CCTATATTGG ATGTGGCTTT AGTCAKACTT ATATTATTTT	1740
tAAAACGATT ACCTACAAGA TTTACATATA AAATTCTATC ATGnCTGC	1788

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GCAAGTTTAG TTAAACAGAT ATTAAAACCA GATCAATATA CAGATGCAAA TTCTCTATA	60
GAGATTAGTT TGCAAACAGG TATGTTTATT GCAGGTGGAT TATCAGGAAT ATTATATAAA	120
ATAAATGGAT TCACTCTAAT TATAGCGATG ACTATAATGA TGTTTCTAAT CAGCATTTTT	180
ATGTTATTTA GATTGCATGT AGATAAACCA ACTCATTCAG AGGAAGAATC AACAAATAGC	240
TTATTGCAAG AATATTTATT AGGATGGAAA TTTTAAAAAG ACAACATGAT GATATTTATT	300

TTTGGAGTTA	TTTCAATCAT	ACCAATGGTG	TTTACAATGA	TCTTTAACAT	ATCATTACCA	360
GGATATGTTT	ATAATGTTTT	AAAACCTTCG	TCTGTACAAT	TTGGTTTTTC	AGATATGTTA	420
TATGGCATTG	GAGGATTATG	TGCAGGTTTA	ATTTTCAGCA	TTCTTTTCGAA	GAAAATCTCA	480
ACTAAAGTAT	TGATATTTTT	GTTATATTTT	ATATTAGTCA	TAAATTCAGC	ACTATTTATT	540
TGGATAAACT	CAGCATTTTA	CTTATTCATA	GGATCATTTA	TACTAGGCTA	CTCAATTTCA	600
TCAATCAGAA	TTTATATGAA	TACAGCTATA	ATGAACACTG	TTTCAGATAA	ATATGTCGGT	660
CGCTCATTTA	CGATATGGAC	GTCAATTTCA	TTGTTACTGC	AAAGTTTAAT	TGCTCCATnT	720
TTAGGAAGAT	GGATTAATGA	AATTAATGAT	AAATTCGGTT	TCTATATTAT	ACTCATTTTA	780
TCCTTACTCA	TATTTGTaCA	CTGCTGCTTG	TTAACAAAAC	AGACAAAATA	AAATATGCAC	840
ATAAGAAGA	GTGACCGTCA	CTCTTCTTTA	ACAAGCGACC	ATTTATCGaT	GGGCTTAGTT	900
CTCTCTGCAC	CCACACTTCA	CTACTTCACT	TTTTCAAATC	ATTTTTTATG	GTCTTAAATA	960
AATCAGTGAG	ATTTGTTGCT	TCGGTAAAGT	CTAGAATTAA	TATCATTTCT	TTAGAACCTG	1020
GATATGGCGA	AACTAATGTA	TTATCTTGCA	ATTTCTGCTG	GGCACTTTA	GTCGCCTTGA	1080
CCAATAATCT	ATTATCATAC	AAACCACCTA	TAACCACGCC	ATCATAATAA	ATAATATATT	1140
CTCCCATCAT	CTTTCTTGTC	TTAACCGCGT	TTGAATTCAC	ATGATTTAAA	AATAAATCAT	1200
GTACATCTTT	CTTAGTCGCC	ATTGTAATCG	CTCCTTCAGT	TTTATGTTTA	ATCACATTGC	1260
TATTAATGAT	TCATTTTCGTG	TTGCTCTTAA	TTTTATCTAT	AATTATATGC	GTAGTTAAAA	1320
TCAAACCTAT	GGAAAAGAAA	ATAATGATAA	CAATGTTAAG	AAATATAGTT	ATAAAATTAT	1380
AGTTTGGAAG	GTATGCGAAT	AGCAGAAAAA	TAGGTATCGC	AAAAAATAAA	TCCCACCAAC	1440
CTAAACTTTT	TAAAGAATGC	TTTAAACCTT	CCATAATATC	ACCTTTATAA	ATTTGTCTTT	1500
GTTATAAGAT	AACTAAAAAA	TCGCTTTACT	GTAAGAGTAG	CCAAAGAAAA	TTCTGAATCA	1560
TATTCATAAG	TAGTGTATCA	TTAATAATGA	ACAATTTAAT	ACTATAATCC	TTGATCTTTG	1620
TATTGATCAA	CTTACCACAA	CATTTATTTT	AGACTACTCT	TAGACTTCCC	TTCAAATGG	1680
TTGCATCTAT	TGAAATTCCT	TTTGTATAAG	TTAGGCTTTT	GTGGTAATAT	CATCATGCAT	1740
AAAAAATCGA	GATACTAATT	ATAAAGAGGG	TATAAATATA	TTATGAAAGA	AAATTTTTTG	1800
AGTGAATTAC	CACGTCCATT	TTTTATTTTG	GCGCCAATGG	AAGACGTTAC	AGATATCGTC	1860
TTTCGACACG	TTGTAAGTGA	AGCAGCTAGA	CCGGATGTGT	TTTTCACTGA	ATTTACAAAT	1920
ACTGAAAGCT	TTTGCCACCC	TGAAGGCATA	CATAGTGTGC	GCGGACGCTT	AACTTTTAGT	1980
GAAGATGAAC	AGCCGATGGT	CGCTCATATA	TGGGGAGATA	AGCCAGAACA	GTTCCGTGAA	2040
ACGAGTATTC	AATTAGCTAA	AATGGGCTTT	AAAGaATAG	ACTTAAATAT	GGGATGTCCT	2100

GTAGCAAATG TTGCTAAAAA GGGTAAGGGT TCCGGCTTAA TCTTAAGACC TGACGTTGCT	2160
GCCGAAATTA TTCAAGCGAC TAAAGCAGGT GGGCTTCCGG TAAGTGTTAA AACACGCCTT	2220
GGCTACTATG AAATCGATGA ATGGAAAGAT TG GTTGAAGC ACGTCTTCGA ACAAGACATT	2280
GCCAATTTAT CTATTCATCT TCGTACACGT AAAGAAATGA GTAAAGTAGA TGCACATTGG	2340
GAATTAATCG AAGCTATTAA AAATTTACGT GACGAAATTG CACCAAATAC ATTGTTAACA	2400
ATTAACG	2407

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

ATGATGnATG GnCCGCCAA GAAGTTGAAC CAGTCTATTG GCTAGAATTG CTCAAAAAGC	60
GAGAcATGTG GTATTCaTAT GTTaGTAgCt ACGCAAAGAC CATCTGTCAA TGTAATTACA	120
GGTTTAATTA AAGCCAACAT ACCAACAAGA ATTGCATTTA TGGTATCATC aAGTGTAGAT	180
TCGAGAACGA TATTAGACAG TGGTGGAGCA GAACGCTtT TAGGATATGG CGATATGTTA	240
TATCTTG GTA GCGGTATGAA TAAACCGATT AGAGTTCAAG GTACATTTGT TTCTGATGAC	300
GAAATTGATG ATGTTGTTGA TTTTATCAAA CAACAAAGAG AACCGGACTA TCTATTTGAA	360
GAAAAAGAAT TGTTGAAAAA AACACAAACA CAATCACAAG ATGaATTATT TGATGaTGTT	420
TGTGCATTTA TGGTTAATGA AGGACATATT TCAACATCAT TAATCCAAAG ACATTTCCAA	480
ATTGGCTATA ATAGAGCAGC AAGAATTATC GATCAATTAG AGCAACTCGG TTATGTTTCG	540
AGTGCTAATG GTTCAAACC AAGGGATGTT TATGTTACGG AAGCAGATTT AAATAAAGAA	600
TAATTATGAG TAAGGAGTTT TATATAATGA CACACTATCA TTTTGTCGGA ATTAAAGGTT	660
CTGGCATGAG TTCATTAGCA CAAATCATGC ATGATTTAGG ACATGAAGTT CAAGGATCGG	720
ATATTGAGAA CTACGTATTT ACAGAAGTTG CTCTTAGAAA TAAGGGGATA AAAATATTAC	780
CATTTGATGC TAATAACATA AAAGAAGATA TG GTAGTtAT ACAAGTAAT GCATTCGCGA	840
GTAGCCaTGA AGAAAtAGTA CGTGACATC AATTGaAATT AGATGTTGTA AGTTATAATG	900
ATTTTTTAGG ACAGATTATT GATCAATATA CTTCAGTAGC TGTAAGTGGT GCACATGGTA	960
AAACTTCTAC AACAGGTTTA TTATCACATG TTATGAATGG TGATAAAAAG ACTTCATTTT	1020
TAATTGGTGA TGGCACAGGT ATGGGATTGC CTGAAAGTGA TTATTTTCGCT TTTGAGGCAT	1080
GTGAATATAG ACGTCACTTT TTAAGTTATA AACCTGATTA CGCAATTATG ACAAATATTG	1140

ATTTGATCA TCCTGATTAT TTTAAAGATA TTAATGATGT TTTTGATGCA TTCCAAGAAA	1200
TGGCACATAA TGTTAAAAA GGTATTATG CTTGGGGTGA TGATGAACAT CTACGTAAAA	1260
TTGAAGCAGA TGTTCCAATT TATTATTATG GATTTAAAGA TTCGGATGAC ATTTATGCTC	1320
AAAATATTCA AATTACGGAT AAAGGTACTG CTTTTGATGT GTATGTGGAT GGTGAGTTTT	1380
ATGATCACTT CCTGTCTCCA CAATATGGTG ACCATACAGT TTTAAATGCA TGGCTGTAA	1440
TTGCGATTAG TTATTTAGAG AAGCTAGATG TTACAAATAT TAAAGAAGCA TTAGAAACGT	1500
TTGGTGGTGT TAAACGTCGT TTCAATGAAA CTACAATTGC AAATCAAGTT ATTGTAGATG	1560
ATTATGCACA CCATCCAAGA GAAATTAGTG CTACAATTGA AACAGCACGA AAGAAATATC	1620
CACATAAAGA AGTTGTTGCA GTATTTCAAC CACACACTTT CTCTAGAACA CAGGCATTTT	1680
TAAATGAATT TGCAGAAAGT TTAAGTAAAG CAGATCGTGT ATTCTTATGT GAAATTTTTG	1740
GATCAATTAG AGAAAATACT GGCGCATTAA CGATACAAGA TTTAATTGAT AAAATTGAAG	1800
GTGCATCGTT AATTAATGAA GATTCTATTA ATGATTAGA ACAATTTGAT AATGCTGTTA	1860
TTTTATTTAT GGGTGCAGGT GATATTCAAA AATTACAAA TGCATATTTA GATAAATTAG	1920
GCATGAAAAA TCGTTTTTAA TATGTTTATA ATAGAGTAGT ATGGGTATTT ATTATTAATG	1980
ACATTATTAC ATGTTAATTA GGAGGCGTTT TTAATGGATT GGATTTTACC AATTGCTGGA	2040
ATTATCGCTG CGATTGCATT CTTAATTTTA TGTATCGGTA TCGTAGCTGT ATTAAATTCT	2100
GTTAAGaAAA ACTTAGATTA TGTTGCAAAA AACTTGACG GTGTAGAAGG TCAAGTTCAA	2160
GGTATTACTC GTGAAACAAC AGATTTACTT CATAAAGTAA ACCGTTTAAC TGAGGATATC	2220
CAAGGTAAAG TAGATGTTT AAACTCAGTT GTAGATGCTG TTAAAGGTAT CGGTGACTCA	2280
GTACAAACGT TAAACAGCTC TGTAGATCGT GTAACAAATT CAATTACACA TAATATTTCT	2340
CAAAATGAAG ATAAAATCTC ACAAGTTGTT CAATGGTCAA ATGTTGCAAT GGAAATTGCA	2400
GACAAATGGC AAAATAGACA CTAC	2424

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 738 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CnATAATATT CnTCAAnCCT TTAAATAGAG GAATAGACTG CCGACAGAGT CCGAGACTTT	60
GTGGGTAGTT TTTTtagTTT TGATAACGGA AGTTAGAGGC TCTCTGTCAA ATTGGGCAGA	120

TGCATTCAGT AACGGAAGTT AGGCTAGTAA ACGTGTCTTA ACTTCCTTTT TGCATTTTGA	180
AGTGTAAAGT TTTCAACATA ATACTATTAG TTCGGTCATG TATCGGACTG ATGGAAAAGC	240
GTTTCACTTT TAATGACTCA TTAAGAACGG CCTGAAAATG TTTGGCGTAT TAAGTGCAAT	300
GATAGTTTTG ACATTTAGTT TCTAATTGGT CATTACTGCC GAGCAAATCT AGTAGAGTAA	360
TCATGTAAAT CTTTAATGTG CCATTTGATT CACTAGCGGT GTTAATAACT ACGGAAATTG	420
CATTTCCGAC TGAAATTTTT GAAAAATATC AACGTACGCT ACAAATAAAA TTTTAACTG	480
TTATAAATGT GTCTCAATTT CATATGTTCA TCGACGATAT GAAGCGTATT ATGGTAAAT	540
GAAGAAATAA TAACTTGTT AATAAATAAA ACATCACGAT TTGATAAAG CACTTTATTA	600
TTGTGTAGAT AATAGTTTTT TAACGAAATA AAAATGGCGA CTGGTTTTAA TAAATCAGCT	660
AATGAATCAC TACACCTATA AGTATGAATA TAGTGATTAG AATGCTTTGT ATAGTTGGAT	720
TTTGCAAAAT TGATGTTA	738

(2) INFORMATION FOR SEQ ID NO: 394: .

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

AAAAGTTGTA ATTAAAGTG GGATTTTACT TAAGnAGAA GGAACTATT TATATGACTA	60
ATAAAGAGn AGATGTCCGC AATATAGCAA TTATTGCTCA CGTTGACCAT GGTAACAA	120
CTTTAGTAGA TGAGTTGTTA AAACAATCTG GTATATTCAG AGAAAATGAA CATGTCGATG	180
AACGTGCAAT GGACTCTAAC GATATCGAAA GAGAGCGTGG AATTACGATT CTAGCCAAAA	240
ATACGGCTGT TGATTATAAA GGTACACGTA TTAATATTTT GGATACACCA GGACATGCAG	300
ACTTTGGTGG AGAAGTAGAA CGTATTATGA AAATGGTTGA TGGGGTTGTC TTAGTAGTAG	360
ATGCGTATGA AGGTACAATG CCTCAAACAC GTTTTGTACT TAAAAAAGG CTAGAACAAA	420
ACCTGAAACC TGTTGTTGTT GTTAATAAAA TTGATAAACC ATCAGCACGT CCAGAGGGTG	480
TTGTAGATGA AGTTTTAGAT TTATTTATTG AATTAGAAGC AAACGnTGAA CAATTAGAAT	540
TCCCTGTTGT TTATGCTTCA GCAGTAAATG GTACAGCTAG CTTAGATCCT GAAAAGCAAG	600
ATGATAATTT ACAATCATT AATGAAACAA TTATTGATTc ATGTACCAGC TCCAATTGAT	660
AACAGTGATG AGCCATTAC AATTTCCAAG TAGCATTGTT GGAACAAT GATTATGTTG	720
GACGTATTGG TATTGGTCGT GTATTCAGAG GTAAAATGCG TGTCGGAGAT AATGTATCAC	780
TAATTAAATT AGACGGTACA GTGAAAAACT TCCGTGTAAC TAAATCTTT GGTTACTTTG	840

GATTAAAACG TTTAGAAATT GAAGAAGCAC AAGCTGGAGA TTTAATTGCT GTTTCAGGTA	900
TGGAAGACAT TAATGTTGGT GAAaCTGTAA CACCACATGA CCATCAAGAA GCATTGCCAG	960
TTCTACGTAT TGATGAGCCT ACTCTTGAAA TGACATTTAA AGTTAACAAT TCTCA ATT TTG	1020
CTGGCCGTGA AGGTGACTTT GTAACAGCAC GTCAAATTCA AGAACGTTTA AATCAACAAT	1080
TAGAAACAGA TGTATCTTTG AAAGTTTCTA ACACAGATTC TCCAGATACA TGGGTAGTTG	1140
CTGGTCGCGG TGAATTGCAT TTATCAATCC TTATTGAAAA TATGCGTCGT GAAGGTTATG	1200
AATTACAAGT TTCAAAACCA CAAGTAATTA TTAAAGAAAT AGATGGTGTA ATGTGTGAAC	1260
CATTTGAACG	1270

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

AAGACCAGGA GAACAmGTAA AACAATATAC AGTTGaAATC GCTCGTAAAT TAATGGAATT	60
TGATATAAAA TGCTCGTGAT TGCTTGTA AA TÆGCAACTG CTGTnGCTTT AGAATATTTA	120
CAAAAGACCT TATCAATCCC CAGTGATTGG CGTAATTGA c CAGGTGCTAG AaCAGCAATA	180
ATGACTACTA GAAATCAAAA TGTATTAGTA CTAGGAACGG AAGGCACAAT TAAATCTGAA	240
GCATATCGTA CGCATATTAA ACGTATCAAT CCACATGTAG AGGTACATGg CGTTGC CT	300
CCAGGTTTTG TGCCACTTGT AGAACAAATG AGATATAGTG ATCCAACAAT TACAAGCATT	360
GTCATTCATC AAACACTGAA ACGTTGGCGT AATAGTGAGT CTGATACTGT CATTTTAGGA	420
TGTACCCACT ATCCATTGCT CTATAAACCT ATCTATGATT ATTTTGGTGG TAAAAAGACA	480
GTGATTTTCGT CTGATTAGA AACGGCTCGT GAAGTTAGTG CATTGCTAAC ATTTAGTAAT	540
GAACATGCAA GTTATACTGA ACATCCAGAT CATCGATTTT TTGCAACAGG TGATCCTACT	600
CACATTACTA ACATTATCAA AGAGTGGTTA AATTTATCTG TCAATGTGGA ACGTATATCA	660
GTGAATGACT AGGAGGATTT TTAATGAAAG AGATTGTTATTGCATCGAAT AATCAAGGGA	720
AAATAAATGA CTTTAAAGTA ATATTTCCAG ATTACCACGT AATAGGTATT TCAGAACTAA	780
TACCAGATTT TGATGTGGAA GAAACAGGAT CAACATTTGA AGAAAATGCT ATATTAAAAT	840
CAGAAGCTGC TGCAAAAGCA TTGAATAAAA CGGTCATAGC TGATGACAGT GGA CT AGAAAG	900
TTTTTGCATT AAATGGTGAG CCAGGTATAT ACTCTGCACG TTATGCTGGT GAAAATAAAA	960

GCGATGAAGC AAATATTGAA AAATTATTAA ATAAGCTTGG TAATACAACT GATCGTCGTG	1020
CGCAATTtGT TTGTGTCATA AGTATGAGTG GCCCTGATAT GGAAACAAAA GTATTTAAAG	1080
GTACTGTTTC AGGTGAAATT GCAGATGGAA AATATGGCGA AAATGGTTTC GGATATGATC	1140
CGATATTTTA TGTACCGAAA TTAGATAAAA CCATGGCTCA ACTTTCAAAA GAACAAAAAG	1200
GGCAAATTAG TCATAGACGA AATGCGATTA ATTTACTTCA AGCTTTTCTT GAAGGTGATA	1260
AAAATGTCTA AATGGATTAT TGTGAGTGAT AACCATACTG AATCAGGGT TTTATATCAA	1320
ATTTATGAAA TGCACCCAGA TGCAGATGTA TATTTACATT TAGGA	1365

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

AATTCCTGGT GCAATAATAA ATAGGATGAA AAAGATTCGG AAAATATGAT AACTCGTAAT	60
CATAGCAACA TCGGCACCAG TAGCTAATGC AACTAAACT ATCTGATTAA CCCCTCCTGG	120
TGCTGCACCA AGaACAATT CATTAATAGG ATTATTATCA AAGAAATGTA TGATATAAAC	180
CATGATTAGC GCACCAATTA TCAACATAAT ATTTTGAATT GTAATTGCGA TTGCTAGTCT	240
ACCTTTTAAA TCTGACAATA AATGCGCAAT TTGAACTCCA ATTCTAATCA TATATATTAG	300
TTGTGCCATG TTCAACAACC AATGATCTAG TGTAATGTT AAACCTGTAG AAAAAATCCA	360
AACAATTAAT ACAATGAGTG GTGCTAATAA TTGAAATGTT GGAAACTTTA TTTTAGACAT	420
AATTAGATAA ACTATAAAGA TAGCTATCGC TAAAATAACT ATTTGCCCTA TGTTTAATAC	480
TTGTGATAAA GGCAAGACTT TTGTTAACTT TCCATTCGCA TGCATGTTACCATCATGAAA	540
AAAATATGAA ATGAACGGTA CTAAAACAAC AACAAATATA ATTCGTGATG TTTGCGTTAA	600
GCTAACAACT AACAAATTAG CACGTTTGTC TTGTTGAGCC ATGACCAGCA TTTGTGTTAG	660
TGCTCCTGGT ATAACACTTA AAATAGCTGT TTCTGTATTA ATACGTGCAA TTTTTTTAAA	720
AACAAATGCC ATTACTATTG CAATTAATAA TATCGAAATA GATACAACAA TAATCGAAAG	780
CCAATTGTTT TTAATATCCA TAACGACATT TTTCGTAAAC GTTGATCCGA TTTGCACACC	840
TAATAGTACA ATACCTAATT CACTAAGTAA GAATGGCCAT TTAATATCAA GTTTGAAAAC	900
TTTTACACAA ATGATTGATG CGATAATAGG ACAAACATA AATGGAAGTA ATACGTGCGA	960
TGAATACAGT AGAATACTAA TAAAAAATGA TAAACGAAC ACAATGAAAT TATTTCTATA	1020
TATCATTGCC ATGTTTTCCA CTTCTTTCAA TAAAAAATAA AATGACTAAA TTGCTGCTTG	1080

AGCTTCACGT TTGTTAAGAT AACAAATATCC GCTAGCAGTT tTGACTACAA AGCATAATG	1140
GaCTTTTCACT ATCAAGTCGC CGCCCATGCC TTATATACAT TTAAAAAnGAG CCTGAACAAA	1200
GTTCAGGCTC TCAATTTGTC CGTATATTTA TTTTACAATA CGACTTAAAG CCGTATCAAA	1260
TGCTTGAATC GTTTTTCAAT ATCTTCTTTC GTGTGTGCCG TAGATAAGAA TGTACCTTCA	1320
AATTGAGATG GnGGnAAAAA CACACCTCTT TGnCATTTCTC GGTACATTTT TGCAATAATT	1380
TCC	1383

(2) INFORMATION FOR SEQ ID NO: 397:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

TCCACTAAAnA TGATTACAAT TGCATTAGTT TGGTGGAGTG CATTTACAAT CTTAACGGGT	60
ATGATTAAGA ACCACGGTTT AATTaTTTAG TGAGATCTT ATTTGGTGTA GGTGAGGCGC	120
CAATGTACCC TTCTAATGCT GTGTTTAATT CATTTTGGTT CTCTAAAAAT GAAAAAGGTA	180
GAGCATCAAG TGCATTATTA GCAGGATCAT ATTCGGACC TGTATTAGCA CCAATAGTTA	240
CAATTGCTAT TGTTAACGCA TTAACTGGC AAGCAGTATT TTACATTTTT GGTGCAGTAG	300
GTATTTTAAT GGCKGTATtA TGGGCGATTA TTGCCAAAGA CTTACCTGaG CrACATAGwa	360
TGGTTAATGA AGCGGAGAAA CGTTTCATTA TGGAAAATCG TGATATCGTA GCTAC	415

(2) INFORMATION FOR SEQ ID NO: 398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

TTTTAGaTaA aTyCAATTnT CyATaCTaAA TgATTnTCTT ATTaCGTCAA TTcGCCTTTT	60
aTTTTATCGT AATCTTTCCa CTGCAAAGCT AAAGCTTCTC CTATTCTAAG ACCAGAATAA	120
AATAACAGTC TAGTTAGCTG ACGAGAAGTA TCATTTGTGA TTTGTTCTAC TTTTTCATCA	180
AATTCTTCAC GAGTGATAAA TTTAGCTTGT GGTTTTGTTC TGGGAATAGG AGTTACCGAT	240
AATGTGGGGT CGTATAAGAG CTTGTAATGC TTTTGGGT AATTGATAAC TGCTTTAAAA	300

CCTGCCCACA CAGATCGTGC ATAGTCAACA GAAAGACCTG CATCGTTTAA CAAATAATTC	360
CTGAAAGCAG TACATTGCGT AGTAGTGATT TTGCCAATAG GGATATTTCC GAACCTTTCT	420
TTTATGTGAG TATTATATTC TGTAAGTTCGC TTTTCTATTG AGCGTGCAGA AAGATTTTCA	480
TTTTTTTAAAC GATCAAAAAA TATATATTCA AAGGGTTGAT TGTCCGAGTA TCCATATTTA	540
ACATTTTGTA TAAATTCGCT TTCAGCTAGT TTGGCATCTT TCTTACGTTC AAACCCACGC	600
TTCATTTTTC GTTTGTTATT ACCGTATACA TCTTTATATC TAATGGAAAA ATACCATTTA	660
CCTGTATTAT CATCCTTATA TACTGGCATT TTGCTTCTCC CTCCTCAAAA TTGGCAAAAA	720
ATAATAAGGG TAGGCGGGCT ACCCGAAATT TAGTACTAGG TACTAAATGT GATATAATAA	780
AATAAAAAGT AGGTGATGTT ATGACATTTA AAAACAATCA TAATTTCAAT GAATTAGTTT	840
TAACGAATGA AGACATTAGA ATTTTAAAAA ATGTCTTAGA AGATGAGTC AGTGTTTATG	900
ATGAATATTC GGTATGTAAT GAAGAATCCG ATTTTGCTTA CTGTTTATTA AGAGACTTAT	960
ATACATTAGA CAGCTTAGCT ATTTGCTCAA ATAATGTTTG AATTATCGAA TTGTACTCTT	1020
CGATTTTAAT ACCATGCATA ATAGAGTTTC TGTGTTCAAT AGCAGCTTTG ACTGAATGTk	1080
TTAAATGTTC TTCTATTAAA TCGTTGTTTk CCAAtTCGtK TAaAAATGTt CyTATATTCC	1140
T	1141

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 706 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

ACTGTGGTAG GTTTTTTATT TTGAAGTATT AATCATAACA GACTAATAAT CATGAGGTAA	60
CTAATAACAC ATATTAACT TGTATTCTTA AACTGGTATA ATAAATTTAT GTTGAAATGA	120
ATATTGTATG ACAGGGTATT CACTTTTATT AAAAGGTAAA ATTAAATAAA GGTTTTATAG	180
AACGTATTTA AATATATGAG GAGTAAACAA ATGGCTGATA GAACGAATAA AGAAATTAAA	240
ACAGGACGCT TTATTGCAAC TGCATCAATC GTATTCTCAA TATTATTG TATTCATTAC	300
TTTGTTTCGT TGGATAATGC GACTGCCAAA GCATTACTTA ATTTAACGAA TCAAAACACT	360
TCAGATAAAG CGATTGATTA CATTTTAAAC AGCTTTAGAT TCACTGGTAT TATGTATATT	420
TTGGCTTATC TAGCAGGCTT CATCACTTTT TGAATCGAC ATACTTATGT GTGGTGGTTT	480
ATGTTTGCAG TTTATGTATC AAATAGTTTG TTTACGTTGA TTAATTTATC AATCACAATT	540
CAAGCAATAA AAGCTGCACA CGGTGCGTAC TTAACATTGC CAATTTTAAT TGTTATTATA	600

GGTTCGGTTG CATTAGCGAT TTATATGCTT GTTGTCTTCTA TCAAACGTAA AAGTACATTT 660
 AATCGCTAGA AAATTGATTT TAACAATAAA AATATGAAAA AAAAnn 706

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

ACACAATCTG AAGATTCACG TTGTGGTGCT GGACATGATC GAAAAATTAG AGCTGAACAA 60
 ATGAnAGAAA TCAGTGATTT TGTTAAAAAG AAAAATATCC CTAAAGATGA AACGGTATAT 120
 ATAGGTGGCG ACCTTAATGT CAATAAAGGC ACTCCAGAGT TCAAAGATAT GTTAArAAC 180
 TTGAATGTAA ATGATGTTCT ATATGCAGGT CATAATAGCA CATGGGACCC TCAATCAAAT 240
 TCAATTGCGA AATATAATTA CCCTAATGGT AAACCAGAAC ATTTAGACTA TATATTTACA 300
 GATAAAGATC ATAAACAACC AAAACAATTA GTCAATGAAG TTGTGACTGA AAAACCTAAG 360
 CCATGGGATG TATATGCGTT CCCATATTaY aCGTTTACAA TGATTTTTCA GATCATTACC 420
 CAATCAAAGC CTATAGTAAA TAGTGCTCAA CTAATAATA ACTTGCTtCG TTCTAAAAGG 480
 ACGAAGCGAG TTATATTGTT AAAATTTGAA TTGACTTACA TTTTAATAAA ATCATCTTAA 540
 CAACTTTAAT TTTTCaTTAA TACAaGTCTT TATCTACAC TCAAACnAGA TTCATACACT 600
 GCACGTCATA ATAAATCTAT CTATTCAAAT ATAAATAAAA GTTACCTACT ACATTCTATG 660
 TAGCAGGCAA CTTTTATTAC TTATTTCTTT TCATTATCAT TAAGTACTTT TACAACTTC 720
 ACATTATGTG TCTTCCAATC AACTTCATAT AATGCTGATA ATTTTCTTC TTTTTTATe 780
 ACATGGTTTT CACCAGACCA ATAGCCCCAG AAACCATGGC GATTCCAATC TATTTTAAAC 840
 TCATCCATTG ATCTTTTATA ATGAACAACA AATTGTGATT TACCTTTGTC TTTTTTATCA 900
 TGTGACATAA CAGCTAAAAA TTCTGGATTA AACCTTCAG ACACAGTTAC AGGCATTTTG 960
 TCTTTAGGTG TGAAATTATC TTTGCCCCAT AAATTTCCAT TTCGTGTAA AGAAAAAATT 1020
 TCACTTTTAG TTCTATTATC ACTATCATTA GTTAATTGTC TCGTATGGTC ATGTCCCATA 1080
 TTATTTATCA AATGTGCTTC TACTTTCCAA CCTACACCTT TATGTGACGT AGATTGATCA 1140
 AGTAATGTAC GATATGATGG TTGTTGATAA CTAATCGTCTCTGAATA 1187

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 847 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

CCAGAATTAT TTTTTCAAAA AGGACAATTT AACAAATGTCG ATAACGTTAT CATAAGCAAA	60
CCGATGAAAG GGACAATGCC TAGAGGTAAA ACGGAaGCTG AAGATCAACA GTATTATAAA	120
ACATTGCAAA CTTCTTCGAA AGATCGTGCA GAAAATGTCA TGATTGTTGA TTTACTAAGA	180
AACGATATAG GGAGAATATC ACAGAGTGGC TCAATTAAGG TGTATAAACT ATTTTTTATT	240
GAGGCATATA AAAGTGTATT TCAAATGACT TCGATGGTAA GTGGAACTTT AAAAAATAAT	300
ACAGACTTAA CTCAAATTTT AACATCGTTA TTTCTTGTG GTTCGATTAC AGGTGCACCG	360
AAAGTGAATA CAATGAAATA TATTAAACAA TTAGAAAGTT CACCTCGTGG TATATACTGC	420
GGACAATTGG ACTATTACTT CCAACTGAAG ATGATAAAAT GATTTTAAAT ATCCGATTC	480
GCACTATTGA GTATAAATAT GGACAAGCGA TTTATGGAGT CGGAGCAGGT ATTACAATTG	540
ATTCTAAGCC AAAAGATGAA GTGAATGAAT TTTACGCAAA AACAAAGATT TTGGAGATGT	600
TATAATGCAA TTATTTGAAA CAATGAAAAT TGATAATGGA CATATCCCTA GACTTACTTA	660
TCATACTAAT CGCATAAAAT GTTCTTCTGa GCGATTAAAC TTTAAATTTG ATGAACATGC	720
ATGGCGAAAT GAATTAAACG ATGTAACAAC AAAGTATCAC AGTGGTCAAT ATAGACTTAA	780
AATCGTATTA AATGCTGAAA GCAAATTTGA AACGATAGTG TCACCTTTAC CTGAGAAAAG	840
TAGTTTT	847

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

TGAAGATGAA GCAGAAGCAG AAGACAATCT GCTACGAGTA CAATCGAAGA AAGAAGAAGT	60
GTATCGTCGA TTAAGTGCTT CTAAGTAAAC AAGCGTTCCT GAAAGtTTAT CATCATGAAA	120
AATGAAATTG ATCATGAAGT TCGTGATGTT AACGAACAAT TTAGTGAACG TCCAATACAC	180
GTAAACAGT TAAAAGATAA AGTGTCTAAA ATTGTGATTC AAATGAATAC ATTTGAAGAT	240
GAAGCAAATG ATGTTCTTGT TAATGCTGTT TATGCAGAGA AATTAATCA ATATGGAAAT	300
AGATATCGTA AGGACTATAG CAATGTTGAT AAGAGCTTAA ATGAAGCTGA ACGATTATTT	360

AAAAATAATC GCTATAAGCg TGCgATTGAA ATTGCAGAGC AAGCTCTTGA AAGTGTTGAG	420
CCAGGTGTTA CTAAACATAT TGAAGAAGAA GTTATTAAGC AATAGAAACT AGTATGTAGT	480
TATACTTAAA TAATATGAGC ACTCTGTCAA ATTGGACTGA TGAGTTTAAT AATTGAAGTT	540
AGCCAACGAT ACGTTGTCTA GCTTCTTTTT TATATGGATA AATGaAAGGG ACAATAAATA	600
TAAATAGCAA TTGTTTAAAG ATAAACGTAA TCAAATGTGT TGTTTTAATT AATATAAGTA	660
GTGAAAAAAG CATAATCACA CAGCTGTTTA AATAGAGTGA AATAGTCTAA TTCTTATTTA	720
ATAAGTAGAA ATAAGATTAT	740

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

ATGCCAATAA TTAAACCATG TAATAAATAT ACGTATAGCG TACGACTACC AATATAAGTA	60
TATAATTTTT TCTTTGTTGA CATTAAATTT AGAAACGCAG TCATTGCGAT AATATAATT	120
CCATATAATA TAAGTCGTTT AAAAGGACTG AATATACTCT GTCCTTCATT TTCAAGTGAA	180
GTATATGGTG AACTTCCCAA TAACCAATCT GCATTGATAG GATGAATCAC GTAAACGATA	240
AAAAACAAAA TAAAGGTAAT GATAGATACT GGTATTAGTT TTTTATTTTT AAAAATAGCC	300
GTATGTTTTT TGGTGAAAAT GTAACCTAGA TAAAATATTG GGAAAAATAC GATTGTCCTT	360
GAAATGCTTA AGTAGCTATC GATGTTATCT GAAAAACCTG CTCCAATAGA TATAATAATT	420
GAAACTGATA GCACTTTATA TGGATTAAAT CTTCTAACTA TTACTAAAAT GACATGAAAG	480
AAAAATAGCG TGATCAAAAA CCATAACGCA AACTGGGT TAAAAGGATC AAGTTGTAAT	540
TCGTCACTTT TACCTGTTAA GAAATAATAA ATTGAAAAGA ATGCAAAAAA TATCATATAA	600
GGTACTATCA AACGTTTTGA AATTTTTTCT	630

(2) INFORMATION FOR SEQ ID NO: 404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

ATTTAAACGT TCAGTTTCTA AAAGTGGAAAC AATCCAAGAA GTACGTAAAC GTGATTTTA	60
CGAAAAACCA AGCGTAAAC GTAAAAAGAA ATCAGAAGCT GCACGTAAAC GTAAATTCAA	120
ATAATTAATA CCTCTGTTGA CTCCCTCAAC ACGAATATTA ATTATATAAA ACAAACATCA	180
CAAGTTAGTG TCTGACACTA ATATGTGATG TTTTTTTGTT GTCAATTTTT AATTAAAAAA	240
AGTTATATAG TTTATAAATA ATCAAATTGA TATTCTATAG GTTCTTATAA CTATAAAGTA	300
TATTCAATTT CATGTATAAT TAATGTGAGG GCGAGGTGAA ATTGTGAGTT ATAATAATTT	360
TTTACAAATG ACAACTATCT TGGAAATCAAC GGCTGGAGAT ACTTGGGTTG AACAAGTTAG	420
CAATATAATT GTTCAACCTA TTTTACGTT AATATAACC TGTTTGACAT TCTTAGGATT	480
TGTATATCAA CTTTACTCTA AAAAAATCAA TGCAGCTGGT ATTATCGCCA CATTATCATT	540
ACTTATTTTA TTTTGGGAT TTCTAATCCA AGGAAATGTC AATATGCATT CTATCTTAAT	600
ATTCTCAATT GCGTTATAT TAGTTGTAAT TGAATTATTT GTAGTTGGTG CAGTAATTGG	660
TATTATTGGC ATGATACTGA TAACTATAAG CATAACAACG CTCGGTGATA ATTTGCTATT	720
TATGCTTGCG AATGTTATCG TTGCCTTGAT TTTAACGATT GTAGAATGGG TGATATTAGT	780
GAAGATTTTC AACAGAAAGA TTCCGTTTTT GGATAAAGTT ATCTTAAAAG ATTCAACTAA	840
TTCTGAGTCA GGTTACAAAT CTCATGATAA CCGCTCGCAC CTCGTAGGAA AGACTGCTCA	900
AACAGTTACA GATCTTCGAC CTGCAGGGAT TATTTTTTGT GAAAATGAAC GTATTGATGC	960
TGTTTCAGAT GGCAACTTTA TTTTGCGBAA TAAAACGGTA AAAATCCTTG AAGTTGAAGG	1020
AACAAGAGTA GTTGTGAGGG AAGTAGATTA ATTAAAAGGA GCATACCAT GTTTAGTTTA	1080
AGTTTTATCG TAATAGCAGT TATTATAGTA GTTGCATTAC TTATTTTATT CTCATTTGTA	1140
CCCATTGGTT TATGGATTTT AGCGTTAgcA GCTGGCGTTC ATGTTGGTAT AGGTACATTG	1200
GTTGGTATGC GTTTACGTCG TGTATCTCCA AGAAAAGTTA TAGCGCCATT AATTAAAGCG	1260
CACAAAGCAG GACTAGCATT AACAACAAAC CAATTAGAAT CGCATTATCT AGCAGGAGGA	1320
AATGTTGACA GAGTTGTTGA CGCTAATATT GCTGCACAAC GTgcTGACAT TGATCTTCCT	1380
TTCGAACGTG CTGCTGCAAT TGaCCTTGCA GGACGTGACG TATTAGAAGC GGTTCAAATG	1440
TCTGTTAATC CTAAAGTCAT TGAAACACCA TTTATCGCAG GTGTAGCAAT GaACGGTATT	1500
GAAGTGAAAG CCAAAGCTCG TATCACAGTT AGAGCTAATA TTGCTCGACT TGTTGGTGGT	1560
GCTGGTGAAG AAACAATCAT CGCACGTGTT GGTGAAGGTA TCGTTTCAAC AATTGGTTCT	1620
AGTAAGCATC ATACAGAAGT ACTTGAAAAC CCAGATAATA TTTCTAAAACAGTTTTAAGC	1680
AAAGGTTTAG ATTCAGGTAC TGCATTTGAA ATTTTATCAA TTGATATTGC TGACGTTGAT	1740
ATTAGTAAAA ATATTGGTGC AGACTTACaA ACTGAACAAG CATTAGCAGA CAAAAATATT	1800
GCACAAGCAA AAGCTGAAGA ACGTAGAGCT ATGGCTGTAG CAACTGAGCA AGAAATGAAA	1860

GCGCGTGTAC	AAGAAATGCA	TGCTAAAGTA	GTTGAAGCCG	AATCTGAAGT	ACCATTAGCT	1920
ATGGCTGAAG	CATTACGTTT	AGGTAATATC	AGTGTTAAAG	ATTATTATAA	TTTGAAAAAT	1980
ATCGAAGCTG	ATACAGGCAT	GAGAAATGCA	ATTAATAAAC	GAACTGATCA	AAGTGATGAT	2040
GAGTCACCTG	AACATTAAGT	CGAGAGGTGA	TAAATGAGT	GTCGGTATTC	TAATTTTTGT	2100
CATATCAGTG	ATCATTCTTA	TCATTACTAC	TATGCGCGAA	AATAGTCATA	AAGATAGACA	2160
AAATCAAAAAG	CCACCTCAA	AAACATCTAC	CGATAATGAA	CCAAAAAAG	GTGGCTTTTT	2220
TGAAGAAATT	GAGCGAACGT	TTAAAGAAAT	AAGTGAAGAA	TTAAATGAAG	AAGAAAAA	2280
ATCATCGAAA	CGAAAATATG	ATGATACGTT	ACCACCTTTA	TTCGATGAAC	TTCCAAAGGA	2340
AGAGCCTAAA	TCGAAACCTG	TTGTAGAACC	TATGGCACCT	AAAAACAAC	AAGAAACAAA	2400
ACCGATGACA	GAGAAACCAA	TCACAGTGCC	TAAAGCAGAA	CCGGTGGAGC	AGAAACATAG	2460
ACCTTCTAGA	CAAGATAATT	CTGACGAAAT	TAGACGTCAA	TTAGAAAAAT	CACTTAGAGA	2520
TGATATTAAA	ACGATTTCGT	CTGACATTGA	TAGAGAAAAA	GAAAAGCAAA	TTGCTAAAAT	2580
GGAAAAACGT	GCTAGAGATA	TTATTGAGGA	TAAATACTTA	TCTGAACGTA	CAAACGTTT	2640
GAAATTAAAG	CAGCTGCTTA	ATTCTCAAAA	TGTCGAAAAAG	ATTGACTA	AATCAGCGTT	2700
CCAATTTGAT	AAAGATGAAG	TAATCAATGG	TATGATATGG	TCAGAAATTT	TAGCTAAACC	2760
AAAACAATTA	TAAAATTTTT	TGAAAACAAG	CACTATCGTA	ATGGTAGTTG	CTTGTTTTTT	2820
TACGTTAAGG	AAAATTAAAA	AACAAAGAGA	ATTTTTCGAG	AAATATTAGT	TATTTAAATT	2880
ACAGCAAAAA	ATTGATTAGT	CTAAAATTGA	ATCTGCTTTT	ATGACAAGGT	GAAAAGTATA	2940
AATGATTATT	TTAAATTAAA	GAAAAATGAG	TAAGTCAATG	CAAAGATGTT	TAAATCAATC	3000
AATTGCATGA	TATAATTAAG	TAGATATTAA	AGCATCATAG	AATGAATATA	AATGATATAT	3060
GAAAAGGAGC	GCGTGTATGC	CTGGAATTAT	ACAAATAGAC	GATATGAACC	AATCTCAAGC	3120
TTTAATTGGA	AATAATGATG	AACATTTAAA	AGCAATTGAA	GAGAGTTTCG	ATGTTGTCAT	3180
CCATGCAAGA	GGACAAGaAG	TTGCCGTAA	AGGTACAAAA	ATAGAAAACG	TAGAAAAGC	3240
GGAATCAGTA	TTAATCAATT	TGCTGAAGGT	TATTGATTTA	GGTAATATA	TTACAATTAA	3300
AGATGTTGAA	GCAGCTATTA	AAATGGCGCA	TAATAACACA	ATTCAACATC	TGTTAGATTT	3360
ATATGATGAA	GAGATAACTA	AAGATGCATT	TGGTAAGACG	ATTCGTGCGA	AAACGATGGG	3420
GCAACGTATA	TATGTTAATG	CCATGAAAAA	TAATGATTTA	GTATTTGGTA	TAGGTCCTGC	3480
TGGTACAGGT	AAGACATTCT	TAGCTGTAGT	TTATGCAGCA	AAGCAACTCC	GTAAAGGTGC	3540
TGTTAAACGT	ATTGTATTAA	CAAGACCTGC	TGTTGAAGCA	GGAGAGTCAC	TTGGATTTTT	3600
ACCAGGAGAT	TTGAAAGAAA	AGGTAGATCC	ATATTTAAGA	CCTTTATATG	ATGGTCTATA	3660

TACTGTTCTT	GGGCGTGAAC	AAACAGAGG	ATTTATTGAA	AGAgGCATTA	TCGAAATAGC	3720
GCCACTTGCA	TATATGCGCG	GACGAACATT	AGAAGATGCA	TTTGTAATTC	TTGATGAGGC	3780
GCAGAATACG	ACACATGCGC	AAATGAAAAAT	GTTTTTAACA	AGACTAGGTT	TTGGCTCAAA	3840
AATGGTAGTT	ACTGGTGACC	AAACTCAAAT	CGATTTACCT	AAAGGTGTTA	AAAEGGACT	3900
TAAGGAAGCG	GTCAGTAGGT	TACACAACGT	TAAAGGTATA	AGTATATTGA	AATTAGATCA	3960
GAGCGATGTA	GTCAGACATC	CATTGGTAAG	TAAGATCATT	GAACATTATG	AAGGAGAGAA	4020
TTAAATGTTT	ACGATAGATT	TTAGCGATCA	CACAGGCTTA	GTTAAAGATG	CTTGGTATAA	4080
ACAAATTGAA	GATTTATTAG	AATTTGCTAA	AAAAGAAGAG	CATATAGAAG	ACGATGCTGA	4140
GCTTTCTGTT	ACATTTGTAG	ATAACAAGA	AATACAAGAA	ATTAATCGAA	CATATAGAGA	4200
TAArGwTAAr	GTTmCaGATG	tAaTCyCaTT	tGCTTTAGrA	GrAGATGAGC	CmGaGATkGA	4260
TtTTAGTGGT	CTTGATATAC	CACGTGTTTT	AGGGGATA	ATTATCTGtA	CGGATGTAGC	4320
GCAAGrACAA	GCAAACAATT	ACGGACATTC	TTTTGAACGA	GAATTAGGAT	TTTTAGCATT	4380
ACATGGATTT	TTGCATCTAT	TAGGTTATGA	TCATATGACT	GAAGCGGATG	AAAAGGAAAT	4440
GTTTGGTCGA	CAAGATACAA	TATTAAACGC	ATATGGATTA	ACACGAGACT	AATTATGAAA	4500
AGGTTTAAAT	ATGCACTTGA	TGGGCTGAAA	ATCTTAATTC	AAAAAGACTA	TAAATTTCTT	4560
TTACATGTGT	TTGCAATGAT	TGTTGCTATT	GTCTTTGGTC	TCGTAATAAA	TATTAATCGG	4620
ATTGAGTGGA	TATTTATACT	CATTGCTATT	GCATTAGTTC	TCACTGTTGA	AGCTTTAAAC	4680
ACTGCTATTG	AATATGTGT	CGATTTAGTG	ACCGTTGAAT	ATCATGATTT	AGCTAAATAC	4740
GCTAAAGATA	TTGCGGCTTT	TAGTGTACTT	ATAGTTTCAA	TATTAGCATT	TATTATAGGT	4800
TTAATAGTAT	TTTTACCACA	TTTTATAGCG	TTATTTTAGG	GAGGCATATA	TGAGTTATCA	4860
ACCTCATTAT	TTTCAAGAAG	TTAGAAAAGC	ACAACAAGAA	TCATTCGC	CATACAGTCA	4920
ATTTAAAGTA	GGGCTTATT	TAAAAmCGAA	AGACgGTAGA	ACTTTTTATG	GTACCAATGT	4980
AGAAAATGCT	TCTTATCCAT	TATCGATATG	TGCTGAACGA	GCTAGTTTGG	TATCGGCAAT	5040
TTCTCAAGGA	TACAGACCAG	GTGATTTTGA	ATCAAtAACT	GTAACCGTAG	ATGCAGATAA	5100
ACCGTCATCA	CCTTGTTGGT	CATGTCGTCA	AGTTTTGAAG	GAATTATGTG	ATGATGATAT	5160
GCCTGTGTAT	ATGACAAATC	ATAAAGGAGA	TATGGTTATG	ATGACAGTCG	CAGAGTTACT	5220
ACCATTTGGA	TTTTCAGGAA	AGGATTTAGA	ATAAATGACA	GAACATAAAAT	CAGGATTTGT	5280
TTCAATTATA	GGTAGACCAA	ATGTAGGAAA	GTCAACATTT	GTTAATAGAG	TGATCGGCCA	5340
TAAAATAGCA	ATCATGTCCG	ATAAAGCTCA	AACAAC TAGA	AATAAAATTC	AAGGTGTTAT	5400
GACAAGAGAT	GACGCGCAAA	TTATATTCAT	TGATACGCCA	GGTATTCATA	AACCTAAACA	5460
CAAATTAGGT	GACTATATGA	TGAAAGTCGC	TAAAAATACA	TTATCTGAGATAGATGCAAT		5520

CATGTTTATG GTTAATGCCA ATGAGGAmAT TGGACGAGGC GATGAATATA TTATAGAAAT	5580
GTTGAAAAAT GTTAAGACAC CAGTATTTTT AGTATTAAAT AAAATAGATT TAGTGCAATCC	5640
AGATGAATTA ATGCCAAAGA TTGAAGAATA TCAAAGTTAT ATGGACTTTA CAGAGATTGT	5700
ACCTATTTCA GCATTAGAAG GGCTAAATGT CGATCATTTT ATTGATGTTT TAAAGACGTA	5760
TTTACCCGAA GnACCTAAAT ATTATCCAGA TGATCAAATT TCAGACCATC CTGAACAATT	5820
TGTAGTGGGT GAAATCATTC GTGAAAAAAT CCTTCATCTT ACAAGTGAAG AAATCCCTCA	5880
TGCGATTGGT GTTAATGTGG ACCGTATGGT T A AGAAAGC GAAGATCGTG TTCATATCGA	5940
AGCAACTATA TATGTTGAAA GASGTTTCGA AAAAGGAATT GTCATTGGAA AAGGCGGTAA	6000
AAAGTTAAAA GAAGTAGGaA AAcGTGCGAG ACGTGAtATA GaAATGCtTC TAGGCTCTAA	6060
AGTTTACTTA GAATTATGGG TCAAAGTTCA AAGAGACTGG CGAAACAAAG TTAAC T TT	6120
TCGCCAAATT GGTTATGTTG AAGACCAAGA TTAATCTTAA AAGTGGTGAA GATAATTGTT	6180
AATGCGCCAA AAAGGGATTA TCATCAAAGC AGTTGATTAT GGTGAATCTG ATAAAATTAT	6240
CACGATTTTA AATG	6254

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

GTTGTTCTAA ATGTTTCTTG nATGAAACGA GTCAATGTAA ACTGATATTG CTGTATTTGT	60
TGCAGCAATT CATATTGGTC TGGTGTTCGA ATAACAGCAG CTTGAGTTGG AGTCGCAGCT	120
CTGATGTCTG CAGCAAAATC ACTTAATGTA AAGTCTGTTT CATGACCAAC TGCTGATATA	180
ATCGGTGTCT TACAATTATA TATTGCACGG ACGA A GCTT CTTCGTTGAA ATTCCATAAA	240
TCTTCTATGG ATCCACCGCC TCGACCTACA ATAATGGTAT CTACACCTAA ACTATCTGCA	300
TATTCAATTT TTTCAATAAT GTCGTCTTTT GCTTTTTTAC CTTGAACCAA AGTACTAATT	360
TGTATTTGTT CAGCTAATGG AAAACGACTA TTTATCGTTG AATGGATATC TCGAATTGCG	420
GCACCTGTAC TCGCTGTTAA AACTGCAATT TTTT T AGGAA ACTTAGGTAT TGATTTCTTA	480
TTGCTTTTAT CAAAACAACC TTCTTCAGTT AATTTTTTCT TTAATGCTTC TAATTTTGA	540
TATAAGTTCC CTATACCATC TAATTGCATT TTATTTACAT AAATTTGATA GTTCCACGA	600
CGTTCAAAAA CAGAAACACG TGCTTCTAAT AAGACTTCAT CTCCTTCTTT AGGTTCGAAG	660

TTTAATTTAG AAGCACTACC TTTGAACATC ATGGCACTTA TAACGCTTTC TTTATCTTTC	720
ACATTAAAGT ATAAATGaCC ACTTGaATGc TTTTTGAAAT TTGAAAGCTC ACCTTTAATC	780
AATACAGATT GGAGATGTGG ATCTTGATCA AATTTATATT TATATATTT CGTTAAAGCT	840
GAAACACTTA AATAATCTGA CATATAACAT CACTCAATTT TATTTTTTTA TATTACTCAA	900
TACACCATTT ATAAATTTAT AATGATCATC ATCACTGAAT TGTTTTGTGA ATTCAACTGC	960
TTCATTCATT ACGACTTTAG CAGGTGTATC ACTGTGTAAT ATTTCATATG TTGCCATTCT	1020
TAAAATAATA CGATCCGTTT TTAATAAACG TGCAATAGTC CAATCTTTTA AATAAGGACT	1080
AATTGTCTCG TCTAATACAG GTTCGTGATC TTTAACGCCA GAAACTAGCC AATGAATAAA	1140
TTCGAAGTCT AAATCTGGAT TATCGTCTTT AATAAAGCTT ATCGCTTCAT TTATCGTTAA	1200
ATCACTGTCC TTCATTTCTA ATTGAATAA AGTTTGAAAA GCTTGCACTC GGGATTCTTT	1260
ACGACTCATT TTTAACTCCT TCAAACGTTT GTATTTTTCT TTATTTAATT ACTGAATTAG	1320
GTATGACATT ACTTTTCAAT AACGATTTGT GTAATGTGAA TATTAATTTG CTTAGGTTCT	1380
ATCGCTGTCA TATTAGAAAT TGAATTAAAA ATTGACGTTT GAATTTTGTTCAGTTTTT	1440
GAAATATTAA CACCATGTTT TAATGCACAA TATACATCTA TATATATGCC ATCTTCTTTA	1500
CTCTCGATTT TTAAATCACG GCTTAAATTT TTACGACTAA CTTTTTCTAA ATTTGTTTCT	1560
TTTAATTCAG CAAAATGGCC AGTGATGCCT TCGACTTCCG AAGTAGCTAT ACTTGCAATA	1620
ACAGATAGCA CTTCTGGCGC TATTTCTACT TTACCTAATT TTGAATTTGA ATAATCAGTT	1680
ACTTTGACCA TGGATTGACC TCCTATTAAC CTTCATCATT CATAATGCTA TTTTGCTCTA	1740
AAAAGTTTGT ATTAAATTTA CCGCTTCTAA ATATATCGTT ATTCAATAAT TTAATATGGA	1800
ATGGAATAGT TGTATCAATA CCAAGAACCA GAATTCACT TAGTGACGA ATGCCAGCCA	1860
TAATCGCTTC ATCTCGTGTC GGTTCATGTA TGATTAATTT CGCTACCATC GAATCATAAT	1920
ATGGCGGTAT CGTATAATTA GTATAACATG CTGACTCTAT TCGAACACCA TATCCACCTG	1980
GTGCAAGATA TTGCTCmATT TTACCTGGTG ATGGCATAAA GTTCTTGTA GGATTTTAG	2040
CATTAATTCT AAATTCAATT GCGTGTCTTG TTAATTTAAT ATCTTCTTGT TTATACGGTA	2100
ACACGTCACC CATAGCAACT TGTAATTGTA ATTTAACTAA ATCAATTCCT GTTACCATTT	2160
CAGTTACAGG ATGTTCTACT TGAATACGTG TATTCATTTT CATAAAATAA AATTTATTAT	2220
CATTTAAATC ATATATAAAC TCAATTGTTC CCGCATTTTC ATAATTTACA GCTTTCGCTG	2280
CACGAACTGC GGCATTTCCC ATTTACGAC GTGTTTCATC ATCTAAAATT GGGGAAGGTG	2340
CTTCTTCCAC TAATTTCTGC ATACGTCTTT GAATTGTACA ATCACGTTCT CCTAAATGAA	2400
TTACATTACC ATAGCTGTCC CCAACAATTT GGATTTCAAT ATGGCGGAAG TTTTCGATGA	2460
ATTTCTCCAT ATAAAGTCCA CCATTACCAA ATGCAGTTTG AGCTTCTTGT TCTGTCATTC	2520

GGAAGCCAGT TTCAAGTTCT TTTTCATCAC GAGCAACACG GATACCTTTT CCGCCACCGC	2580
CAGCAGTAGC TTTAATGATG ACCGGATAGC CAATTTTTTTT GGCGATTTTC TTAGCTTCTG	2640
AGACGTCTTT CATTAAACCG TCACTACCAG GAACAACCTGG AACATTGGCT TTGATCATTT	2700
CTGCCTTAGC AACATCTTTG ATACCCATTT TTTGGATAGA TTGATAACTT GGTCCAATGA	2760
ACTTCAATTG GcATgctTCG CATAATTCTG CAAAATCAGC ATTTTCAGCT AAAAAGCCAT	2820
AACCCGGATG AACGCCATCA CAACCTGTAG AAGTTGCAAT AGATAAGATG TTCGGAATAT	2880
TTAAATATGA ATCTTTAGAC AAAGTGGGAC CTACGCAATA TGCTTCATCA GCAATTTGAG	2940
TATGTAGCGC ATCTTTATCC CCTTCAGAAT AGATTGCAAC AGTTTGGATG CCTAAATCAC	3000
GACAAGCGCG AATAATCCTA ACTGCGATTT CACCGCGGTT TGCAATAAA ACCTTTTTCA	3060
TTATTTCAACC TTAAATAACG GTTGGCCATA CTCTACCATT TGTCCGTCTT CTACTAAGAT	3120
TTCAACAATT TCACCTGAAA TTTCTGCTTG AATTTCATTA AATAGTTTCA TTGCCTCTAA	3180
AATACACACT GTTGTTTCAT TTGAAACAGT GTCCCCAACT TGCACATATG CTTCTTCGTC	3240
TGGAGATGGC GATTTGTAAA ATGTACCTAC CATAGGTGCA TTAATTGTTT TGTGATTATC	3300
TGAAGTTGGC TTTGGAGCTT CAGTTTTATT GCTATCAGTT GATTGTGCTT GAGGCATAGG	3360
CATTGCCGCA GCTTCAACTG GCATTTGTGA GATTTGTGGC GTGATAATCT CAGTTTCTTT	3420
TTCTTTCTTA AGCGTCACTT TGCCTTTAGT ATCTTCAATA TTGATTTCCG TTAAAGTTGA	3480
TTTATCCAGA ATTTCAATTA ATTCTTTGAT TTCTTTAAAG TTCATTATTA CTGACTCCTT	3540
CAGTTTGTTT TCATCTACCC GTCTATTTTA CTTGAGACAA CTCTTCAATT CAAGCATGTT	3600
CATATTGCTG GCGACATTAT AAGTCTATCC CAAAGTTATA ATAAAACCAC ATTTAAATT	3660
AAAAAFACTT GTGTATTTAT TACTTAACAT TGAATCATCT TAACTCTTGA	3710

(2) INFORMATION FOR SEQ ID NO: 406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

GCTGATGTTT GTTGCCTTTn TCCACCAGAC AATTCAGAGG GATATTTATC ACTAATATCC	60
AATATATTTA ATGCTTCTGC TACTTTTTCA TAACGATTTA ACATATGTTC TTTATCTAAC	120
TTCTGTACCG TTAGTGGTAA CATTATGTTT TCTTTAACAG TCAATGTATG CAGTAAATTA	180
TACTCTTGAA AAATAAAACC AATATCATGC TTGCGTATAT CAGATwATT CTTGTTTGAA	240

AGCTTTTCTA ATTTTTTTTCC TTTTAATGTA ATAGAACCTT GTGAAATATA ATCAATTGAA	300
CTTAAACAT TTAATAATGT CGTTTTCCCA GATCCAGAGG GACCCATAAT AGCAATAAAC	360
TCGCCTTCTT CAATAGACAT ATTGATATCT CGCAACACTT CTTGTGCCAT TTTTTTAGTT	420
CCATATATTT TTGTTAATTG TTTTACTTCT AAAATTGCCA CTTTAACACT CCTATAATTT	480
ATCTTAACTT CATTTCTTTT AGGCTTTGGC ACTTGATCTT TCAATTTAAC ATATGATAA	540
CATCTATCTT ATTATAACGT TGAAGCTGCA TTGATGTATC AATTCTAAGT AACAAAACGC	600
ATGTTTAAAA TGACAAATTT GTCACTTCCG ACATGCGTTC AACAAATTCA TTTTGTAATG	660
GGAAAATCAA TCTGACAGTT GTCCCCCTAC CAACAGTCGA CGTGACTTGC AGGTGAATAC	720
CTAATTGATC CTTTACACTA TTTACTAAAT ATAGACCCAT ACCTGAAGAC GTCGTTTCAT	780
TTCTGTTAGC CGTTGACGTA AATCCTCGTT CAAATATTCG CGGCATATCT TTTTTACTAA	840
TACCTCTGCC ATAGTCTTTA ATATATAACG AACATGTTG ATCATTTAAT TCTGTCCCAA	900
TTTCAATATT AAAATTCTCA CTATATTTCA ATGCGTTTCA CAAAATTTGT CTAATAATCA	960
TACGACACCA TTTTATATCT GTATAAACAT AATCATCCAC TTTAAAGTCA ACATCAAAAC	1020
CAATACCTTT AACCTGACTA ATATGTCTTG TTAATTGTAT TTCATCAATG ACCATGCGTT	1080
TAAGTGACAC GTAATCAAAA TACATATCTT TACGTTGAGA TTCTAATCTA GTAATATACA	1140
GCTGTGTATC TAGCATCGAG TTTATACGAG ACCATTCATA TAGTAATGCT TGTWTTCTTT	1200
CTTGATTTTT TTCTTGATCA ATTAATAATT TCATAGCTGT CACAGGtGTT TTTATGTCGT	1260
GCACAAATTC TGTAATGGTT TGTTCATGCA TGTTC AATTG CAACTGTTGC TCAACAACCT	1320
TTTCTTTGTG CGCTGAGATT TGACGATATA AATAATCAAC TGTATGACGT TGAAATGGCG	1380
TTTCCGCTAA ATCTTTATGT TTAATTTCTT CTATTTCTTT ATCTTTGTCA AAATGCTTAT	1440
ATAATTTTAC TTCTTTAAAA TATGTCAATA AAAGAAAAAT CATTGTTAAA CTAAATTCA	1500
AAGAAACAAT ATAAAATAAA CTGTCTATTG GAAAATCATA ATCGATAGA CTArTGCCTA	1560
ACATAAGGAA GTTTAAAAAC AATATCCAAA AtATCCAGTT CATGCGAGAT TTCAAAAAAT	1620
AAGCTACCCA TTTCAAATTA TTCATGAGCC ATATATCCTT TnCCnACTTT TGTTTCGATT	1680
GCACTATCCA TACTAATTTT AGATA	1705

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1722 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

TCAATATATC	TTAAAATTCA	ATGATTAAAT	CnATTATCAC	TAGACATnAA	ATACATAAAT	60
CCTATTCCCC	ATTTTCATTT	nTTAATTCAT	AAATGAATCA	ATAACCACCT	AATAACAAAT	120
CATATTATAC	ACCTTTGTTT	TCTATTTTTC	TAAGGTTTAA	AAAATATTTT	TAGGTAAACC	180
TAAAAATAGA	TGTAATAAAA	AGCCTCCTC	AGATATTTAT	ATATCTATGA	AGACGTTTAA	240
ATACATTATA	GATGGTCTGG	TTCTGGGTGA	ACGTATACTG	AGGAAAtACC	TTTTTTGTGC	300
AAATGATGTT	CGACATTGTC	ACAAATTTGA	TGCGCTTCTA	CTAAGGAAAG	GTTAGCATCT	360
ACAACAATTG	TGACATCAAT	AAACACACTA	CTTCCATGGT	AACGCCCTT	AATACTTTTA	420
ACTTCTTGTA	CTTCATCAAC	TTCTAAAATA	TCATTGCGAT	ACGCTTCTAA	TTCAGTTTCA	480
TTGAAACCAT	CACTCAACAT	AAAAATTGCT	TCTTTAAAAA	TACCAAAACC	AGTATAAACG	540
ATTAGTAAGC	CTAGTAATGT	TGCTAAAATA	ATATCGACAA	TTGGGAAACC	GATTTGCGTA	600
AAAATTAATC	CTATCGCTGT	TCCAATGCTG	ACTAACTAT	CCGATAAATT	ATCTTTGGCA	660
GCCGAATTTA	AAGAACTACT	TTTCGTTCTT	TTCGCTAGTC	TTTGATTGAC	TGCAAATACA	720
ATCAACATTA	CAAGACCACT	GATTAAGCTG	ACGATAATTG	TTATTGCGTT	AGGTACAACG	780
TCATCTTCTT	TGAACAAACG	AGGTGCATTT	TGAATAACTA	CTTGGATACC	TACAAACATA	840
ATGACAAATG	ACACCAATAA	TGAAGAAATA	TTTTCAGACT	TCAAATGGCC	ATAAGGATGA	900
TTTCGATCGG	CAGGTTTAAT	TGAAATTTTC	AATCCAATAA	TAACAGCTAA	AGAAACGATA	960
ATATCTGTCA	TATTGTTTAA	TGCATCGGCT	CTTACAGCTG	CAGAGTTAAA	GACAAACCC	1020
GTGACATACT	TAACAATAGA	TAAGATTATA	TATACAATTA	AACTCAAATA	AGCACCGCGT	1080
TGCGCCAATT	TAAGATTTTC	ATTATGAGAC	ATGCGTTGAA	CCACCTTGAA	TTAGTATAGT	1140
AACAATATTA	TGAATGATTC	ATTTTAATTT	TACAACGTTT	TTAATTTTTA	TAAATTTTTA	1200
TAAAATTAAA	CTAATTTATT	CATTCGCAAC	CCCTAAAAAT	AATTTTTTAGC	CTTTCTGCGA	1260
ATTTTATGAG	CTAGAAAGGC	GCCCAACTCT	CCCTGTTTGT	TAACTTTCGC	CTCGAAAGTT	1320
TCTATGTTGG	GACCCTATGC	ATTAGTAGCG	AAGcTATCTA	ATGTGTTCCCT	TTATTTTCTG	1380
CGAAwwTTAT	GAGCTAGAAA	GGCTTATGCA	GTTGACtTT	TACGTCCAAC	TGCGTTCCTC	1440
CGTCTTCTTC	AAATTTATTT	GTnAGAAAGG	CACCCAACCTC	TCCCTGTTTG	TTAACTTTTCG	1500
CCTCGAAAGT	TTCTATGTTA	GAACCTATG	CATGAGTTGC	GAAnTATCTA	ATGTCGTGAA	1560
CTAATTATAT	AGAAGAAAAA	GTGCATCAAT	GACAAATTAA	ATGAGATTTT	TACTCTACCA	1620
AACTCTCTTC	GAAAGACAAT	TTTCTCCTCT	ATTTATTAGC	AACTATTGCA	TTTCTCCATA	1680
TAGTACTTCC	TTACTTAAAA	TACGCTGAAT	GTCTGAATTA	AA		1722

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

GCGAGACCCC CTGAGGGAGC AGTGCCCACT CGAAGACCCG AGGCTGAGAC GGCACCCTAG	60
GAAAGCGACc ATTyCAATAC GAaTTgTGAt AAATAGAGAA CAGCAGTAAG ATATTTTCTA	120
ATTGAAAATT ATCTTACTGC TGTTTTTTTA GGGATTTATG TCCCAGCCTG TTTTTTGTGA	180
TTTTTAATAA TTTGAATATG GAAAATGTAT TATTCTCTCA TTTGTATAGA TTGTATTTAA	240
TAAGTTAATG TAATCCTTGA GCTCACGATT AATAAAATTCCTATAACCTTA ATTATTTTCT	300
CGATACAAAG GGTTATTAAC TTTAATATAA GTATAATGAT GTGCCTCATC TTCAAGACGC	360
ATTGTTGTAA CACACTTATA ATCTATAAAT GGCGCGAACA TGGTATCTTT AATTTCaTTT	420
ATGCGATTCT CATTTACTTG ATTAGATTG TGTGTCGAAA GTACAAGTTG ATCaAAAATG	480
TTATCTAGTA CATCACGAAC GATATACCAC ATATGTCTTT CTAAGTTTGA ATCATTTGAT	540
GCTTTAGAGA TTGTAAGAAT TAATTCGCCT AAATGGTTTT GAACGGTAGA ATAAAAGGCT	600
TTGTTAAACA CAGACGTTTT TGAATCAGTA AGAATTCTTG ATTTTTCATG GAAATGAGAT	660
GTA CTGTATA CCATTTCAAT TAGTTGTGCT TTATCAATTC TTAAACCTTC AAAGTCTCTA	720
ATATACATCG TGTCCAATAG ACCATCTTTC CGAAATGTTG CAATAGCATT TTGCAAGTGA	780
GCCTCTAATG CAATGCCATA TTTAGTAACT AGTGGGATTA CGAGACCAAG CAATGCTTTA	840
CTATAAGTTT CAACCCACGA TTTGCGCGAT GATTCAAAT CAGACAAGA TGCAGCTGAT	900
TGATAACGTT TAATCAATGT CACGATAGGT GATTCATTGT TAAATGGGTA GGTTGCAACT	960
AAGCTTGAAG GAATCAATGG TGTGACTTCT TGTGGAATCA TTTGGTATAT ATTTTTTCTA	1020
AATAATGTAC CTAATTgnTC nTTCGTTTCAG TTTGATAGTC TGCTTCGTCT TGCTCATTAT	1080
AAAAATGAAT ACCAGCAACT TCATCAATAA TTGTTGATGC ATAGGACTTA AATATGACAT	1140
CTTTCTCCAA AATATCATTT AAAATACGTG TCATTAGTGG ACCATTGTGC GTCGTTTGTT	1200
CTGATAATGT ACGAATCTCA CCTGTAATAT GAACGTTTGT CGACAATTTG ATGTGTGGCG	1260
ACATAGCTGG GTATTTAGGA ACTAATGTG TGAAAGATAA ACCAGCATAA TAATCCaACG	1320
TATGTTTTGC TTCAATGATT AATTCTTTAT CTA CTCTGCTG TTGATAATCA GAATGTAATA	1380
CGTCATCTAA TTGCCATGGA TGAACAATCA TAATGTGATA ATCATTAAAG TTAAACTTTG	1440
GCGTAAATTC ATTTTCTAAT TGTTTAATTA AGTCCGAAA TAGTTGATGA ACAETGTAT	1500
CATAATCTTT AGACAGTGAC ATAGTACGGC TTAATTTACT GTGAATCAGT ACTATTTTCA	1560

ACTTAATAGG	TTGATTGAAT	TCTGAAGAAT	ATAGGAATGT	TTGTAATGCA	TTTAAACCTT	1620
TACGTAATTT	AGCCCCAGGA	TGTAGCGGAT	GACCTTCAAT	AACGGCTTGC	TCTGAACGCA	1680
AGTAACTATC	TTCGCTATTT	TCGATAATAT	TAAATAAAGG	TGCAGAATCA	TGTTGCATTG	1740
ACAGTGCTTG	ATAGCTAATT	GCAAATGTCA	TATtAGTtGC	ACTGTTTATT	AAATCTTGCT	1800
GAAATTGATC	ACTAGCAGCA	TTTTTTAAAT	CTGGTGCTTC	AATTAAAATA	CACTCAAGAA	1860
TTTCATTTGG	ATGGTGTACT	CGTGTAATCG	TATTTGAAT	GTCATCTTTA	ATGTAGAAAG	1920
GGCCTTCAAC	ATCAATTCGA	TCAAAGGCGT	GTTCTCCAGT	GATAGGAGCA	TATAATGTTT	1980
GCTTAGCTTG	TGGGAAGTGG	ATTTCTAGTA	TATGAGTCGT	TGAGATATCT	AACATAATCA	2040
AATCACGACT	CAATATTTTC	TTACTTTGAG	TGCGCGCTTT	AACTAAGTTT	TCGCGATGCA	2100
TTGATGTGAC	CAATCTCTGA	GTGACTTTAT	CTCTTCCTTG	TAAAATCATC	TCTTTAAAAA	2160
TATTAGCCCA	ATCGCTATTA	TGTTGTTGTA	AAAATAAATA	TGTTTCTTGT	TCTTCTTTGT	2220
TAAATTTTAA	TGTCGTCTCT	TTAAAAATTA	AGTTCAAGTT	CATAATTCAC	CTCTATGAAA	2280
TATTTTACAA	AAGCAAGATA	GATTTGTATA	ATCCATATTA	ATGATAATGA	yTCTTATTAT	2340
CAACAGAATG	CGGGTGTAAG	TTTTATGACA	AAATATTTTT	TTAGCAGTTC	TTTTCTACTA	2400
TTTCTAGGTA	ATTGGATTGG	ACAAATAGGG	CTAAATTGGT	TTGTACTTAC	CACTTATCAT	2460
AACGCAGTTT	ATCTGGGGAT	TGTCAATTTT	TGCAGACTTG	TACAATATT	ATTACTAAGT	2520
GTGTGGGCAG	GGGCAATTGC	CGATAAATAT	GATAAAGGGC	GATTGCTGAG	AATTACAATT	2580
TCATCATCAT	TTTTAGTAAC	TGCAATTTTA	TGTGTGCTCA	CGTATAGTTc	ACTGCAATTC	2640
CAATTAGCGT	CATTATTATA	TATGCGACAT	TAAGAGGGAT	TTTAAGTGCG	GTTGAAACAC	2700
CTTTAAGACA	AGCAATCTTA	CCAGATTTAT	CAGATAAAAT	ATCTACTACA	CAAGCTGTmw	2760
CATTTCAATC	ATTCATCATT	AATATTTGTC	GTTCAATAGG	GCCTGCCATT	GCTGGTGTCA	2820
TATTAGCAGT	CTATCATGCG	CCAACAACAT	TTCTTGACA	GGCAATTTGT	TATTTTATCG	2880
CAGTTTTATT	ATGCTTACCA	TTACATTTTA	AAGTAACTAA	AATACCTGAA	GaTGATCAA	2940
GaTACATGCC	GTAAAAAGTT	ATTATAGATT	ACTTCAAATT	ACATATGGAA	GGTCGACAAA	3000
TATTTATAAC	ATCATTATTG	ATTATGGCGA	CAGGTTTTTC	ATATACGACA	CTTTTACCAG	3060
TTTTGACAAA	CAAAGTATTT	CCGGGGAAAT	CTGAAATATT	TGGTATCGCTAT	GACGATGT	3120
GTGCCATTGG	TGGTATTATT	GCAACGCTAG	TTTTACCTAA	AGTACTTAAA	TATATTGGTA	3180
TGGTAAATAT	GTATTATTTA	AGTTCATTTT	TATTTGGCAT	TGCTTTGTTA	GGTGTGGTAT	3240
TTCACAATAT	TGTCATCATG	TTCATTTGTA	TTACATTGAT	TGGGTTATTT	AGTCAATGGG	3300
CACGTACGAC	AAATCGCGTT	TATTTTCAAA	ATAATGTTAA	AGATTATGAA	CGTGGTAAAG	3360

TACTGAGTAT TaTTATGATG GgATAGAGGT ATGaTTCCAT kGGGAAGTCn ATTAATGAGT	3420
ATATGTGCAG ATGTGTTTGG CATTGTTAGA ACTTTTTTCAA TAATGGGAAT AAGTACTATA	3480
TGCATTACAA TGGTATTCTA TTTTATAAAT AqAAGTTGA AGTTAAAGTT GGAGGAAAGT	3540
AATCATGGTA TATCTTGAAT GGGCAAAGGC AGATAGAAAT ATTCAATATC GTGTAATTAA	3600
CGCCATTATT AAAGAACGTA TTTACCCCGA GCAAACATTT ATTTTCGCAA AAGGATCTTT	3660
AATTGAAATT CAGTATCATA TGCATGTGTT GACTATTGAA GTTGTTAGAA AAAGTGCAT	3720
AGAACGCTAT GAGTTTACAG GTGATATTAC TTATTTAAAT AAAGGTGAAA CGTCATTAAT	3780
TATAACTTTA GAAGGTTTAT TAGATGTGTT GAATCATGAC TTTGATATCC CTATTTTCTAGA	3840
GCGACTACGC GAAGAGTTAA TACACAGTCG AGATAGTTTA GTTGAAACAT ATAAGCAAAT	3900
GTCTCACAGA CAAACGTTAA TAAGTCmAAG TTTTAAATTT TCAAGGTTAC CACAAGATAT	3960
TAACTTTTTT TCakGGTtAC AACATGTAAA AGATAGTGAT AAGACAGATG ATTTAACTTA	4020
TTCTGAGAGT TTGGTACCAG AGGGGCATCC AACACACCCT TTAACCAAAA CGAAATTGCC	4080
CTTAACATATG GAAGAAGTAC GAGCATATGC ACCTGAGTTTAAAAAGAAA TCCCTTTGCA	4140
AATTATGATG ATTGAAAAAG ACCATGTTGT GTGCACAGCT ATGGATGGTA ATGATCAATT	4200
TATTATTGAT GAAATAATTC CCGAATACTA CAATCAGATT CGTGTGTTTT TAAAGAGTTT	4260
AGGTTTGAAA AGTGAAGACT ATAGAGCGAT TTTAGTACAT CCTTGGAAT ATGATCATAC	320
GATAGGGAAA TATTTTGAAG CATGGnTTGC TAAAAAATA TTAATTCCAA CGCCGTTTAC	4380
AATACTTcCA AAAGCaACTT aTCatTTaGG ACGATGTCTT TAATTGATAA ACcATACCAT	4440
GTAAgTTGC CCgTCGATGC aCAAGCAACA AGTGCCGTTA GAACAGTCTC AACTGTGACT	4500
ACTGTAGATG GACCAAAGTT AqGTTATGCT TTACAAAACA TGTTGAATCa ATATCCaGGA	4560
TTTAAAGTTG CTATGGAACC GTTCGGTGAA TATGCAAATG TTGATAAAGA TAGGGCACGT	4620
CAGCTTGCTT GTATTATAAG ACAAAGCCT GAAATTGATG GAAAAGGTGC AACAGTAGTT	4680
AGTGCAAGTC TAGTTAATAA AAATCCAATA GATCAAAAAG TTATCGEGA TAGTTACTTA	4740
GAGTGGTTAA ATCAAGGAAT TACTAAAGAA AGTATTACGA CATTTATTGA ACGATACGCT	4800
CAAGCATTA TCCCGCCTTT AATTGCTTTT ATTCAAATT ATGGAATTGC TTTAGAAGCA	4860
CACATGCAAA ATACAGTAGT GAACTTGGGG CCACATTTTG ACaTTCAATT TTTAGTGAGA	4920
GATTTAGGTG GTTCTAGAAT TGATTTAGAA ACATTACAAC ATCGTGTATC AGATATTAAA	4980
ATTACAAATG ATAGTTTAAT AGCTGATTCT ATAGATGCAG TGATTGCAAA ATTCCAACAT	5040
GCTGTTATTC AAAATCAAAT GGCAGAATTA ATCCATCATT TTAATCAGTA TGATTGTGTT	5100
GAAGAAACCG AATTATTTAA CATAGTACg CAAGTAGTAG CGCATGCCAT TAACCCAACA	5160
CTACCACATG CAAATGAGTT AAAAGATATT TTGTTTGGAC CAACAATTAC TGTCAAAGCG	5220

TTGTTAAATA TGAGAATGGA AAATAAAGTA AAGCAATATT TAAATATTGA GTTAGATAAT	5280
CCGATAAAAAA AAGAGGTGTA GTACTACATG GCACACGTTA ACATAAATAT ATCAAGATT	5340
AAaTATAACG CCAAAGTACT TCAAACAGTT TTTCAAAGTA AAAATATGCA ATTCACACCA	5400
GTAATTAAGT GCATAGCTGG TGACCGTACA ATTGTAGAAA GCTTAAAAGC GTTAGGTATC	5460
AATCATGTTG CAGAATCCAG ATTGGATAAC ATAATTAGTA TTGCAGATAC AGGATTTAAC	5520
A	5521

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

AGGTCGTCTr GCaGmAGmGm TATTTGACGA TCTTGCTTTC CCAAAACACG ATGATGATTT	60
TAACATACTG TCTGATTATA TTGAGACACA TGGTGATTTT aCATTGCCAA TGTCTGTATT	120
TGATGATTTA TATGAAGAAT ATACGGAATG CTAAATTTT TAATATAATT TTTAATAATA	180
ATAGTTAGAA CCAGGGTGAT GCAATTCGTT ATCCTGGTTT TAATTTAAAA TAACTAAGT	240
TGTGACTAAA AATTAATCAA TTATAGTGAA ATATGGTGCG CTATCTTGCA TAAATTGATA	300
TGATTAACTA CACAGAATTT AAAAGTACAT AATACATAAT AAGGAAGTGA TACAATGAT	360
GATAAGCAAC ACACATCTTC ATCCGATGAT GAACGCGCTG AAATTGCAAC AAGCAATCAA	420
GACCAAGAAA CTAATTCATC GAAACGCGTT CACTTAAAAC GTTGGCAATT CATATCAATA	480
TTAATTGGTA CAATCCTAAT AACAGCTGTC ATCACAGTTG TTGCATATAT TTTTATAAAT	540
CAAAAAATAA GTGGTTTAAA CAAAAGTAT CAAGCAAAC TAAATAAAAT TGAAAATGTG	600
TATAAAATCT TAAATAGTGA TTATTACAAA AACAGGACT CTGACAAGTT AAGTAAAGCT	660
GCAATTGATG GCATGGTCAA AGAATTAAAA GATCCTTATT CTGAATATTT AACAAAAGAA	720
CAAACGAAAT CCTTTAATGA AGGTGTTTCA GGTGATTTT TAGGTATTGG TGCAGAAATG	780
CAAAAGAAAA ATGATCAAAT TATGGTTACT AGTCCTATGA AGGGATCTCC AGCAGAACGT	840
GCTGGCATTG GTCCTAAAGA TGTCATTACT AAAGTAAATG GAAAATCAAT TAAAGGTAAA	900
GCATTAGATG AAGTTGTCAA AGATGTTTCGT GGTAAAGAAA AACTGAAGT CACTTTAACT	960
GTTCAACGAG GTAGTGAAGA AAAAGACGTT AAGATTAAAC GTGAAAAAAT TCATGTTAAA	1020
AGTGTTGAGT ATAAGAAAAA AGGTAAAGTT GGAGTTATTA CTATTAATAA ATTCCaGAAT	1080

GATACATCAG GTGAATTGAA AGATGCAGTT CTAAAAGCTC ACAAAGATGG TTTGAAAAAG	1140
ATTGTTTTAG ATTTAAGAAA TAATCCAGGT GGACTACTAG ATGAAGCTGT TAAAATGGCA	1200
AATATTTTTTA TCGATAAAGG AAAAAGTGT GTTAACTAG AnAAAAGGTAA AGATACTGAA	1260
G	1261

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

AAATATATTG AAnAGAnAAT TACTAAGATT AAATCnTCTT AAATATCCC TGAAATAACG	60
TCCTAAAGAT TAAAGGAAAG AGGTTATAAG TTATGCCAAA ATTAATTTTA TGTCGTCATG	120
GACAAAGCGA GTGGAATGCT AAAAAGTGT TTAGTGGATG GGAAGATGTT AATTTATCTG	180
AACAAGGTAT TAATGAAGCG ACTAGAGCAG GTGAAAAAGT AAGAGAAAAT AACATTGCCA	240
TCGATGTAGC TTTTACATCG TTATTAACAC GTGCTTTAGA TACAACGCAT TATATTTTAA	300
CTGAATCTAA ACAACAATGG ATTCCTGTAT ATAAAAGCTG GCGTTTAAAT GAACGCCACT	360
ATGGTGGATT GCAAGGCTTA AATAAAGATG ATGCTAGAAA AGAATTGGA GAAGAACAAG	420
TACATATTTG GCGTCGTTCT TATGATGTGA AACCACCTGC TGAAACCGAA GAACAACGTG	480
AAGCTTACTT AGCTGATCGT CGATATAATC ATTTAGATAA ACGTATGATG CCTTATTCTG	540
AAAGTCTGAA AGATACTTTA GTTCGAGTGA TACCATTTTG GACAGATCAT ATTTACAAT	600
ATTTGCTAGA TGGTCAAACG GTATTAGTTT CTGCACACGG AAATTCAAT CGCGCATTGA	660
TTAAATATCT TGAAGATGTG TCAGATGAAG ATATCATTAA TTATGAAATT AAAACAGGTG	720
CACCGCTTGT TTATGAATTA ACGGATGATT TAGAAGTTAT AGATAAATAC TACTTATAAA	780
AaAAGAGCTG CATGTACACA AGGAGTGAGT GTATATGcAG CTCTTAAAtA TGTGAAGTAA	840
TGTAAGGAAA TAGTTAAGTA TAGAGTTTAT ATTAACGAGC TAGGGATACT CGAAAATATA	900
GTTAGACATA CAATATAGTC AAATTAAAAC AATTATTTTC CTCTTTTATG TTGCTTAATA	960
ATCTTTAAAG CACGCTTTCT TGTTTTAATG TTAGGGCTAT TTAAATTACG ACGAGCAGTC	1020
TGTAAATCTA ATTTATCTC TATCCCTCCT TGTAATATA TTATGACCGA TAACTACTCA	1080
TATGTAAATA GTAATGATTA CGTTTTAAAG AAATTGTAAT AAAGTCGTGC TAATTTTTTG	1140
GAAAATGGGT ATAATTACCG GATATCTAAA AATGTGTGTC GTTTTTTAGA TGGTGAGGGG	1200
GAAGCTTTAA ATGTCGAAGA AACAAAAATT AACGATGATT ATTACTATGC TGATGGTGG	1260

ATTTTTTGGG	TTATTAAATG	AAACACTATT	AGTGACGGCT	TTACCAAGTA	TTATGAAAGA	1320
TTTTGAAATT	TCATATACAC	AAGTTCAATG	GCTGACAACA	GCTTTTTTAT	TGACTAATGG	1380
GATTGTTATT	CCTTTGTCCG	CGCTTGTTAT	ACAACGTTAT	ACAACAAGAC	AAGTGTTTTT	1440
AGTGGGTATT	TCTATCTTTT	TCTTAGGTAC	ATTACTCGGC	GGCTTGAGTC	CGCACTTTGC	1500
AACATTATTA	GTTGCTAGAA	TTATTCAGGC	GTTAGGCGCA	GGTATTATGA	TGCCATTGAT	1560
GATGACAACG	ATTTTGGATG	TTTTCCAACC	ACATGAACGC	GGTAAATATA	TGGGGATATT	1620
TGGTTTGGTA	ATTGGTTTAG	CACCAGCTAT	TGGACCTAT	CTTTCAGGTT	ACCTTGTTGA	1680
ATATTTTAAC	TGGAGATCGC	TTTTCCATGT	TGTCGCTCCA	ATTGCAGCTG	TGACATTTTT	1740
AATTGGaTTT	AAAACGATAA	AAAATGTTGG	AACTACAATT	AAAgTACCTA	TTGATTTTTAT	1800
TTCTGTCATT	TTTTCTGTAC	TAGGTTTCGG	cGGGTATTG	tATGGAACGA	GTTCaATTTc	1860
AGAAAAAGGT	TTTGATAATC	CTAcGtATTA	GTATCTATGA	TTGGAGGCGT	TGTTTTAGTC	1920
GCATTATTTG	TAWTACGTCA	ATATCGGCTA	TCAACACCAT	TATTaAATTT	TGCTGTATTT	1980
AAAAATAAAC	AATTTACAGT	TGGTATCATT	ATTATGGGTG	TCaCAATGGT	ATCGATGATT	2040
GGTTCGGAAA	CGATTTTACC	TATCTTTGTG	CAAAATTTAT	TGCATCGTTC	AGCTTTAGAT	2100
TCTGGATTAA	CTTTATTACC	AGGAGCAATT	GTTATGGCAT	TTATGTCGAT	GACTTCGGGT	2160
GCTTTATATG	AAAAGTTTGG	TCCTAGAAAT	CTTGCTTTAG	TAGGTATGGC	GATTGTTGTT	2220
ATTACTACGG	CTTATTTTGT	TGTAATGGAT	GAACAAACAT	CAACATCAT	GTTGGCAACA	2280
GTTTATGCGA	TTCGAATGGT	TGGTATCGCG	TTAGGATTAA	TTCCAGTAAT	GACCCATACG	2340
ATGAATCAAT	TAAAGCCAGA	AATGAATGCA	CATGGTTCAT	CTATGACAAA	CACAGTACAA	2400
CAAATTGCTG	GTTCTATCGG	AACAGCTGCA	TTAATTACTA	TTTTATCCCA	TGCAAGCAAA	2460
AACTTTTCTC	CAACTATGTC	AGACTATA				2488

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

TTTTACAATT	TCAGATATCT	CTAAACACA	TACCGATCCA	ATGGCCAAAA	TTATTCGTCA	60
AAAATTGAAA	AAACTAGGAA	TTCGTAAAGG	GATTCCAGTT	GTATTTTCAG	ATGAAAGTCC	120
AATTGTCATA	AGAGAAGATG	TAAAGATAT	AGTTGGAGAT	AAAAATGCTA	TCAATCGAAA	180

AGGACAAATG CCACCTTCTT CAAATGCCTT TGTGCCAAGT GTTGTGGAT TAATTTGTGC	240
AAGTTATGTG GTGAATGACG TATTAAAAGA TATTCCAGTT CGTCGCATTA AAGACAAAGG	300
GCAATAATTC ATTTTGAAAG GGATAATTTT CAACGTAAGG CAAGTGTAC CACACCATAA	360
AACTAAACT GACTAGTTCG CAAGCATAGT AGAATATGCC TCGTGTACTA GTCAGTTTTG	420
ATTTGATTAT AGCTAAAATA TCAAAGGTAA TCGATTTAAT CTTATTTTTA CGGCCTTTGT	480
TTAAGTAAGT TGTTATATAT TTCTTTGAGT TGTGTTCAC TTTTAGATGT CGTTTTTGGT	540
TCGTAATAAA TTTTGTTTTT TAGTTTATCA GGTAAATATT GCTGTGAAAC ATAGCCATTA	600
ACATATTGGT GTGGATATTT GTAACCAATA GATCGGCCTA GATCTTTAGC ACCTTGATAA	660
TGTCCATCTT TTAAATGGTT TGAATTTGG CCCACATGAC CGTTTCTAAT ATCGGACAAT	720
GCACTATCAA TGGCACTCAT TGCTGAATTT GACTTAGGTG ATAAGCATAG TTCGATTACT	780
GCTTGGCTTA GTGGAATTCT AGCTTCTGGT AAACCTAGAC GTTCTGCTGA TTCAATAGCA	840
GCAAGTGTTT TCTGACCAGC ATTAGGTGAG GCTAAGCCTA TATCCTCATA GCTAATTACA	900
AGTAATCGTC GAACTATTGT AGGTAAATCT CCAGCTTCAA TTAATCGTGC TAAATATGT	960
AAAGCGGCAT TGACGTCGCT ACCACGGATA GATTTTTGGA AAGCGCTCAT AACATCGTAA	1020
TGCATGTCAC CATCCTTGTC ACTTACAAAT GCACCTTTTT GTAAACAGTC TTTAGCATCT	1080
TGCAATGTAA CATGTCGATA ACCGT	1105

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

TAACGTCGAA CTTGAGCTGT TACGTTATGA CTCATAATTA TTTTAGCATA GTCATTTAAA	60
TAAACTTCTG TTCTGTCTGT TGGATAAGCA AATTCAAGCA ATTGACTGTA ACTATCATT	120
ATGACTTCTT GATCAACATG ACTATCAAAA TATACAGCAT AATAATAAGT ACCATCAACC	180
ATATATAACA AATCTTCAAA CTCTGTAGTT ATGATTGTC TATGATATGC ATAATTAATA	240
ACATCTTCTA AATCGTTAAA TTTCACAATG ATTGTTCTTG TATTTTTACG TGCTGAAGAC	300
TTTTGACGTT TAGAACCTTG AGCTTCTTTT TCTTTTGTTT GTTGCTCGAA TAATCTTCT	360
AATTGATCTT CACCTTCTAA TGTTTGAGCT AACAATTCTT GAACTTGTTT ATCAAATk	420
TCAGTTGCAT CATCATCAGA CATATTCATC ATATCTTCAT TTTTAGATTT AGAAATTGTG	480
ACTTCGACAC CTTTTTCAAA GGCATGTACT TGAATCCATA ATGGACCTnC TACAACAAAA	540

TCTTCTACTT CGTTAATTTT ATCCATCATT GAnCAAAAG

579

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1342 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

GTGGTGAAAC TTCTTGCTTT GTAATTTTAT AAAGTGGATC AATATCACTC TGACTTACAT	60
CAGGTTGAAC TGTCATCTTT TTAGTTACTT TGTTTTCAAG CGTAATATTT GCTAATTcTA	120
GgtTTTACAG AATAATGAAT GTCATCAGCT AmCCCTTTmm CtTGATACTy CTCTTGATAT	180
TTTCCAGCTT TAGCATTTGA TAAATCAATC ACTACETTA AATCTTCTGG ATTTTCAATT	240
TTTATTATCT TTGATTGTGG TCCTGAAATA GTCACATTAA CTGTTTCAGG CGCTTTTGTT	300
AAATGCAAAT CTTTAGTGTT ATAAAGAATT TCAACGGGTA CATCTTGAAT CGTTTTACTA	360
GACTTTTGAC CAAGATTACC AGTGTTAAAG ATATTTCCAA AAACATTGTT AACAGATAAA	420
AAGAAAAACA ATGCCAAAAG AAAGGCAATA AATCTCAAGC CCCATTTACT TTCTAGCATA	480
TTATTTTACA CCTTTCTTTT GAAAGCGTGT GCCAAACCAA TGTTTCAGCAA GCAACTCTTC	540
AAAAATTTTCG TTTGAAATGT CTCGTCGTAA TTTTCCATCA AATGTTACCG AAATATCACC	600
AGTTTCTTCA GATACAATAA CGGTAAATGC ATCAGATACT TCTGAAATAC CAACCGCAGC	660
TCTATGTCTT GTACCCAAAC TTTTAGATAT CTTAGGACTA TCAGACAATG GCAAATAACT	720
TGCTGCTGCT GCAATCTTCG TGCTTGAAT AATCATTGCA CCATCATGTA AAGGTGTGTT	780
AGGTATAAAG ACATTAATTA AAAGTTCTTG CGAAATATTT GAACCATTG CAATACCTGT	840
TTCAATATAA TCTTGAAGAC CTGTTTCTTT TTCAAAGACA ATTAATGCAC CTATACGTCT	900
TTTAGCCATA TATTGCACAG CCTTTGAAAC CGATTGAATC AATTTCTCTT CATCTTTACT	960
ATACGTATTA GAAGTATAGC GTTTTAAAAA GCTACCTCTA CCAAGTTGTT CTAACGCACG	1020
TCTAATTTCT GGTGGAATA TTAATAATTA AGCTAATACC CCCATTGAA TAACGATATC	1080
GAATAATTTA GATGTTGCAG TCAAGTTCAA TATCATACTT ATCTGCTGAC CAATAACAAT	1140
TACTAATATC CCTTTAAGTA ATTGTATCGC TTTAGTTCCC TTAAAGACCG TGATGAGAAG	1200
ATAAAGTACA TACCAAACTA TCAGTAATC AAGGATACTC GTTACAATTT TTAACGTACT	1260
GAGGTTTTGA AAAAAGTTGG AAAAATCCAT AACATCTCCT CCGGGTAATA TTTTCCATA	1320
ATACCCATTA TACCAATCAT TT	1342

(2) INFORMATION FOR SEQ ID NO: 414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

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CTGTATAAAG ATGGAGGTGT TTTGCATGGT AAAACGTACT TATCAACAA ATAAACGTAA      60
ACATAGTAAA GTTCATGGTT TCAGAAAACG CATGAGCACA AAAAATGGCC GTAAAGTTTT      120
AGCGCGCCGT CGTCGTAAAG GCCGTAAAGT TTTATCTGCA TAAGATCACT GACTCATCAG      180
TGAtCTkTTT TTTCGTTTAA ATTAAGAATA AATAGAAATT TATGTTATAA GCTCAATAGA      240
AGTTTAAATA TAGCTTCAnA TAAAAACGAT AnATAAGCGA GTGATGTTAT TGGAAAAAGC      300
TTACCGAATT AAAAAGAATG CAGATTTTCA GAGAATATAT AAAAAAGGTC ATTCTGTAGC      360
CAACAGACAA TTTGTTGTAT ACACTTGTA TAATAAAGAA ATAGACCATT TTCGCTTAGG      420
TATTAGTGTT TCTAAAAAAC TAGGTAAEC AGTGTTAAGA AACAAGATTA AnAGAGCAAT      480
ACGTGAAAAT TTCAAAGTAC ATAAGTCGCA TATATTGGCC AAAGATATTA TTGTAATAGC      540
AAGACAGCCA GCTAAAGATA TGACGACTTT ACAAATACAG AATAGTCTTG AGCACGTACT      600
TAAAAATTGCC AAAGTTTTTA ATAAAnAGAT TAAGTAAGGn TAGGGTAGGG GAAGAAAAC      660
ATTAACCACT CAACACATCC CGAAGTCTTA CCTCAGACAA ACGTAAGACT GACCTTAGGG      720
TTATAATAAC TTACTTTAAA ATGTATTCAC ATCGTTGAAG GAGGCGAGTA GCAATATGGA      780
TTTAGATACA ATTACGAGTA TTTCAACACC AATGGGTGAA GGGGCAATTG GAATTGTTTCG      840
ATTGTCTGGA CCGCAAGCCG TTGAAATTGC TGACAAATTA TATAAAGGAA AACATCTTTT      900
AAATGATGTT CCATCACATA CGATTAATTA CGGTCATATT ATTGATCCAG tCTAAAGAAG      960
TGGTTGAAGA AGTTATGGTG TCTGTGTtAA GAGCGCCAAr AACATTTACA CGCGArGATA     1020
TTATAGAgAT TAATTGTCAT GGTGGtATtk TAACaTTAA TAGAGTGCTG GGA              1073
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(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

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CTTTACCAAT GCCAAATCCG AAGTAAAGTA TAGCAATAAA GATTACTAAT ACAATTCTGT      60
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AAATGGCAAA	TGGAATTAGT	TTGATTTTGT	TAATTAGATG	CAAGAATGTT	TTGATTGCAA	120
TTAGTCCAAC	AGTAAATGCA	GCTAAAAAGC	CTAAAATATA	AAAAGGTATA	TCAGCATCT	180
GAATATCTTG	ATAATGTTTT	AATAAAGATA	AACCACTAGC	TGCTAACATA	ATTGGAACAG	240
CCATAATAAA	TGTAAAGTCC	GATGCTGCTT	TATGATTTAA	TTTCATTAAT	ACCCCAGTTG	300
AAATTGTTGA	GCCTGAACGG	CTGAAACCAG	GCCACATAGC	TACTGCTTGA	gAAATACCAA	360
TTACAAATGC	TTGGAAATAA	CTGATTTGAT	CTACTGTTTG	TGGGTTTTTA	ACTTTAGCTG	420
AGTATTTATC	AGCAATAATC	ATATAGATAG	CACCTACGAA	TAAGCCAATC	ATAACAGTTG	480
GCACACTAAA	TAAATGTTCT	TCGATGAAAT	CATCAAATAG	TAAGCCTAAA	ATACCTGCTG	540
GCACCATACC	CACTAATACA	TGTAATAAAT	TTAAACGTT	TGGCTTTGAA	CGTCTTTGTT	600
GATCGTTATC	TCCTTCAACA	TGTTTGTGTT	TACCAATATG	TAAAATCTCT	AAGAAGCGTT	660
CGCGGAACAC	CCATGCTGCT	GCAAAGACGG	ATCCTAATTG	GATGACGATT	TTAAATGTAA	720
ATGCTGACTG	AGAACCTAAA	AATTCAGATG	ATTTTAACCA	CATATCATCA	ACTAGGATCA	780
TATGTCCAGT	AGAGGAAACA	GGTGCAAATT	CTGTTAATCC	TTCGACGACC	CCTAAGATAA	840
TACCTTTTaT	TAATTCAATG	ATAAACATAA	TGTACCCACT	TTCATTACTC	AATTTAATTT	900
ATTTAAATAT	CAAAATTACC	ATATCATGAT	AGCATATTCA	TTTAAAGACA	TGCTAGTTAT	960
AGTTATAATA	CTAGACTAAA	GATGTATATA	TTCATTTTCT	TTTACATGTA	AAACTACAAT	1020
ATTTTATTGA	GCTATTTAAT	TTGATTTTAA	GGAAAACCTT	TTATAATAGG	TTTAGGTGAT	1080
ATAATTGTGA	AAAAATTAAC	AACAATACTG	TTTCAATATA	AAATTTTTC	GGTACTCATG	1140
TTCTTGGTCA	GTA CTGGTCT	CGGCATAATC	GTTATAACGC	AAAAATTTT	AATAGCAGAT	1200
TTTTTAGCTA	AAATTATAAG	ACATCAATTT	CAAGGTTTAT	GGATTGTATT	ATTTATTTTA	1260
TTAGGTGTTT	TACTTTTAAG	AGCAACTGTG	CAATTTCTAA	ATCAATGGTT	AGGTGATACA	1320
TTAGCATTTA	AAGTTAAGCA	TATGCTTAGA	CAGCGGGTTA	TTTATAAAAA	TAATGGTCAT	1380
CCAATCGGTG	AACAAATGAC	TATACTCACA	GAAAACATTG	ATGGTCTAGC	ACCTTTTTTAT	1440
AAGAGTTATT	TGCCTCAAGT	GTTCAAATCA	ATGATGGTTC	CGCTCATCAT	AATCATTGCA	1500
ATGTTTTTCA	TCCATTTCAA	TACCGCATTA	ATTATGTAA	TAAGTGCACC	ATTTATTCCT	1560
TTGTTTTATA	TTATTTTCGG	TTTGAAACG	CGAGATGAGT	CAAAAGATCA	AATGACTTAT	1620
TTGAATCAAT	TTAGTCAACG	GTTTTTAAAT	ATTGCTAAAG	GTTTAGTGAC	GTAAAGCTA	1680
TTTAATCGTA	CAGAGCAAAC	AGAGAAGCaT	ATTTaCGACG	ATAGTACTCa	GTTTAGAACT	1740
TTAACAATGC	GCATTTTaCG	CAGTGCTTTT	TTATCGGGAT	TAATGCTCGA	ATTATAAGT	1800
ATGTTAGGTA	TTGGATTGGT	TGCATTGGAA	GCAACGCTAA	GCTTAGTAGT	ATTCATAAT	1860

ATTGATTTTA	AAACTGCGGC	AATTGCGATT	ATTTTAGCGC	CTGAATTTTA	TAATGCAATT	1920
AAGGACTTAG	GGCAAGCGTT	CCATACTGGA	AAACAAAGTG	AAGGTGCCAG	TGACGTTGTG	1980
TTTGAGTTTT	TAGAACAACC	GAACATAAAT	AATGAATTTT	TATTAAAGTA	TGAGGAAAAC	2040
CAAAAGCCAT	TTATTCAGTT	AACAGACATA	TCATTTTCGAT	ATGATGATTC	TGATAGATTG	2100
GTATTAAATG	ATTTAAATTT	GGAAATATTT	AAAGGTGATC	AAATTGCACT	TGTAGGTCCA	2160
AGCGGGGCAG	GTAAATCCAC	TTTGACACAT	CTTATGTCAG	GTGTTTATCA	GCCAACAATA	2220
GGTACTATAA	GTACAAACCA	GCGTGATTTA	AATATAGGAA	TACTTAGTCA	ACAGCCATAT	2280
ATTTTCAGTG	CTTCTATAAA	AGAGAATATT	ACGATGTTTA	AAGATATAGA	AAATAATACT	2340
ATTGAAGAAG	TGCTAGACGA	AGTAGGTTTA	TTAGACAAAG	TGCAATCTTT	CACAAAAGGC	2400
ATTAACACAA	TAATAGGTGA	AGGAGGCGAA	ATGTTATCTG	GTGGACAGAT	GAGACGCATA	2460
GAACTTTGCC	GTCTTTTAGT	TATGAAGCCA	GATCTCGTTA	TATTTGATGA	GCCTGCAACT	2520
GGTTTAGATA	TTCAAACAGA	ACACATGATT	CAGAACGTTT	TGTTTCAACA	TTTTAAAGAT	2580
ACAACGATGA	TTGTCATTGC	ACATAGAGAT	AATACAATTC	GCCATTTACA	ACGACGCTTG	2640
TATATAGAAA	ATGGAAGACT	GATTGCTGAT	GATCGCAATA	TTTCAGTAAA	TATAACAGAA	2700
AATGGTGATG	ACTTATGAAA	ACACGACTAA	AATTTCAAGT	AGATAAGGAT	TTATTGTTAG	2760
CTATAGTTGT	TGGTGTTTGT	GGAAGTTTGT	TTGCGCTCGC	ATGTTTTTTC	TTAAGTGGTT	2820
ATATGGTGAC	ACAAAGTGCA	CTTGGTGCGC	CACTATACGC	TCTGATGATT	TTAGTCGTTA	2880
CAGTAAAATT	GTTTGGGTTT	TTAAGAGCTA	TTACTCGATA	CGTAGAGCGC	CTTATTTCTC	2940
ATAAAGCTAC	ATTTACAATG	CTACGTGATA	TTCGGGTACA	GTTTTTCGGT	AAATTAGTAA	3000
ATGTCATTCC	TAATGTTTAC	CGTAAACTGA	GTTCTAGTGA	TTTAATTTCA	CGTATGATTA	3060
GTCGTGTTGA	GGCATTACAA	AATATAKATT	TACGTGTTTA	TTATCCACCA	GTCGTCATCG	3120
GTTTGACAGC	GCTAGTTACA	GTCATAGTTT	TGGCGTTCAT	TTCAATCGGC	CATGCG	3176

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

TCTTTATTTT	AATTTCCAAT	TGAATTTTTT	TATTATTTAC	GCATAGCTCT	TAAAATTAAC	60
GTTACGATTG	CAATTAAGAT	AATTGAACCA	ATTAATGCTG	GCAAGATGTA	AATACTTCCT	120
AATTCAGGAC	CCCATTGTCC	GAATAGTTTG	CCACCTACCC	ATGATCCAAT	AATACCTGCG	180

ATAATATTGC CTAAAATACC ACCTGGGATA TCTTTACCCA TAAAGCACC AGCAGCCCAT	240
CCAATTAAGC CACCGACAAT TAACATTCCA ATAAATCCAA ACATAATTTT CAGTCTCCTT	300
TTTCTATTTA TTTTGC GTTA TTCTAAGTAG TACCCCTTAT TTACAATTCT AAAACAAATT	360
CAAATTATTT TTATCCAAAT ATTTTAAAA GTAGTAATTG AATATCAATT TTATTCAATG	420
TAGCTATCGT TATTTAAAGT CTCTGTACCG ATAATATCAT ATACATTTAC ATTATTTTTT	480
CTGCCGAATT CATAGCTTGA TTATTTTATG TTATAGGACT AgAATATACA CATATTATTA	540
GAGCATCTTT GAATTTTAAA TCAAGAAGCG AGGTTAATGA ACAATGAATA TGCATATTTT	600
ATATaACTTA CGAACTAAAC ATAATTAGA AATTGACGAA TTAGCACAGC AATTAAATGA	660
GAAATATGGT ACTAAATATG AAGCACATCA AATTTGGGAA TGGGAGAATC ATCACCATGA	720
ACCTAAATTT AAAGATGCCA TGCATTTAGC TGACTIONCTTT GATGCACCAT ATGAAATGTT	780
TTTAGAAAGT AAGGTTAAAG AATATCAGAA ACATTTAGAA GAAGTCGATA TCGCATGGA	840
TAAATAGATG CAAATAAACC CTCACAACAC GTTTGGCATA TATCCTTTCA AATCTATACT	900
GGATATATTA CATTACGTTG TGAGGGTATT TTATTAATTA ATATGAATTA AGACATTTTA	960
CAAGCGTTAA TGCAACGAAT CTTTTTAGTG ATCTTGCTCA CTCTTTAATA CTTTACCGTT	1020
CTTAGCATCA ACAGTAACTT CTTGTTTTTT ATTACCTTTT TTCAAATCGA TATTGTAAAC	1080
AAGTTTGCCA TCATCTTTTT CAAGTGACCA TTCTTTAATA TCACCATCAA ATTCTTTTTG	1140
TCCTTCTTTA ATGGCTTTTT TGTAATCTAT AGCATCGCTA TATTTAAAGT TATCATTTTC	1200
ATTCATTGTA TCTTCTTTTT CAGTCTTTTT GTAACTACT TTTTATTTT TATCAGCAAC	1260
AAGTACTTCT GACTCTTCAC CAGATTTTTG TTGCGTCACT TTATAAGCCC ATTCACCATT	1320
AGAATTTTCA AATGAAATTC CTTTCAACTT TTGGCCTTTG TAAGTTTCTT CAGCTTTTTT	1380
CACAGCATCT TCTGGGCTTG TTTTAACATC TTTTAAAGCA ATAACATCTT TTGTTGTAT	1440
AGTGTCTTGA TTAGTATTTG ACTCTGTTGA TTTTGTTTCA TCTTTTGGAG TATCATTGCC	1500
ACATGCAGTA AGCACCACCG CTGACATTGA TAACACTGCT AATGATTTTA ATTTCATAAT	1560
ATCACTCTCT CTCCTATTT TTGAAACTCA TAACAAAAGC TTATATGCTA TATAGATTGT	1620
ATTACCCCTT GTTTTAAAT TTATTCATAA TTATTACAAA TATTTTAAA TTAATCGTCA	1680
TGCGTTACTT TCGTTCGTAC TCCTTTTATA AATGAACCAT GTAATATAAG CATGCTATTA	1740
TCGACTCAGT TTGTCTAATG CTTTCTTTGG TACTTCTTCC TTTTCAACTT CTTCAAAAGT	1800
TTCTACATGA TGACCTTTAT GTGTAATTTT CAAGTATCTATGCGGTTTAA CATCAAATGT	1860
AGCAGTATAC ATTAATTGCG TCTCTTTCCC TTCTTTATTA AAAACACTTT GACTATAACT	1920
TCGGAGTTGA TCATCCATTC TAGTAGACAC CTCTGTCGTT TTAACATAAG AATCATCCTT	1980

CTTTACTAAT GGGTTAAATT GATCTGTTAT ACCATGGGAG TCTATTGTTT TTAAAATGAA	240
TAAAGCAgCA TAAGCGCCAA TGATAGTAAG TACAAGATAt GTkATTGTTT TTAAAATCGT	2100
TTCAAAAAGA	2109

(2) INFORMATION FOR SEQ ID NO: 417:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

GTTACATAAA TGAAAACAAA AAAGATAATT TTACTGCTTA TGCTACACCA GAACATAATT	60
ATCAATTTGG TGGTGCTATG ATAGAAAGTG AAAAATTAAG CGAGTTACTA AAGCCAGCCA	120
ATCAGTTAAA ATCACCAGAT GATATAAAAA AAGAACTAAA TAAAAAGAAG AGTCACTAAA	180
GTTAGGAGTT ACTTTAATGT CCAAAAAACA TGTTTTTATA ATTATTGGTG TCATATTGTG	240
TATATGTACA GTTTCTACGG TCATGCATTT TAAAATGAAA TATATGAAA AAGAAAAACA	300
AAAAGCGATT TACTACAAAG AACACAAGA ACGTATTACA CTCTATCTTA AGCATAATAC	360
TAAAGAAACG AACACGATTA AATCTGTACA TTTCACAAAC TTGGAAACAA GTCCTATGGG	420
AAGTGCTGTG ATTGAAGGAT ACATCAATGA AAATAAAGAA GATGATTTTA CTGCTTATGC	480
ATCGCCTGAA CATAATTATC AATTTGGTGG CGCTATGATA AAAAGTGAAG GAGTAGATAA	540
ATTATTAAAA CCAGCACATG AAAGAAAATC ACCAGAAAAA ATCAAAGAAG AATTAGATAA	600
AAAAGAAGGC CACTAGGGTC TTCTTTATTT TTGATTTAAT CTTCCAATAA TCTATGTCAT	660
TGCTATCGAA GGTGTTTCGC AATTAAATA AATCACTTCA TCATCACCAA TACTTCCCCA	720
GTTTTGTACA GTACATTAAC ACAAACGAAC CACGTTAATT TAAATGGAwT AaTAGTTTGG	780
CCATTATAAG AACAATATAT ATCGAnTAAC AAT	813

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 640 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

AAAAGCAATC GTTGGTGGTG CTAAATTCAT CGGCAACTCA TATGTAAAG CTGGTCAAAA	60
TACACTTTAC AAAATGAGAT GGAATCCTGC ACATCCAGGA ACACACCAAT ATGCTACAGA	120

TGTAGATTGG GCTAACATCA ATGCTAAAAT CATCAAAGGC TACTATGATA AAATTGGCGA	180
AGTCGGCAAA TACTTCGACA TCCCACAATA TAAATAAGCA ACATGAACAT AGGATCAAAA	240
GTCATCCCC ACTATCAATC ATGGGGGATG ACCTTTTGATC CCTTTTTTAT ACATACAACA	300
GCAAAAATAG CGGTGATTGT TTACCATCAA TTTTAACAAT CACCGCTACT TTTGCTTGTA	360
ATTCATGATT CAATTTTTGT TGTGTGCACA ACGACACTAA ATTATGTGTT TGCTATTGTC	420
GTGTTACAAC GATATGCGTC GTTGATTTAA CTTATCAAGT AATTGATTTA AATTGTCTAA	480
TTCGACTTCC GATAAACATT GACATCTTGC TTCAATCAAT TCGCAACGTG CATTATTTAT	540
TTGTGAAATT AATGTACGTG CTTGATCAGT CAAAATTAAT TCTTTACATC TTAAATCTTC	600
GCTAGATTGT TGACTTGTGA TGTACCCnnt CAAAATAAT	640

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

nTAGTTTTAA ATATAGTAGT CTTCAAATAT ATCATTAGCG TTTAATACTA CCTTAGCACC	60
TTCTTGATA CGTAATAAAT TACCTTTTGT CATAGGATTA AACATAGATC CAGGTAAAC	120
ATAAACATTT CTATTTTGCT CTAATGCAAA ATCTATCGTG ATGTGACTGC CACTTTGTTC	180
CTTAGCCTCA GTAATTAAAA CCCCTTTTGA CAAACCGCTG ATAATTCTAT TGCCTCAGG	240
AAATCTATAT TTAGCGATTG GTGTATGTGG TGGATATTCA GATATAACTA AACCTTTTTC	300
TTCTATTTTA TTTCTTAATG CTAATGTACT TTTGGGATAA TGTGTTTGAT GGCCAAAGGC	360
TAAAACTGCA ATTGTAGGGA GATTGTATTT TAAAGCTATT TGATGTGCCA TTGCATCAGC	420
TCCTTGAGCA AGGCCGAAA CAATTGTAA ATATTGCTT TTATCATTTG ATAATAAAAA	480
TTCTAAAGAC TGTGGGTAT AACTTGTAGA ATCTCTTGCA CCTACTACTG CCAAATGATG	540
CATATTATTT ATTAATTTGA TGTTCCTTT ATAGAAAAGA AGTAATGGAA ATTGATAAT	600
TTCTTTTAAT AGCACTGGGT ATTCAGAATC CATATATGTA ATGTAACCTA CTTTAAATTT	660
CTGCAGTTCT TTAATAATAT CGTTATGATC AAGTTTTATA AAAGCATAGT ATTTACGTAA	720
TAAATGAACA TTTTCTTCCC TATTCACCCA TTCACATAAA TAACTATCTT TTTTCTTCC	780
CTCCTCTTTA ATTACATTAG GATATGCCAT TAAAAATTGA TGAATTTGTT TAGTCGAAAA	840
GTGTGCCCAG TATAACTTAA GCAAAAATAG TTTAATCAAT AAATCAACTC CTTTTTGTA	900

TCATACAAAA TCATATTCTA TTTTGTGTTT ACATTTCTAA TACAAAAACA TTGTCGATGT	960
AATGTTATTT TAAGGAGTAA AAATACTGAC TTAAAAAGTGAAAAGTATGT TGGAAAGAAT	1020
TTAAAATTTT AATTTCCAAC ATACTTTATA ATTAAACCTT ATAAATAAGT TTTGCAAATT	1080
TATATAGAAT TGGTCTTACT GGTGATGA AATCACCAAT TAATTCTTCA ACATGTGCAT	1140
TAAAACCCTT TTAAATTG	1159

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 420:

TCAATCAGCG ACTACAAGAA GTGCGGGTCT TCAAACAATT GATGTGACAA CACTAAGTGA	60
CCCCACTAAT ATTATCATGG GTATTTTAAT GTTTATAGGA TCTTCGCCAA GTTCGGTTGG	120
TGGCGGTATT CGTACAACAA CTTTCGCTAT TTTAATTTTG TTTTAAATTA ACTTTAGTAA	180
TAATGCCGAT AAAACATCCA TTAAAGTTTA CAATAGAGAA GTACACATTA TGGATATTCA	240
ACGTTTATTT GCAGTATTTA CAATGGCGAC AATTTTAACA TTTTATAGGAA TGCTAATTAT	300
ATCAGCTACT GAAAATGGTA AGCTTACATT TTTACAAGTA TTTTGTGAAG TCATGTCTGC	360
ATTTGGAAC TGTGGACTAT CGCTTGGTGT CACAAGTGAT ATAGTGATA TTTCTAAGGT	420
CGTACTAATG ATACTCATGT TTATAGGACG TGTGCTTGA ATATCATTTA TCATTATGAT	480
AGCAGGACGT CGAGAACCAG ATAAATTCCA TTATCCAAAA GAACGTATTC AAATAGGATA	540
ATATAATAGC AATCTAAGTT TAGTTAATGT AGATTTTAAC TGGAACCTAG ATTGCTTTTT	600
TAGTTTGTAT TTTTAACTTA TTTTATAAGA CGATTGGTTT CGAAAATGGT AAAGTAGTAA	660
CAATGAGAGG TGTAACATGA TGGAAAAAAA TGAAAACATT AATGTAGAGA TTTTAACTAC	720
GTCAGATATG CATAGTCATT TCTTAAATGG TGATTATGGT TCAAATATTT ATAGAGCTGG	780
TACTTATGTT AACCAAGTAA GAGACAAAA TCATCGCGTC ATTTTATTAG ATAGTGGCGG	840
AAGTTTAGCT GGCTCGTTAG CGGCCTATTA TTATGCTATT GTTGACCTT ATAAACGACA	900
TCCAATGATA AAGTTAATGA ACAGAATGCA TTATGATGCT AGCGGTGTGA GTCCAAGTGA	960
ATTCAAGTTT GGTTTATCAT TTTTAACTCG TTCAATTGCT TTGGCACGTTTCCATGGTT	1020
ATCAGCAAAT ATTGAATACA ATGTTACTAA GGAGCCTTAT TTTTCAACTC CATATTGTAT	1080
TAAACATTTT GGTGACTTAA AAATTGCTAT CGTAGGCGTC ACAGCAGATG GTTTAATGGA	1140
AAATGAGTAT TCTGAAATGG AGCAAGATGT ATCTATTGAA AAGACATTAG TGGCATCAAA	1200

ACGTTGGATT AGATATATCC ATGAAGTTGA AGAGCCAGAT TTTTGGATTG TAATTTATCA	1260
TGGTGGATTG AATAAAATTA GTAATAGTAC GAAAAATAAA AAGGCAAGTT CGAATGAAGC	1320
TGAAAAATTA ATGGAAGAAC TCGGTGTTAT AGATTTAATG ATTACAGCTC ATCAGCATCA	1380
AACAATAGTA GGTCAAGATC ATGAAACGTA TATGTTTCAG GCTGGTCAAG ATGCCAAAGA	1440
GCTTGTACAT CTTTCGATTA ATTTTAAAAA GAGAACAACA ACTTATGATG TTGAAAGCAT	1500
TGATTCTAAA GTGATTGACT TAAATGAGTA TGAAGAGGAT CAAGAATTAT TAGATTTAAC	1560
ATTCTATGAT AGAAAAGCAG TGGCTTATTG GTCACAGGAA ATCATAAGTG ATAAAGETT	1620
GATGTTATCA GTAAATGGGT TACAAGATTT AGTCTGTCAA ACACATCCAT TTTCGCAATT	1680
ATTACATGAT GCAATTCACC TTGCATTTGA TAATGATATA ACATGTGTCC ACGTGCCTAT	1740
GaACGGAGAG AAGGGGTTGA GTGGACAGAT TCGAAATGAA GrTTTGTATC aTGCATACCC	1800
ATaTCCAGAT aAGCCAtGGG tATGACAATT aGTGGTCAAA ATaTCAAGGT ATnTTGGGGT	1860
ATAGTTATTC ACCATTAGG	1879

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2710 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

AATCCCCCT TTTTCCCCT CCATTTTnCC ATCCACTGGT CCTTACGGGA CCATATTATT	60
TnAAATTGGA nAAATTATt TTAAAGaTTA TwAaACTCT TtAATCATTt TrGTGAATTA	120
AAAAAAGTAG TGCAAAAAGC AAAATATACT TTATACACTA CAAATCATTt ATTTATAATA	180
AAGTTTCACC AAAAAATGTT CCAACTAATG AAACCGCTTG TTCAGCAGTA TGATTATTAC	240
TGTCAATCAA TGGATTTACT TCAACTAAAT CCATTGAGGA AATTAAATGT GATTGATGCA	300
GTAATTCCAA TGCAAAATGG CTTTCTCTAT AACTAAGACC ACCCAAACT CTAGTACCAG	360
TGCCTGGCGT TTCAAGCGGA TCTAAAGCAT CAACATCTAA AGATAAATGA ACGCCATCAA	420
CATTGCGTGA CTTCAAATAT TCTATTGTAT TTTCAATTAC TTCCTTTATC CCCAATTTAT	480
CAATATCTGA CATAGTAAAT GTTTTAATAT TATGATCTTT GATAAATTGT CTTTCACCTT	540
TATCTAAATC TCTCATACCA ATTAGTACGA TGnTTTCTGG CTTGATTACA TTACnATTTA	600
ATTCTAAAAG TTCTTTGGGA CCTTCGCCGTG TCAAATCCT TAGAGGCATA CCATGAATAT	660
TTCCACTTGG TGACTCTTCA GGTATATTTA AATCACCATG EcATCATAC CAAATAACAC	720

CTAAATTATT	ATAATGTTTA	CTTATTGCTG	ATACTGAACC	TACCGCAATA	GAATGATCTC	780
CACCAAGAAC	TAGAGGAAAT	CTGTTATTTT	CAATTGATGC	TGAAACCTCT	TTATTTAATT	840
TTTGATTAAC	ATCTATAATT	TCATCATAAT	TTCTTAATCC	TTTTTGTTCA	CTATGAAATT	900
TTTCAATGTT	CACAGCAGGt	ACCTTAATAT	CCCCCTTGTC	ATATACATCA	AGGTCTAATT	960
GCTTTAATCT	TGAAATTAAT	CCAGCATATC	TAATTGCTGT	TGGTCCTAAA	TCAACACCTA	1020
ATTTTCTTTG	TCCAAATGTT	GATGGTGCAC	CTATAATATC	AATTGCTTTT	GTCTTTGTCA	1080
TAAGCGTCCC	CCTTTGCTCT	ATGAATTAA	AGAATAATGT	ATGCGCTTAC	CATTATCAAG	1140
CAATAGCTAC	ACATATAATC	TGTTTATCTT	ATTACTTCAT	AAAAAAAGGT	TCTTCATCTT	1200
TTATGGTGGG	AAGGTAAAC	TTCCTGCTTT	TTTTAATACA	CAAAAAGCGC	AATTGCCTCT	1260
ATAATTTAAA	GTGACCAAAC	CCAAACTAAA	GGAGACAAGT	GCGCCTATg	GTAATGATAC	1320
CTTAGAATTA	CTAAGAATAA	AAGATGAAAA	TATAAAATAT	ATAAACCAAG	AAATTGACGT	1380
CATTATCAAA	GGAAAAAAG	CAACAGTGGT	TAATGCTGTA	CTAACGTATA	AGCCTTCGGC	1440
CTGTTATTGT	TGTGGAGTTA	AAAATGAAGG	ACAAATTCAT	AAACATGGTA	AGCGTGTTTC	1500
TCGTATTACT	TTACTTAAAA	CTCAAGGGTA	TAACACATAC	CTCAACTTAG	CTAAACAACG	1560
TTTTAAATGC	TTAGAATGCA	ATGGcACTTT	TACTGCTAAA	ACGTCAATTG	TTGATGAGTC	1620
GTGTTTTATC	TCAAGATGTG	TTACTCAAAA	AGTTATAGAA	GAAGCTACTA	AAGTTAAAC	1680
AGAGATTGAT	ACTGCAGAAG	ATAACTGTAT	CTCTCCATCT	ACTGTAAGTC	GTATTAGAAC	1740
TAAAGCGGCT	AATTCATTAC	GAATTAAACC	CTTTAATTGT	TTGCCAGAAC	ACATCGCTAT	1800
GGATGAATTT	AAAAGCGTTA	AAAATGTAAC	TGGATCAATG	AGTTTCATTT	TTATAGATAA	1860
TGATACTCAT	GATGTTATAG	ATATTTTAGA	AAATAGAACT	ACAAGATTCT	TGCGTgCTA	1920
TTTCGAGCGA	TTCGATTTAA	AAAATCGACA	ACAAGTTAAG	ACGGTTACTA	TTGACATGTA	1980
TGAACCCAT	GTCCGATTAT	TTCGCGACCT	ATTCCTAAT	GCAGCTATTA	TTTTTGACAG	2040
ATTCCATATC	GTTCAACATT	TAAATAGAGA	ACTTAATAAG	TATCGTGTAC	AAGTTATGAA	2100
TGAATACCGT	AATAAAAAAG	GACCTGATTA	TACAATTTTT	AAGAATAACT	GGAAAGTCCT	2160
ATTGATGGAT	ACTAGTAAAA	CCATATTTAG	TAAATACAGA	TGGAATAAAT	CTTTTAAGGC	2220
TTATAACGC	TCATCTGACA	TTGTAGAATT	CATGCTTTCA	AAAGACGATA	TACTACGACA	2280
CTCCTACGAA	CTTGTCCAAG	GATTACGAAA	AGACCTAÆG	TTATGTAATT	GGCCTAAATT	2340
TATTAATCGT	TTAAATTCAG	TTAGTAAAAA	GTCTGTGAGT	AAGGGTGTAT	GGAAAGTGGT	2400
TAAATATTAT	AGAAAACATC	AAAGGATGTT	AAGAAATACA	ATTTATTACC	CAGCATTTAA	2460
TAATGGTGCT	ATAGAAGGAA	TTAATAATAA	GATAAAATTA	ATCAAGTGAA	TTTCTTTTGG	2520
TTACAGAAAT	TTCAACAAC	TTAAAGCACG	TATAATGATG	aTTTTCAGCT	TGTACAAAGG	2580

AGaAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC GCCTAATAwA nGGGskCTAA	2640
AAGTTgTATT TTTAAAAATA GTTCCTTTAA ATTATATACC CnCCACATTT GGGGGAGGAC	2700
CTAAAAAAGC	2710

(2) INFORMATION FOR SEQ ID NO: 422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

CATTTTAATT GtTaAAATTC CAAAAAAtGT ArGTGGATTw AAAGrAAACC CtGTGTTTTT	60
AAAAGGtACC ATTaAAATAg TTCCGATTGT ACCATCCCAC GTGAAAtTTT TAgTAtTGCC	120
GGTGaGAGAA AATGCCAATG CAATCATCGC AGTTCATAATCATCCATCCG GTGATGTAAc	180
GCCCTCACAA GAAGATATCA TAACAACAAT GAGGTTGAAG GAGTGTGGTT TGATTTTAGG	240
GATAGATTTA TTGGATCATA TTATAATCGG TGATAATAGA TTTACCAGTC TTGTAGAAGC	300
GGGTTACTTT GATGAAAATG ATTGAAGTTG ATAGAATTAA TGACGTATCT TGTGTATAAT	360
ACCTACGAAG TACTTTCATT GGAGGAAAAA TAGTGACTCT ATTTATTATT ATCGGGGTTC	420
TCGTGCCAAT GGTTTATACC ATGCAGTTAA ATATTAAAAA TGAACCTGTa ACAAAGCGCA	480
ATCTTTTAAT AACATTAGCT TTATCTACGT TAGGTATTTT AGTAACCGCG TTAGCAGGTG	540
TAATCGTTAC GAAACAAGCT TTCCTTTAT TAAGTGTAGC AATTGGCTCA ATTTTACTG	600
GAATCGTTTG GGGCCTTTTA CTAAGTGGTA GcTACGCGCT GATACGATTT TTATCTAACG	660
CATTTGGGCG TAAGTAATAG TAATCTGTTC ATCAAGTAGT ATCCGTGCTT GAAAACAAAC	720
TAAAACTCCT AATGTGGAAC TAGTTAAAAA ATTCTAAACT AGTACATgG GAGTTTTGTT	780
ATGCAGAATA AATTTAATTG TTAAATTGAA AGTGCGGTAA AAATCCACTA TTTATTTGAA	840
AAAAATCGAG CAACCAATT AAACCTTGAT ATCCTAAGTA AATACATAAT AAAACAAGTC	900
CGACATAAAT TAAAAATCGC AAAATAGAAA GTCCAACCTCT AAAAAGGAGG ATGACTAATA	960
GTGCTATTAA AATAATTGt AGTATACTCA ATGCTACAAA CCTCCTArTA CGCTTTTAA	1020
TCCATAA	1027

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

CGGCACATTT TTAATTTATA CATATTTTAA AACTAAGTAA CAGTTTGAAG AAATCGTAGT	60
TCAATAATGT TAATTGTGAA AATGTATATA AACATAAAAA AATCATGTAT AATATATGTT	120
GTTAATTAAA CAGTTCGAAA GCGAGATGAC ATTATGGGAC GTAAATGGAA TAACATTAAA	180
GAAAAAAAGG CCCAAAAAGA TAAAAACACA AGTAGAATAT ATGCGAAATT TGGTAAGGAG	240
ATTTATGTTG CAGCAAAATC TGGTGAACCC AATCCAGAAT CTAACCAAGC TTAAGGTTG	300
GTGCTTGAAC GCGCTAAGAC ATATTCAGTG CCGAATCATA TTATTGAAAA AGCAATAGAT	360
AAAGCTAAGG GTGCTGGAGA CGAAACTTT GATCACCTAA GATATGAAGG ATTTGGCCCA	420
AGCGGATCAA TGCTAATTGT TGATGCGTTA ACAAATAATG TAAATCGTAC TGCCTCTGAT	480
GTGCGAGCTG CTTTGGTTAA AAACGGCGGT AATATGGGTG TATCTGGATC AGTTGCTTAT	540
ATGTTGTCAT GTGGCCACAT TTGGTATTG	569

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

TGGACCTATA AAATGGATGC ATCCAAATAT GGATGnGGGG TAnGGCGGGa AAATAGGaGG	60
TTATATAGTA AGTCATTTAA GTCGAATAE CATCCTTTTT AAAATGAAAA AAATAGAAAG	120
CTCAATAGTT TGTTAAAGCC TTAAATAGC GTCGTTACGC AATTTTAGAA TGCTAAAAAT	180
TGTCACAAAT TTCAAATTAC GTGCTAAAGC TTGAGATATC AATATTTATT GGCGATAGAG	240
TGTAATTTGA CTCCGCTTAC ATCTCAGTTT TATGTTTGTA ATTTGGTAGC ATAAATTAT	300
AATAAAATAA AATTGTTAAT CTTTAATTTC AGTATAGATA TTTTACGTG TAGTCACGTG	360
TAAATAAAT TCAATTAGGT TAGGAGACAT AATTATGAAA ACATTTGGTA AAAAGGTTGT	420
ATTAATCGGA GATGGATCTG TAGGATCAAG CTATGCCTTT GCAATGGTTA CGCAAGGTGT	480
TGCTGATGAA TTTGTAATTA TTGACATTGC AAAAGACAAA GTAAAAGCAG ATGTTCAAGA	540
TTTAAACCAT GGTACAGTCC ACAGTCCTTC ACCAGTTGAT GTGAAAGCAG GTGAATACGA	600
aGaCTGTAAA GATGCAGATT TAGTTGTTAT TACAGCTGGT GCACCTCAAA AGCCAGGTGA	660
AACACGTTTA CAATTAGTTG AAAAAAATAC TAAGATATG AAGAGCATCG TTAAGAGTGT	720

TATGGATAGT GGCTTTGATG GATATTTCTT AATCGCGGCA AACCTGTAG ACATTTTAAC	780
AAGATTTGTA AAAGAATATA CTGGATTACC AGCAGAGCGT GTTATCGGTT CAGGTACTGT	840
ATTGGACAGT GCACGTTTAC AATATTTAAT TAGCCAAGAA CTTGGTGTTG CACCTTCAAG	900
TGTTGACGCT AGTATTATTG GCGAGCATGG TGATACTGAA CTTGCAGTTT GGTCAACAAGC	960
AAATGTAGCA GGTATTTTACG TATATGACAC ATTAAAAGAA CAACTGGTA GCGAAGcTAA	1020
AGCGGAAGAA ATTTATGTGA ATACACGTGA CGCTGCTTAT GAAATTATCC AAGCTAAAGG	1080
GTCAACATAC TATGGTATTG CATTAGCATT GATGCGCATT TCAAAGCCA TTTTAAATAA	1140
TGAAAATAAT GTCTTAAATG TTTCTATACA ATTAGATGGT CAATATGGTG GTCACAAAGG	1200
CGTTTACCTA GGTGTACCAA CATTAGTTAA CCAACATGGC GCAGTTAAAA TTTATGAAAT	1260
GCCATTAAGT GCCGAAGAAC AAGCGTTGTT CGATAAATCT GTAAAACAT TAGAAGATAC	1320
ATTTGATTCA ATTAAATATT TATTAGAAGA CTAAGCCTAT TTTAAGTATT AATTAGAAAT	1380
ATATTAATGG TAAGAGGATC TATTAGTGTT GCAGTAACAC GTGGCACTGA TAGGTCCATT	1440
TTTTTAGCAA GCATTGATAG AGGCAATACT TTTGCGTAAA ATAATAATTG AATAAAGTAT	1500
TATGACTCGT GAAAATTTAG TGACATGAAT AAAAATGTTG AGGCGTCATT GAGTATAAAG	1560
GAAAGTAGTT CTGCATTAAT CACGAaGTAG AGCATGACmA CGAGGAATAA CTATAGGGaG	1620
ATGGTTTTGG AATGACGAtG TCTTGTATCA ACATGGTACA TTAGGTACGT TAATGGCTGG	1680
CTTACTAGAA GGCACAGCTA CAATTAATGA ATTGTTAGAA CATGGGAATT TAGGGATTGC	1740
AACGTTAACA GGGTCTGATG GCGAAtAATA TTTTtagacG GAAAGGCATA TCATGCTAAC	1800
GAGCATAAAG AATTTATAGA ATTAAAAGGC GATGAGAAAG TACCGTATGC ATCGATTACT	1860
AATTTTAAAG CGAGTAAGAC ATTTCCATTG CAACAATTAT CACAAGATGATGTATTTGCA	1920
CAAATTAAAA ATGAAATGTT AAGTGAGAAT TTATTTTCGG CTGTTAAAAAT TTATGGCACA	1980
TTTAAACATA TGCATGTACG AATGATGCCT GCTCAGCAAC CGCCATATAC ACGTTTGATT	2040
GATTcAGCAC GCAGACAACC TGAGGAAAAA AGACAAGATA TTCGTGGTGC CATTGTTGGA	2100
TTTTTTACAC CAGAATTATT TCATGGCGTA GGGTCTGCTG GTTTTCATAT ACATTTTGCG	2160
GATGATGAAA GAGCTTATGG TGGACATGTT CTTGACTTTG AAGTGGATGA CGTTGTCGTT	2220
GAGATACAAA ACTTTGAAAC ATTCCAACAA CATTTCCCGG TAAATAACGA GACGTTTGT	2280
AAAGCGAAAA TAGACTATAA AGATGTGGCA GAGAAATTA GAGAAGCTGA ATAGTCTAAT	2340
ATAATTAAAA GACCTTAGCG ATATTAGGAA CAGGTGGTTC TAAATGCATC GTTAAGGTCT	2400
TTTTATATTA TATATGTGCT TACATATTTT GTTGATACGC GCGTAAAAAG CTATAAATAG	2460
TATCAAGATA TGGGGTGTCA AGAATGTGTT CACGTGCACG TCGATAAATA AAGCCTTA	2520

TCGCTTCGAC TTCAAGAGGT TGCTGATGCG CAATGTCGTA ATACATGCTC GTTCCCATTT	2580
CGTCGGGATA ACCTTGATAT ATAGTCATAA TAGTATCGAC AGTTTGTCT GAAAAGTTTA	2640
ACCCCTCTGC CTGTGCAACA CGACAACCAT CTAGTAATAG CTGTCTACAC AGTGTACGTA	2700
TTTCAGGATT ATGCATGATT GCAACGGTCT GTCTACCGAG TGCTGTGATA GAATTAATGC	2760
CCAAGTTAAC TAACAATTTA TACCAAATAG CTTGTTGAAT ATTTGCTTCT AATACAATGT	2820
CGATTTGACT GTCTTGGACC AAATCTCTAA ATTGTCGAGT TAATGCATTA TCTTGTATAC	2880
GTAATTGATA ATCTCTGAAG TGCGTAACAA CATCGCCTTTCTTTTGACCA CTTATATAGA	2940
CAACTGCTTG GCATACGTTT TTAAATGAAA TATGTTTCGAG TTGACCATAA CCATTTTGGG	3000
CTAAAATGAT GAGCGTGTCC TCATGTGCAA GATGAGTTAA ATGAGGAATA ACTGCATCAA	3060
GTTGATGTGT TTTGACTGCA ATAATAATAA CATCAAATGT GTTTGTGACA TCTTCATAAC	3120
CTTTCACAAC AATATCTTGT GCAGGTGCAT GTGGTACAGT ATAATATGTT ATTGTTTTGG	3180
CGTGTCTCCC GATAAGCGTT GTATGAGGCA ATGATTGTTG TAATTCATAG GCAATAGTTG	3240
TACCGACAGC GCCTGGGCnn TTAC	3264

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

AGAACGAACC TTAAATAGT ACGTGTGAC CACGAAGTGT CATGACAAAT TGATAAAACG	60
AATAGTTTTT CATTAGTTCA TTGTCACATC AATCACTTTT GTkTCACCTT TAATCACAGC	120
ATTTTCATCA TAAATATTAA TTGAAGCTGC TTGATCAGTG TTAGTAATTA TAATTGGTGA	180
AATTACAGAT TTAGCGTTAT TATTAATATA TTCAAGGTTG AAETTACTA ATGGATCTCC	240
GACGTAACT TCGTCACCAC TAGACACTAA CACTTCAAAT CCTTCACCGT CTAATTGAAC	300
TGTGTCTAAA CCGATATGAA CTAATAATTC TAATCCGTTA TCTGCTTTTA ACCCAATCGC	360
ATGCTTAGTT GGAAAGACAT TGTCAACACG TCCTGCAATT GGAGACACAA CTTCTCCTTC	420
AGTTGGATTA ATACCAAAC CTTGCCCCAT CATTTTTTGT GCGAATACAG GATCTGGAAT	480
ATCTTCAATT TTCACGAATT CTCCAGTTAA TGGTGCATAA ATTGCGATAT CTTTCTGAAC	540
TTCTTTGCCT TTTCCGAATA ATTTTTTAAA CATACTTTCC ACTCCTACTT ATCAAAATGT	600
GATATTAAAT CGCCATAACC CAATCTTCT AACTTTTCAT ATGGAATAAA TTGAATTGCA	660
GCGGAATTGA TACAGTATCT TAAGCCGCCA CTTTCTTTAG GTCCATCATT AAAGACATGT	720

CCTAAATGAC TATTTGATTC TTCTGAACGC ACTTCAGTTC TCAACATACC AAATGATTTG	780
TCGACTAATT CTATAA	796

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

ATCCAGCAAA TCTTTCTTAT CACGTTCTGT AATTTTCTTA GTATCCATCT TGATTAGCTT	60
TGATAACTTT TCAGCCGTAT CCAACATTTT CGATTGTGTT GTTTTTCGAC CCCTAGTATA	120
TGTAATAGCC ATTTTAGAAG CATTATCAAC TAAACTTTT CCATTTCTGT CTAAAATACG	180
ACCTCTTGGC ACAGACTCAT TCACTGTAAT GTTTTCATCA TTTTATATAA TTTGTTTATA	240
ATGTGAGCCT TGTGCGATTT GTAAATAACC TAAACGTAGT ACTAGTACTG CAAAATATAA	300
TACAATCACA CCAAATATAA AGTTAATTCT CTTGTTAATT GTATTTTGAA CGATTTTCATC	360
ATTTGATTTT TCTTTTAGTC TTTTAAQA AACTACCTAC CTCTATTCAA AGTCTTTCAC	420
TTTAAATCAT ATATGAATTT AGAAATTATT TCTATCTTTT TGACAAAAAA ATAACGGTCT	480
CATTtAAGAG ACCGAACAAG TAATCATACT TTATTTTGTT GCATTATATA ATTCGTCAAC	540
TTTTTCCCAG TTAACACAT TCCAAAATGC GCCAATGTAG TCAGGGCGTT TGTTTGATA	600
TTTTAGGTAA TAAGCGTGTT CCCATACGTC TAAACCTAAA ATAGGTGTTT TACCCTCAGT	660
TAATGGATTA TCTTGTTTTG GTGTAGTCAC AATTTCTAAC TGGCCATTGT TTACGACTAA	720
CCAAGCCCAA CCTGAACCAA AGCGTGCAGC TGCTTTGTCA GCAAATTCTT TTTTAAATTC	780
TTCTAAAGAA CCCCATTGTT CTTTAATTTT TTCTACTACA GTACCTTTTTT CTTCTGAGTT	840
TGGTGAAAGT AACTCCCAGA ATAATGAATG GTTTAAATGT CCACCGCCAT TATTACGTAC	900
AGCAGTTTGG ATGTTAGCTG GTACACTGTC TAAATTAGCA ACAATTTCTT CAATAGATTT	960
AGATTCTAAA TCTGTACCTT CTAAGTCAGC ATTTATTTC GTAACATACG TGTTATGATG	1020
TCTGTCATGG TGAATTTCCA TAGTTTCTTT GTCAAAATGT GGTTCATATG CATCAAATGC	1080
GTATGGTAAT TTTGGTAATT CAAAAGCCAT AAATAATCAT CCTCCTAAAA TGTCTGTAAG	1140
TAAATAATAA CAAGCAGTGA CTGGTTCAAC AAAGAATTTG CTTAAATTCT ACTACTTATT	1200
ATTTTCTCTA CTCATTTAAT ATAACATAA TCAAAAATAA TTAAACATTT TGTATATAA	1260
AAGTTAACAG ATTTGCCATA AAATCATACG AACGGAGTAT GAAATGAACC TTTATCTTCT	1320

ATAATTTAAA	AAATGAGATT	TATGCATACA	TCGGACCAAA	TGTGCATAAA	TCTCATTTCT	1380
TTATATTAAT	CTTGGcAAGA	CTCACATACA	CCATAAACTT	CAAGTTTGTG	TTTGTGAATA	1440
TTAACACCAG	GTAGTGATAA	TTTTATCTGA	TCTATTGGAC	AATAATCTAT	TACCTTTGTA	1500
TCTCCACACT	TTTCACAGAT	AAAATGATGA	TGATGATGGT	TTGTACAAGC	GATTCTAAAC	1560
TTCATTTTAC	CATCAAGTTC	TGTATTTTCA	ATAATTCCTA	A ACT TTTAAA	TAAGTGCAGG	1620
TTTCTATATA	TTGTGTCGAA	TGAAATTCCA	GGATAATTTT	CATCCATAAC	TTGTTGTATA	1680
TACTTTGCGT	TTATATACTT	ATCTTCTTCG	ACAAAAATAT	CTAACATATC	TTTACGTTTA	1740
TCTGTATATT	TTAAACCGTT	CTCTTTTAAA	ATTTTAATAG	CATCATTTGT	ATTCATTGAT	1800
ATTAGCTCCC	TTTTTAAACT	TCATTTCGCAT	TTTCTGATAA	GCCATTGTAA	TCATAAGTAA	1860
AATAACAAGT	AGAACTACAA	TTACACCACC	CGGAGAAATG	TCCATATAGA	AAGCTAGGAC	1920
TAAGCCTAAT	ATTACTGATA	ATTCACCTAA	AAATACACTT	AGTAATATCA	ATTGCTTAAA	1980
ACTTTTTGTT	ATTCGCATAC	TTATTGCAAT	TGGTAACGTG	ATTAACGCAC	TTACTAACAG	2040
TATCCCTACA	ACACGCATTG	AGGCAGAAAT	AACCATCGCT	ACAATAACAA	TAAATAAAAA	2100
TTGAATCCAT	TTAGGAATGC	CAATGACTTT	ACTATATTCC	TCATCAAATG	ACAATATAAA	2160
TAATTCTTTA	TAAAACAATG	TAATAAACAG	AACAACTATG	ATGGCAATGACAATAATCGT		2220
TGTTAAATCA	CTTATATTCA	CTGCGCTTAT	TGAGCCAAAT	AGCAATCCAA	CAATTTCTTG	2280
ATTGAACCCA	TCAGCTAATG	AAATGAAGAT	TGCACTCAAG	GCGATACCAG	CACTCATTAT	2340
AATTGGAATA	GCAATTTCTT	GGTAAGCAGT	GTATGACGTT	CTTAATTTTT	CAATTAGAAG	2400
CGCACCTACT	ATTGCGAATA	AGATTCCAAA	CCACATTGGA	TTAATAAATA	CTAGTGTTGG	2460
CATAATAGTA	AGTAAAAACA	TACCGAAAGA	TATACCACCT	AAAGTTACAT	GACTTAGAGC	2520
ATCAGCTwTA	AGTGATAGTC	GTCTAACAAc	GATAAAAGCA	CCGaTTAGAG	GCGCAATAAA	2580
ACCTAtCAAG	ATAcCACTAA	TTAAAGAGTA	C TC ATAAAA	TCAAAATTCA	ATAATGCATC	2640
TATCAATTGT	GACACGCCTT	TCCATTTTAA	ATAAACTCAA	ATCTTTATTA	ATTACAACAT	2700
TCTCGATTAT	GCTGATGATC	GACAAAACGT	ACAGGATGTC	CATAAATTTT	TGAAATTTCA	2760
ACTTCATCAA	GTGATTTAAA	CTCATCAGTT	GTACCATGGA	AATGCAAATG	CTTATT TAA	2820
CATGCTACTT	CAGTAGCAGT	ATCTGCTACA	ACACCGATAT	CATGAGTAAC	TAAGATAATG	2880
GTGATACCTT	CTTGTTTTAA	TTGATCTAAA	GTATTATAAA	ATTCACCTAC	ATGTTTTGCA	2940
TCAATACCAT	TCGTTGGTTC	ATCAAGTACT	AATACTGcAG	GTTCTGAAAT	CAATGCTCGA	3000
GCAATCATTa	CAGTTTGTTG	TTGACCACCT	GATAATTCTG	CTATATTTTT	ATGAATTAAA	3060
TCACTTATAT	TCAGTCTTTC	TAGTACTTTA	ATCACTTTTT	CATTATCTTT	GCTATTAAAT	3120
GTTTGAAAAA	GACGTTTTGT	CTTTGTTAAT	CCGCTTAAAA	CAACTTCTTT	AACACTTGCT	3180

GGGAAACCTG AATTAAAGGC ATTTGCTTTT TGTGATAC A AGCTTAATTT AATTGATGTT	3240
TcTTATTTTT AAAATCAATA CCTTCAACAA AAATCTCACC ACTTTGTAAA GGTAATAACC	3300
CTAGAATCAA CTTCAATAAT GkTGATTTAC CAGCACCATT TGGkCCAACA AwTGctAAAA	3360
ATTCACCTTT ATTTATTTTG AATGnnnTAT ATT	3393

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 427:

TAATTTTTTTG CTTCGCCATT ACTACGCACT ACCTTTACAT TATCGTTCTC AAGGCTCATC	60
CCCTGTTTCT TAGCCTTTTC GTATATGCGT TCATAAGAAG AATTCTTTTT GATTTAGAT	120
TGTAAAGCAC TGTTTTCACT TGATTGTTTA TCTATTTTAT AATCTAAATC TGCAATCTTT	180
CCTCGCGTAT CATACGCATC CATTTTTTAAA GATAGCATAT AAATACTTAA CATAGCAATT	240
ACAGTAATCA AAGTTATGTA TAAAACTTTT TCAAATTTAG TTAATTGTAC AACCACTTTT	300
CTCGAAACAG TCTTCTTTTC GGGCTTAGTT TGTGGTTGTT GCTTCGGTAT ACTATTATAA	360
ACTTGTTCTG CATATGGTTG GTACACTTTT TCTACAGCCA TATAAATTG CTCCTTATTT	420
AAGTATTTCA GCTACACGTA ATTTTCGCGCT TCGTGCTCTG TTATTGTCAT CTAAATCTTC	480
TTCTGTAGCG GTAATCGGTT TACGATTAAC ACGCTTTAAC TTAGGTGTAT ATGCTTCTGG	540
TATAACTGGT AATCCTCTTG GTACCTCTGG ACCTTTTTCA TATTCTTGGA ACACCTGTTT	600
ACATAAACGA TCTTCTAAAG AATGGAAAGT GATTACCGAA ATCCTGCCAT CTACTTTCAC	660
TAATTCAATC GCTTGTTCTA TTGAATCTTC AAAAGCTGAC AATTCATCGT TTAAGTCAAT	720
TCGTAGTGCT TGAAATACTC GTTTTGCAGG ATGTCCGCCT TTTCTTCTTG CTTTTCAGG	780
AATACCTTCT TTTATAATGT CAACTAATTC TAATGTTGTT GTTATTGGTT GTTGTTTCGG	840
ATGTGCTTCG ATTCTTCGAG CTATCTGTTT TGAAAATTTT TCCTCGCCAT AGCGATAAAA	900
AATCTTCACT AACGCTTCAT ATGACCAATT GTTAACAATT TCATATGCTG TTAGTTCTTG	960
TGTTTGGTCC ATACGCATGT CTAATGTTGC GTCATGGTGA TAACTGAA C CTCGTTCTGG	1020
AATGTCGAGT TGTGGGCTTG AAACACCCAA GTCGTAATAA ATTCCATCTA CTTTTTCAAT	1080
GTTTAAGTCT TTTAATATTT GAGTTAATTC ACGGAAGTTG CTA	1123

(2) INFORMATION FOR SEQ ID NO: 428:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 838 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

TATATCCTCC AnACCATAAA AATGGAATTA TAGTGAAGAC CGCTATGATC CAGGATGACC	60
ACGTATTATA GAATCTTTCg ATAGAGAAAC GAATCaACGT ATCCgACATC aCGAAATGAA	120
ATTAGAAGAT TATAAAGATG AGTTAAGAAG AGAATATCTA AAACAATCTG ACAGAATTGA	180
AGGAGATGAA TAAGCGTGGG ACTTGATTTT AGTGGTTTAC CAGATTTAGC AGTATTGGAA	240
CAAATGAAGG AAAAAGAACA GATTAGTAG GTTATTGCGC CTGAACATGT TCGTATGCAT	300
CATGATCATC AAAATAAGCT GAAAAGTGAT GAGAAAATAT TACTTGACCA AATGGTAAGT	360
CATTTCAAAA AATTTGAAGA TGATTTTAA AATGCGGCAC AAGGGGCTTG GGTGAAAAAT	420
GCCACAGACG AATTAAAAGA TATTAGTAAT GATTTAGAAA AAATTCAAGA TATAAAGTA	480
TAAAAAGGTA TTAAGAAACA CAATAAGTAT ATAATCCATT TAATAATAAA TGAATTATAT	540
AGTTCATAAT TTCGACTATA AGTGGCTATT AGCCATTATT TTTCGGGATC TATGTCAAAT	600
CGGACTAATG AATTCAATAA TGAAGTTAA GCAACCAATC TTTGTTTAAAC TTCTTTTTTA	660
TTTTTTGGAA AATAAAGTTT TGAACATAAT AAAATTTGAT TATGTTTTAA CGAATTTTGA	720
TGTTTCTTGA ACTATATATC ATCTAGTCGT CATTTACAAT TGGTAAATAT GACTTCAAAC	780
TGkATGAAGG TGATGGCGAT TAAAAGGCTC ATCCGTAGGT TCTAAAGAAC TAGAnTTT	838

(2) INFORMATION FOR SEQ ID NO: 429:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

nGTGTTCAAA TAATAGAATG GCTAATACCC CAACAATAAA TAGGAATAAA TATGTTGATG	60
TCGTAATTTT AGTAAATAAT GAAAATCTAA AATTAGTAAC CCTATTTTGA ATATAAGCTT	120
TAAC TTCTAA TAATACTGGG AAGCCGATTG ATCCTAAAAT TATTAAAAAT ATA ACTATCG	180
CTTG TACAAA ATAATCATGT GCATAAGGAA TTAATGACTT ACCTGTAATA TCTAACCAC	240
CATTGGTAGT GGCAGAAATA GAAACAAAAA CACCTTGCAT GATTGCATAT TTAAATCTG	300
GATTATCTCG ATAAAAGTAA AATGCTAATA ACATGGCTCC TACGAGTTCG ATTACAAATA	360

TTGATTTTAC AATATCAATA ATCAATTTGA CGGTACCACT CATTGTGTTT TTGTTATTAT	420
CTAACATAAT TAACTGACGT TCTCTAATTC CAATATGTTT ACCTAGTACC ACCCATAACA	480
TCGTACCAAT TGCCATGACG CCAATTCCAC CAATATTTAA TATCACGAGG ATAATTAATT	540
GTCCAAATGT AGAATAGGTA TCGACAATAC TTATCGGAGA CAATCCAGTA AACTAATTC	600
CGGATACGGC AACAAATAAT GTGTCAATTG GATTTAATTC TACACCTGGT TTATGaACAT	660
ACGGTAAGTT TAATAATAAA AATGCAATGA CAATTGCGAC GATATAGTAC AATACAATAC	720
CTTGTTGAGG GCTTGATCTT TTTAAAAACT GGCTAAAAAT TGACACGTTG TTCACCTCAA	780
CATTATTTTA GTTTAATATT AATTTCTTTC TCTTTACCAT CTCTATAAAT CTTCGCTGTA	840
ATTGATTTCA AGTCATCTTT ATGACTAAAT ATAATCTGCC TAAAGCGTAA ATCATCTTCT	900
AAAAGTTTGC CATCTAATTC AGTAATTACA TCACCTTTTT TCAGACCAGA TTGATCTGCT	960
AAACCATTGT TGTCAACTTG ATCTACAACA ACACCGTTCT TAACTTTTCC TGGCAATTTA	1020
ACTGCTTGTC TTTCAAAACT ATTTAGACTG ACAATATTCT TCATTTTAAAC ACCTACATCG	1080
GGATAGTCAA TTTTACCTTT tGTTTCTAAA TCTTTTACAA TCTTTtGTAC TTCATTAAaCA	1140
GGtATTGCAA	1150

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

AAGAATATTT AGGATTTTAT GTTTCGCAAC ACCCAGTAGATAAAAAAGTTT GTTGCCAAAC	60
AATATTTAAC GATATTTAAA TTGAGTAACG CGCAGAATTA TAAACCTATA TTAGTACAGT	120
TTGATAAAGT TAAACAAATT CGAACTAAAA ATGGTCAAAA TATGGCATTG GTCACATTAA	180
ATGATGGCAT TGAAACTTTA GATGGTGTGA TTTTCCCTAA TCAGTTTAAA AAGTACGAAG	240
AGTTGTTATC ACATAATGAC TTGTTTATAG TTAGCGGGAA ATTTGACCAT AGAAAGCAAC	300
AACGTCAACT AATTATAAAT GAGATTCAGA CATTAGCCAC TTTTGAAGAA CAAAATTAG	360
CATTTGCCAA ACAAATTATA ATTAGAAATA AATCACAAAT AGATATGTTT GAAGAGATGA	420
TTAAAGCTAC GAAAGAGAAT GCTAATGATG TTGTGTTATC CTTTATGAT GAAACGATTA	480
AACAAATGAC TACTTTAGGC TATATTAATC AAAAAGATAG TATGTTTAAT AATTTTATAC	540
AATCCTTTAA CCCTAGTGAT ATTAGGCTTA TATAACTTTy ATCAACTAAT AAATTATGAT	600

ATAGTAAACT GATGGTTAGA TATTTyTyAA CCATCAGTTT GCGTktAET TAGTTTTTTA	660
TGCTTATTAT TTTTATGAGT TTCACCTTAC ATTATTGATT AATCCATAAG AATAATTAGC	720
ACAAAAAGCA GTATACATAA ATTGAGTAAA GAATTTTGTC GATATAACCG nGCGGAAAAA	780
TAATAACnTT TTGGATn	797

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

TTTCCAAGAG AAGTTGCGGA AGTAATTAAT AAAACGCATC ATAATAAATT GGTCATTTTCG	60
ATGATTTTCGk CACAAATCGA TGCGGATAGA ATGGATTATT TACAACGTGA TGCGTATTTCT	120
ACAGGTGTAT CATATGGTGC TTTTGATATG GAGCGTATTT TAAGATTAAT GCGACCTTCT	180
AAAGATGAAG TACTAATCAA AGAAETGGT ATGCATGCAG TTGAAAACCTT TATTATGAGT	240
CGTTATCAAA TGTATTGGCA AATTTACTTC CACCCAGTTA GTCGTGGTGG AGAAGTGCTG	300
CTTAATAATT GtTTGAAACG CGCAAAACAG CTTTATAATG AAGGCTATGA ATTTAAGTTG	360
CATCCACATG ATTTTATTCC ATTTTTTGAA GAGACAGTTA CGATTGAACAATATGTTGAA	420
CTCGATGAAG CGGTAGTTAC GTATTATTTG GAAAAATGGA CAAAAGAAGA TGATGCTATT	480
TTAAGTGATT TAGCAAGTCG ATTTATTAAT CGAGACTTAT TTAAATATAT TCCATTTGAT	540
GGCTCAATTA TTACAATATC AGAACTGCAA GAACTGTTTG AAGCAGGTGG TATTAATCCA	600
GATTATTATT TTGTGAGTGA AGCATTTTCT GATTTGCCAT ATGACTATGA TCGACCGGGG	660
TCAAATCGCA AACCGATTCA TTTATTAAGA CAAGATGGTA CGATTAGAGA AATAAGCAAT	720
CAATCATTAG TCATTCATAG TATTACAGGC ATTAATCGCC AAGACTATAA ATTATATTAT	780
CCTAGAGAAA TGGTTGCAA GATTAAAGAT AACAATTA GAGAAGCTAT TGAAAATTTG	840
ATTAATGAGC TTAATTAAAC AGGGCTAAAA TTGTTATCGT TAAATATGGA GGTTATATCA	900
TTGTCTGAGA AAAAAGGCTT TAATTTTAAT ATCATAAAAA ATGACCTCT AGATGGTCAT	960
AAAGGTACAA ATATTGGTTC AATTAGCTTA GACAATATTG CACCAGTTTT TATCGATTET	1020
GCTAACAAAG AAGCATTTAT TGATATTGGA GGCATGCATG CTCGTGCCAA AGTTGAAAAA	1080
GGTGTGAAAT GGATTACTGA TAAAGCTGCT GTTGAAGGCG ATGAAGCTAA AGaATATTGG	1140
TTGTGTTGGG TAACAACAGA ACGTAATGAA CAAGGACCAT ATTACGCTGG TTTAACAGCG	1200
TGCTATTTAT TAGTGAATAA AGCAATTCGT CGTGGTTATA AAAGTATGCC TGAACATGTT	1260

AATATGATGG ATAAATCAAT GAAACATCAT ATTATCATAG ATCAAATTGG TGACGAGAAT	1320
AAAGCTATTT TAAAAGACTT TTTAATGAAC CATGATGAAG GTATGTGGAA GCATTCTTCT	1380
GATGCTTTAC ATCAAGCATT TAATTAAATA TTAGAACTAAAATTTCCCA ATTAATCTAT	1440
AAAGATATGA TTCATTTCTC AATGAC	1466

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

TTGTACGAAT ACAAAGTTGC ATTAATATAG AATCATTTAT GCTTTTTAAT ATCACAAAAC	60
AAATTGATTA AACTAGCTAA AATAGTCAAA ATTGGAATCA AGATTACATA AATATCATAA	120
CCTCTAGATA TTAGTATACA TAATATAATT AGCGACCCTA TTATAATTGC TAAATTATAA	180
GCCAAACTAA TTTTATATTT CATTTCAATT CCCACCTTAA TAGCATTTAT TAAAATTCTA	240
TAATGTTTAC ATAGACTTCT TAACAACTT TAACCCAGCT AAGCTAAGTA TTGAAATAAT	300
TACACCTCCT AATATAAATA TATTACTTAA GCTTAGTAAA GGTATAATTA TACTTATCAG	360
TCCTAAAGAC AATGTATCCG CTGcATAATT CGatGtAGAT GAGATACTAA ATACTTTCCC	420
CATCAAATGA TTTGGCGTTT TTATTTGAAT GGCAACTGAT CTTGTTAGTC CCTCTATAGA	480
TTGTCCAAGT CCCAATAATG TTGCACCTAT ATATAATATC GCACACTTG GAAACACATT	540
AATAATCGAT AAGCCAATTC CCCAACTAA AACACCAATA CTAAATTTAA AGATTAATCG	600
CTTTTCTGAC AGCAAACCCA TAATCAATGA CATTAAATAA GATGCTATAC CTAAACATGA	660
TGTAGCTAGT CCATATACAC CAACGCCCTC TTTTAATATA TTGGAAATAA ACAATGGTAA	720
TACAACACGC CAAAGGCCAG TATTAATCAA TATGCAGGCA AATTGGATGA TTATAATAAA	780
TGGAATTTCT TTAGATTGTT TCAAGAATTC CCAAGTTTCA GAAAAATCTT CTTTGTAGTG	840
TCTATCAATC ATGTTGTTAT TTGTATATTT TAAAAGTGCA TTAAAAATAA ATCCTAAAAA	900
TAGCAATATA CTACAAATAA AAAAGACGCC AACATTACCA ACTAGTATTA CAATGACACC	960
AATTAAAGCA GGTAAAATAA TATTTGAGCC TCTTTGCAAA CTATCGATTA ACGCATTACT	1020
TGTTGCTAAA TGCTCCTCAT CAATAATTTT AGGAAGAATT GCCCTAAACG CAGGATCCGT	1080
ATAGCAGTTA ATAATGGTGA TAGCTGTAGA TATGGTTAGA AGCGTCAGATAATTTAAATT	1140
TGATGTTATT GCAAGTAAAG GAATAATTAT TATAATCAAA CTTAGTATAA GATCAGATAG	1200

ATAAAGTATT TTCTTTTTAT TATGTTTATC AGAATATGCG CCACCGAAAA TACCAAATAT	1260
AATAAATGGA AGTGTTTGAC TCATAACCAT CATTGATAAT TTTAAAGATG ATTGGTTTGT	1320
CAATTCAACA GTAAACCAAA TTATTTGTAA CGAAAACAGC ACAAAACAAC TCCGACGTAA	1380
GArATTACCA ATCAATAAAT ATGTAAAGTT TCTATTTTTTC AAAACTTCTA AATACAACAT	1440
ATTTATCACC TCTCATAAAA ATAATTGAAT GCATCCACCA GCTTTTTTTAG ACCTTCTTCT	1500
AAACTCTCTT TATCCAAAGC GCAATTAATT TAATATAAT TTAGTCAGTT AAATATCAAT	1560
TATTTGAAA TATACATACT ACTTGAAACA CCATACATAA CCCCCAAAAT GACTACTCAG	1620
AGGTTATATT CTACTAATTA TGATTATATT AAATATGAAA ATATTATCAA AAAAATCAAA	1680
TTTATAACAA AAATACACCC CTAAAGTTA GGTCTTTCAA TCCAACTTTT GGGGTGATA	1740
TCATTCTCAT CATATTCTAG GTTGTTTTTA ACAAACTAAA TATAGTGAAT GCAAATCAAC	1800
TATTATTTAA ATTATGAATT ATTTTAATTC TTTCTTCTAC GAGCCAATAA CATTAATCCA	1860
GCAATTCCAA TTATACTACT AAAGATCAAA CCTTTTTGCG TGCTTTCTAA ACCTGTTTTT	1920
GGTAATTCTG CTGTTTTTTT CTCTTGATTA GCTACTGATT CTTTAGCAAT TTTAGATTTT	1980
TTAACTTTAT CATTTTTATC CATTGAATGA ACTGGGCCAT TTGGTTTTGC TCTGTCTTTC	2040
GATAATCCTG GATTGTTAGG ATTTACTGGG CCACTTGAT GAGTTGGTCT GCTCGGCTTC	2100
TCTGGGTTTT CAGGTCCTTT TGGATCTTTT GGTCTCTCT CACCGAACTC TACAATCTTA	2160
TCTACTGGTT GTTTtGTGAT CTCTTCTGTT GGTGACCCT CGCCAACTTT TTCACCTGTT	2220
AATGGGktCA CTGTGawTGG TGktGTGawT GTCyTACTTC CTGGktGTCC TTCTTGTTTC	2280
ACTCGCTCTT CACCAGGTTG TAAT	2304

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 433:

GTCTTAATAT TTTACAAGAT ACAGCCTGAC AATATTTATA TTACAAACCA ATATGGTAAA	60
GAGGCTGTGT CTCGATTAAA AAGAATTTTA GAGCAAAGTA TACCTAATAA AGAATATATT	120
GATTTATCAG AGATATCATT AATTACATTT TTAAACCAG AATATAATAA ACAACATGTG	180
AATGAGGAGT TTAATCTTTT ATCTTCTTCG AAAATAAAGA ATTTAGCCAA AGAAAATGAT	240
GGTATTATTA TTTATTTAAA TTTTAAGGAT GTTAATTATC AACTGaTAaG TGAAGGCAAT	300
ACTTTTTTTT CTGCAAAACC ATATTTGCAT TGTGTGTTCA ATAAAGATAT TTTAAATATG	360

GATAAAGTTG ATATAGAAAA TTTTTTCAAA AGTATAGAAG TAAATACAG TAAATAAGAT	420
CAATTATTGA ATCCACCGAC CAGCAGATTT TTTTAAAAA TTAATACCCC GTTAATACCC	480
TTTGCTTCAA TTTGATGAAA ATCAATGAAA TTCAAAATTG AAGAAATCCT TTAATATCAA	540
GGTGTACGAC AGTCTATATA ATCATGCGAA ATTCTAAAAT TTTCTGAcGT AAAAAACAA	600
ATTCyTAAAG CAGCTCGTCG TTCACCTCAA TTCTCAAAAC GTTAATTGTC GGACGATATA	660
TATACAAAAC ACCTCGATGT TATGTGAGG TGTTTTTTTG CGTTTGTGTG GGGAATATGG	720
AATAGAGTAT AAATGAATTA ATGTCTCAGG TATAGAATTA ATTCAACTAT GAATTATTGA	780
TTTACACGTA TAATTTGTAC ATCTTACAC AATCAAAAGT GTrCATTATT AAATTGTCAT	840
TTAGCTTGCG GAGACCGTAC GATAGTGTTT TAATAATAGA TATTCAAGGG AAAGAGCTAT	900
CGGATGATAA CCAGATGATA ACTCAAGAAC CATGrTTTAA GAGTGTTATC AAAATAAGGA	960
GTGACTTAAT TGAAAGATTC TATATTTTGG AAGAAAGCTT TTATTyCTE TTATTTTATT	1020
GTTGsGATGC TGGTGTCTTCT ACTTTTTTAGG TTTTATATTA AaACAGATAA CTTTTCTATA	1080
TATTTAATGA GTATCTTCTT AATTTGTTTA GGAAGTCTT CTATCATTTA TAACTATAAA	1140
ACCAATCGAT AAATATAAGT ATGAAATGTA TAAGTCACAG TTAGATCTAA GTCTTGCTGT	1200
GGCTTTTTAT ATCTCCATAA AACGACAAAT TCAAGCCCGA CATAAACAG CATTTTCAGC	1260
CCACCATAAA ACGACAATTT CAGCCCGCCA TTGACTAAAC ACCACATCCC AAAAATATCG	1320
TAACAATCCT CTACATCAAT CAATCCAACA TCCCTCATAA TCACAACGCA CAAAATCTAT	1380
TCATGCATTT TTGGAATACT TAGTATTACAAATAACGATT TTTATTCATC TAACAAAGGT	1440
TATATAATGT ACTGAAGGCA ATTTTTATGT ATTACAAATC TAATCGTACA TGTAATAATT	1500
TGATAAACAT CATTAATTTT GCGTAACTAT CATTAGATTA CAAATCACAA AGTAATTACA	1560
TGTAATACAC ATCTATACAT CACATTTGAA GGGAAATGaA TATAAATGAC TGATAAAAG	1620
TACACTGCAG CCGATATGGT TATTGATACT TTGAAAAATA ATGGGGTAGA ATATGTTTTT	1680
GGTATTCCGG GTGCAAAGAT TGAATATCTA TTTAATGCTT TAATTGATGA TGGTCCTGAA	1740
CTTATTGTCA CTCGTCATGA ACAAACGCC GCAATGATGG CGCAAGGTAT TGGAAGATTA	1800
ACAGGCAAAC CGGGTGTAGT ACTTGTTACA AGTGGTCCTG GTGTAAGTAA TTAACTACT	1860
GGATTATTAA CCGCAACATC TGAAGGGGAT CCTGTATTAG CGTTAGGTGG CCAAGTGAAa	1920
CGnAnATGAT TTATTACGAT TAACGCATCA AAGTATTGAT AATGCTGCGC TATTAAAATA	1980
TTCATCAAAA TATAGTGAAG AAGTACAAGA TCCTGAATA TTATCAGAAG TTATGACAAA	2040
TGCAATTCTGA ATTGCTACTT CAGGAAAAAA TGGCGCAAGT TTTATTAGTA TTCCGCAAGA	2100
CGTTATTTCT TCACCAGTTG AATCTAAAGC TATATCACTT TGCCAAAAAA CAAATTTAGG	2160

AGTACCGAGT GAACAAGATA TTAATGATGT CATTGAAGCG ATTAAAAATG CATCATTTCC	2220
TGTTTTATTA GCTGGTATGA GAAGTTCAAG TGCAGAAGAA ACAAATGCCA TTCGCAAATT	2280
AGTTGAGCGC ACGAATTTAC CAGTTGTAGA AACATTCCAA GGTGCAGGTG TAATTAGTCG	2340
TGAATTAGAA AATCATTTCT TCGGTCGTGT GGGCTTATTC CGCAATCAAG TTGGTGATGA	2400
ATTATTACGT AAAAGTGATT TAGTTGTTAC AATCGGTTAT GATCCAATTG AATACGAAGC	2460
TAGTAACTGG AATAAAGAAT TAGAAACACA AATTATCAAT ATTGACGAGT TCAAGCTGAA	2520
ATTACTAATT ATATGCAACC GAAAAAAGAG TTGATTGGTA ATATTGCTAA AACGATTGAA	2580
ATGATTTCTG AAAAAGTGGA TGAGCCATTT ATAAATCAAC AACATTAGA CGAATTAGAA	2640
CAATTAAGAA CACATATTGA TGAAGAACT GGTATTAAAG CGACGCATGA AGAAGGAATT	2700
CTACATCCAG TGGAAATTAT TGAATCTATG CAAAAGGTAT TAACTGATGA TACTACTGTA	2760
ACAGTTGATG TTGGAAGTCA CTATATTTGG ATGGCACGTA ATTTCAGAAG TTACAATCCA	2820
AGACATTTAT TATTTAGCAA TGGTATGCAA ACGCTTGGTG TAGCATTACC GTGGGCAATT	2880
TCAGCTGCAC TTGTGCGCCC TAATACGCAA GTTGTGTCCG TTGCTGGCGA TGGTGGCTTT	2940
TTATTTTCAT CACAAGATTT AGAAACGGCC GTACGTAAAA ATTTAAATAT CATCCAGCTT	3000
ATTTGGAATG ATGGAAAATA TAACATGTT GAATTCCAAG AAGAAATGAA ATATAAACGT	3060
TCGTCAGGTG TAGACTTCGG TCCTGTAGAT TTTGTAAAT ATGCAGAATC ATTTGGCGCG	3120
AAAGGTTTAC GAGTTACTAA TCAAGAAGAA TTAGAAGCGG CAATTAAAGA GGGCTATGAA	3180
ACAGATGGTC CAGTATTAAT TGATATACCT GTAAATTACA AAGATAATAT CAACCTTTCA	3240
ACAAATATGT TACCTGACGT ATTTAACTAA AATAAAGATA AATGTTAAAG AGGAGTGGGA	3300
GATTTTATGA CTAATGTTTT ATACCAACAT GGTACATTAG GCACATTAAT GGCAGGATTA	3360
TTAAAAGGAA CTGCATCAAT AAATGAATTA TTGCAACATG GTGACTTAGG TATCGCTACA	3420
CTAACAGGTT CAAACGGTGA GGTAATCTTT TTAGATGGAA AAGCTTACCA TGCAAATGAA	3480
CATAAAGAAT TTGTAGAATT AAAAGGTGAC GAGTTAACAC CATATGCAAC TGTAATAAA	3540
TTTGTAGCAG ATACAAGCTA TGAAACGAAA GATAAATCTT CAGAAGCAGT TTTTGCAGAA	3600
ATTAAGGAAA AGATGTTGAG TGAAAATTTA TTTTAGCAG TAAAAATTC AGGCTTATTT	3660
AAAAAATGC ATGTACGTAT GATGCCGGCT CAAGAACCAC CTTATACACG TTTAATCGAT	3720
TCAGCTAGAA GACAACCTGA ACAAACCTGAA ACGTATGTCA AAGGTTTCAGT CGTTGGTTTC	3780
TTTACACCAG AATTATTCCA TGGTATCGGA TCAGCAGGAT TTCATGTACA CTTTGCGAAT	3840
GATGATCGTA ACTTTGGTGG ACATGTCTTA GATTTTGAAG TAGAAGATGT TAAAGTAGAA	3900
ATCCAAAATA TAGAAACATT TGAACAGCAT TTTCCAATTC AAGATAAAGA TTTCATAAA	3960
GCAAATATTG ACTATAAAGA TATTGCAGAC GAAATTAGAG AAGCTGAATA ATGAATCCAG	4020

AAATATAATG ACGGTTTATG AAAATTGACT TCATAATGCG CGATTTAGAA ATGATAGTTT	4080
GTAAATATGA TTAACCATGA CTACAATAGA ACAAATATAT TTATAATTAC GTCTAAGTAA	4140
TAAAATAAAT CCCTTCACTA TTAGCAGTAG TGAGGGGATT TATTAGGTTT CAGATATTTG	4200
AGATTTGCTG TTATGTTTAG ATTATAAATT GTGGTACACA TCATATAAA ATTTACTATT	4260
GTATAGGCCA ATCTGTTACT ACGAGAAGCA AACAACAATA ATTTACAAGT TCAATAACTA	4320
AAAAGACAAA CGCCAATTTT TCAGCGCTTG CCCTATAAAA CTATTTTCAA ATTATTATTT	4380
AACTACAATT TGTATCTGTT TGATTGTACT TGGATCAATT GAATTTTTAG CGTCGTCATT	4440
TTTCTTTAGA TTCACTACTT TTTTATTACC ATCATTCAA GTAAGCGTAT AAGTTGCTGT	4500
TTGGGCATTA TTAATTTTTT CTGTTGTAAC ACCACGTTGA GAAGCTAATT CATTTTTTAC	4560
TTTACTGTCA ATTTCTTGAT AAAGAACATT TTTATTTTCT GGAAGATAA AGTAAGTTCTG	4620
ATGTAATGCA GTAATACCAT CTACTGAAAT TGTGTAAGGA ACAGTGTGAT AACCATCCAC	4680
AGTCATTTCT TTATAGCCGT TATTACTATC TGCAGATGCT TCGTGACTCG GTA	4733

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

AATAAATGGT AATTTTATAT CATCAACGGC TACAAATGGG GCAGTTTCAT ATATAAATAA	60
ACACATCTAC TCAACTGnTC TTAATTAATT AATAAATGAT TTACAGATG ACATATAACA	120
GCCATTATTA GnTTAATTCT AATAGTTTAT TTAAATTTTC TTCGGTTGTC GCCCAACTGG	180
TTGCGAATCT AACAACACGA TGTTGATCAT CGTATTTTTC CCAAACAGCA AATTTAACTT	240
TTTGTTCTAA CTCTGCTATT TTCTCGTTAC TTAAATAAAA AAATTGTTGA TTGTTGGAG	300
AATCAAAGTA AAGACGATAG CCTTTATTTT TAAACCCGTC TTTCATCTTA TTTGCCATTT	360
CGATAGCATG TCTGCTTATA TTAAATATA AATTGTCCGT AAATAATTCT AAAAATTGTA	420
TGCCTGTTAA CCGTCCTTTT GCTAAAAGGG CACCGTGGAT GCTTGATTCG AGTGGTAAAT	480
TGTTTCGGTT CATTATTTTT CGTAAACA ATGGCTTCCC CGCATAATGC ACCTATCTkC	540
GTACCACCTA TATAAATAC ATCACAATAT TTAGCGrTgt CTTTAATAGT CATATCTGAT	600
TGGTCACTCA TCAATCCATA CCCTAATCGT GCACCATCCA TAAATAATGG AAGCTGATAT	660
TGCTTACATA CTTTGCATAA CTCTTCCAAT TCTGaTTTAG AGTATAATGT GCATATTCT	720

GTAGGATGAG AAATATATAC CATTCTGGG AATACCATAT GGTCTTTTT AAAATCACTT	780
TTAAATGTCT CCATGTAAGT TTCAACATCT GAAGCACTAA CTTTTCCTTC CTTAGAGGGT	840
ATAGTAATTA CTTTATGTCC ACTATATTCA ATTGCACCGC CCTCATGCAC AGCAACATGA	900
CCAGTGTCTG CTGAAATGAC CCCTTCGTAA CTTTCTAACA TTGAATTAAT AACAACCTGA	960
TTGGTTTGTG TTCCACCTaC TAAAAAACGA ATTGTAGCAT TTGGaCAGTC AATTGTATCT	1020
TTAATCTTTT CAATTGCCTG AGCTGTGAAT TGaTCAAAGC CATATCCCGA AGCTTGATACA	1080
AGATTTGTAT CTACTAATCG TTTTAATACT TTTCATGAG CACCTTCTAA ATAATCATTT	1140
TGCAATGAAA TCACTACATT TCCCCCTAAA ACTAATATCA ACATTTTAAT AAGATAAACC	1200
AATTTCAAAA CTAGTTCGAT ATTTAAAATG TATTATGGAT GGnTAAAGTT TGTATCGCAT	1260
TATCGCGAAG TTGnATAAAT ATAT	1284

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

ACAGCTTTTG GTAArGGAGA AAwTCAaTat GAAACAGTAT AArGCGTATT TaATCGATTT	60
AGATGGCACA ATGTATATGG GAACAGATGA GATTGATGGA GCAAnACAAT TCATCGATTA	120
TTTAAATGTA AAAGGCATTC CTCATTTATA CGTAACTAAT AATTCAACAA AAACACCTGA	180
GCAAGTAACT GAAAAATTAC GTGAAATGCA CATTGATGCT AAACCAGAAG AGGTTGTAAC	240
GTCAGCGTTA GCCACTGCTG ATTATATTTT AGAACAATCA CCAGGAGCAT CAGTATATAT	300
GTTAGGTGGG AGTGGTTTAA ATACTGCGTT AACCGAAGCG GGACTTGTCA TTAAAAATGA	360
CGAGCATGTT GATTATGTAG TTATTGGACT TGACGACAA GTTACATATG AAAAGCTTGC	420
GATTGCAACG TTAGGTGTAA GAAATGGtGC AACATTTATT TCTACAAATC CTGATGTATC	480
AATTCCTAAA GAGCGTGGTT TATTACCTGG TAATGGTGCT ATTACAAGTG TTGTAAGTGT	540
ATCGACAGGT GTATCGCCAC AATTTATTGG TAAACCAGAA CCGATTATTA TGGTTAAAGC	600
ATTAGAAATT TTAGGATTAG ATAAATCCGA AGTTGCTATG GTAGGCGATT TGTACGATAC	660
CGATATTATG TCTGGTATTA ACGTAGGTAT GGATACGATT CATGTACAAA CAGGTGTATC	720
TACGTTAGAA GATGTGCAAA ATAAAAATGT GCCACCAACG TATTCTTTTA AAGATTTAAA	780
TGAAGCAATA GCTGAATTAG AAAAATAGAT ATAGTCATTT TATAAAGTAG GTGAATTGAT	840
TTGGTAAAAA TAGTTGTTTC GAGGAAAATT CCAGATAAAT TTTATCAACA ATTAAGTAAA	900

CTTGGTGACG TTGTTATGTG GCAAAAATCA TTAGTGCCTA TGCCTAAAGA TCAATTTGTG	960
ACaGcCtTCG TGACGCAGAT GCTTGTTTTA TTACATTAAG TGACAGATC GATGCAGAAA	1020
TTTTAGCGCA ATCACCAAAT TTAAAAgTAA TTGCGAATAT GGCTGTAGGA TA	1072

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

TAAAACTTA CTTTAACACC ATTCCTTTTT AACTTTTTTTC GTGTTTCnTT TnCTTAAGTC	60
CATCCATATT TTTAATGATG TCATCTGCTG TTTTATCTTT TAAATCTAAC ACTGaGTGAT	120
AmCGAATTTG TAGCACAGGA TCAAATCCTT TATGGAATCC AGTATGTTCA AATCCTAAGT	180
TACTCATTTT ATCAAAGAAC CAATCATTAC CAGCATTACC TGTAATCTCG CCATCATGAT	240
TCAAGTATTG ATATGGTAAA TATGGATCGA TATGTAGGTA TAGACAACGA TGTTTTTTTAA	300
CATATTTTGA TAATTCATTA AAGAAAAAGT GTACGAGTTC TTGATTTTCA TAATCAATCA	360
CTGGACCGCG ATTTGAATAA AAATACTTGA ACACTTTCAT AACAGGTACA GCAGTAAGtA	420
AGCAAGCTGC AATGACCTCG TTATTATTGT TTTTTATTCC CACTAAATGT GTTTCATAAC	480
CTTCAGCAAG CTTTAACTCA TAGTGGCCAA CAGTTTGCGT GaAAT E CTG TATGGCATGC	540
TATCTGTAAa GGCACCAAAC TCTTTAGCTG TTAAATTTGT AAACCTCATT ATCATTACTC	600
CTATTTGTCT CTCGTTAATT AATTTTCATTT CCGTATTTGc AGTTTTTCTA TTTCCCCTCT	660
GCAATGgCA AAAATAATAA ATCTAATCTA AATAAGTATA CAATAGTTAA TGTTAAAACT	720
AAAACATAAA CGCTTTAATT GCGTATACTT TTATAGTAAT ATTTAGATTT TTGAATACAA	780
TTTCAAAAAA AGTAATATGA ACGTTTGGGT TTGCTCATAT TACTTTTTTT GAAATTGTAT	840
TCAATTTTAT AATTCACCGT TTTTCACTTT TTCAAACAGT ATTCGCCTAA TTTTTTTAAA	900
TCAAGTAAAC TTAATTATTC AATGTTT G T GGATAGATTG TAAATATTTA ATGATTTTCT	960
CACGCGTGTT AGATTTAAAT CGCTTAACGA TTTCGCTACC AATGACAATG CCATCTGCAA	1020
CCTCTTTTAT ATCTGCAACA TGTTGTGGTG TTCTTATACC AAATCCTGCG ACAACTGGCA	1080
CATTGGCTAT CGCTTTAATT GACTCAATTT TTCGTTTTAA TTCTGGATGA AAGCACCGT	1140
TTTGCCCTGT TGTCGCATTC ATCGTCACAG TATAAATAAA GCCTTCCGCA TGGGATACGA	1200
TATCTTTTAT ACGTTTGTCA TCAGTAGTCA TCGCAACTAA CGATATGATT TTGACGCCAT	1260

AGTGA	CTAAA	TTGTT	GTTTT	AAACG	CTGCG	ATAAT	TCATA	TGGTA	AATCA	GGAAT	AATTA	1320
AGCCG	TAGAC	ACCAG	TATCT	CGACA	TTTTT	CAAAAA	ACGC	TTGTT	CTCCA	TAATG	ACAAA	1380
TAATAT	TATA	ATACG	TCATT	AATAC	ATAGT	TACAC	TTAAT	TTGAT	CACCA	TGTTTT	TCTA	1440
ATTGAT	TGAA	AATATA	AATCT	ATCGT	GATGC	CTTGTT	TAAT	CGCTT	GTTGA	CCTGCT	TCCA	1500
TGATA	ACTGG	ACCAT	CAGCA	ACCGG	ATCAG	AGAA	GTAC	TCCAAT	TTCA	ATTAT	ATCTG	1560
CACCAT	TTTC	ACTCA	ACAAT	GTTGC	ATTTT	CAATC	AAATC	TTTAT	TGCCC	ATAAT	ATAAG	1620
GTATA	AAATA	TTTAG	TCATT	TGCA	AAGACCT	CGCTC	TACCA	TATAT	TGTCT	AATTG	TTTCC	1680
ATATCT	TTTAT	CGCC	ACGTCC	AGAA	ATAGTT	ACTAC	AATAA	TATCT	TCTTT	CGAC	ATCGTA	1740
GGCGC	TAGTC	TTTCA	ACATA	ACTCA	GTGCA	TGTGC	ACTTT	CAATT	GCAGG	TATA	AATACCT	1800
TCATG	TTTTG	TAAAG	TTGAT	TAAAG	CATTC	ATTGCT	TGTG	TATCA	CTAGC	ATTTT	CAAAA	1860
GTTACT	CTAC	CAATG	TCGTG	GTAAT	AAGAA	TGTTCT	GGTC	CAATA	CCAGG	ATAAT	CAAGT	1920
CCTGCT	GAAA	TAGA	ATGTC	TAGTT	GCACT	TGCCC	ATCTT	CATCT	TGAAT	TAAAT	ACATT	1980
TTAGT	ACCAT	GTAAT	ACGCC	AGGTG	ATCCT	TTGCC	AATTG	CAAGT	GCATG	TTTAT	CAGTA	2040
TCATC	GCCTT	GACCT	GCGGC	TTCA	ACACCG	TATA	ATGCA	CATCA	TCTTT	AATA	AATGGA	2100
TAAAT	GTAC	CGATT	GCATT	TGAG	CCACCA	CCGAT	ACATG	CAAT	TGC	ATCC	GGAAGT	2160
CGACCT	TCTT	TCTT	CAATAT	CTGT	GATTTT	ATTT	TCTTAC	CAATC	ACACT	CTGAA	AATCT	2220
CTAACA	ATCG	TTGGG	AACGG	GTCT	GACCT	AATGC	AGAAC	CTAAT	AATAA	ATGT	GATCA	2280
TCTAC	ATGAC	TTACCC	AATA	TTGCA	ATGCT	TTATTA	ACTG	CATCC	GATAA	AGTCC	CTGA	2340
CCATCT	TCAA	CTGCC	ACAAC	CTTTG	CACCA	AGTA	ATTCCA	TTCTA	AAATAC	ATTA	AGTTGT	2400
TGTCT	TTTAA	TATCT	TCACT	TCCC	ATAAAG	ACAAC	AAGTT	CCAT	ATCAA	TAATG	CAGCA	2460
ACCGT	AGCAC	TAGCT	ACACC	ATGTT	GACCC	GCACC	AGTTT	CAGCA	ACAAG	CTTCT	TCTTG	2520
CCCATT	TCTTT	TAGCA	AGCAA	CGCT	GACCT	AACGC	ATTAT	TAATTT	TATG	GGCGC	CTGTA	2580
TGATTT	AGAT	CCTCT	CGTTT	CAAAT	ATATT	TTAGC	GCCAC	CTAGG	CTTTC	AGTAT	ATGAT	2640
GCAGC	ATATG	TAAGT	GGTGT	CGCGC	GTCCCT	ACATA	CTCTG	ATAAA	TAGTA	TTCC	AGTTCT	2700
CTTTG	AAACT	CTGGG	TCTGC	TTTTG	CCTCT	TTATA	AGCTT	TTTTC	AACTC	AATA	ATTGCT	2760
GGCAT	TAAATG	TTTCT	GGAAC	ATATT	GCCCT	CCAT	ATTCAC	CAAAG	AAACC	TAAT	TCTCT	2820
GCTTCT	GTTT	GTATTT	GTTT	ATTC	ATTGTC	TCTAT	CTCCT	TTCAC	AATAT	TTACA	ATTGC	2880
TGTCAT	TTTTT	TCTAT	ATCTT	TTG	CCCCATT	TACTT	CTATA	CCTG	ATGCAA	GATCA	TAAACC	2940
TTGAT	GTGAT	AATTT	AAGTT	GATTA	ACTGT	TTGA	ATATT	TCAG	AGTTAA	TGCC	TCTGC	3000
TATCA	AAATA	GGTAT	GTCTT	TTATG	TGCTT	CAAA	ATAGTC	CAGT	CATATG	TTTG	ACCGGT	3060
ACCAC	CATAC	GACAC	TGAGG	GTGTG	TCGAT	AATA	AAATAAA	TCTAC	GGAACC	CTTT	ATATTT	3120

ATTTATGTTT TGGATTATGT TTTTCATCTnG AGtAAAGCT TTAGTGATTT TAATGCTTGA	3180
ATATkTCTTT TTAATTTTCCT GTAtAAAAtC AATAGATTct GtGTAACTGT ATTGTGkTAA	3240
wTGaCGwATg CtTAAwACgT GTGCCAATGG T	3271

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

ATAATGAAAT AATACTGTGT TTTATCTGCG AAATGTAtCA TTTTCTAATc GTTCACAGT	60
AAAATGAAAA GATAAAGTGT GTTTTTACTT GAATTTTGAC TAAAATTACT CTATATTTAT	120
TAATTGAGCT ATGCTTATTA TTACAATTTG ATTACAAATT TTAAATTTGT TAATTGAATG	180
ATAATATTAA ATAAAGAAAC TTACACAAGC AAATATGAGT TGTAGCCCAA AATACTTGTT	240
AAATCAAAGT TGAAAGCTAC AAATAATGAA AATTATAAAC TTGAATCTGA AAGTAATTAC	300
TATAATTATG ACAATGTTAA CTTTTAAACG CACTTATTAA TTAAC TACAT AATGTTAATA	360
TCTAATTTAT TCAAGTACTT TCGCAAGATT TATTATCTAA ATAACGGGGG AAAGAATCAT	420
GAGTtCACAA AAAAgAAAAT TAGTCTTTTT GCGTCTTCT TATTAACCGT AATAACGATT	480
ACCTTGAAGA CGTATTTTTT TTATTATGTT GATTTTTCTT TAGGTGTTAA AGGTTTAGTA	540
CAAACTTAA TATTATTGAT GAATCCTTAT AGTTTAGTAG CACTGGTTTT AAGTGTGTTC	600
CTATTCTTTA AAGGCAAAAA AGCATTTTGG TTCATGTTCA TAGGCGGCTT CTTATTGACG	660
TTCCTATTAT ATGCCAATGT TGTGTACTTT AGATTCTTCT CTGATTTTTT AACGTTTAGT	720
ACTTTAAACC AAGTAGGTAA CGTAGAATCT ATGGGTGGTG CGGTTAGTGC ATCATTCAAA	780
TGGTATGACT TTGTTTATTT CATTGATACG TTAGTTTACT TATTCATTTT AATATTTAAA	840
ACAAAATGGT TAGACACAAA AGCATTTAGT AAGAAATTTG TTCCTGTCGT AATGGCGGCT	900
TCAGTAGCAT TATTCTTCTT AAACCTTAGCT TTTGCTGAAA CTGACAGACC AGAATTATTA	960
ACACGTACAT TTGACCATAA ATATTTAGTG AAATATTTAG GACCTTATAA CTTTACAGTA	1020
TACGaTGGTG TTAAACTAT CGAAAATAAT CAACAAAAAg GCTAgCATC TGAAGATGAC	1080
TTAACaAAAG TATTAAAtTA TACGAAAcAA CGTCaAACmG AGCCTAACCC rGAwTATTAT	1140
GGGGTGGcAA rGAAGAAAA TATTATTArG ATTCATTTAG AAAGTTTCCA AACCTTCTTA	1200
ATTAATAAAA AGGTTAATGG TAAAGAAgTA ACACCGTTTT TAAACAAATT ATCAAGTGGG	1260

AAAGAGCAAT TCACATACTT CCCTAACTTT TtCCATCAAA CAGGTCAAGG TAAAACATCT	1320
GACTCTGAAT TTACAATGGA TAACAGTTTA TACGGTTTAC CGCAAGgTTC TGCCTTTTCA	1380
TtaaaaGGAG ATAATACGTA TCAGTCATTA CCAGCAATTT TAGATCAAAA GCAAGGCTAC	1440
AAATCTGATG TCATGCACGG TGA CTATAAA ACATTCTGGA ACAGAGACCA AGTATATAAA	1500
CACTTTGGTA TCGATAAATT CTATGATGCA ACATACTATG ACATGTCAGA TAA	1553

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

ACAAAATCAA TCAGCAAAAT GATTGGATTA AGACGCAAAT TGAGCGTTCA ATGGAAGGCG	60
AAACAGTTGG CATTAATGAT CAAAATATAG AAATATATAG TGAAGtTgA GATTTATACC	120
ATACACTCGT ACCTTTAAAT CAAGAATTGC ATAAGTTGCG ACTTAAAACT CAAAAC TTAA	180
CCAATGAAAA TTATAATATT AATGATGTGA AAGTTAAAAA GATTATTGAA GATGAACGTC	240
AAAGACTAGC ACGAGAACTT CACGATTCTG TTAGTCAGCA ACTTTTTGCG GCmAGTATGA	300
TGCTATCTGC TATCAAAGAA ACGAA tTAGA ACCACCATTA GACCAACAAA TTCCTATTTT	360
AGAGAAAATG GTTCAAGATT CGCAGTTAGA AATGCGTGCT TTGCTGTTAC ATTTAAGACC	420
GCTTGGTTTA AAAGACAAAT CTTTAGGTGA GGGTATTAAA GATTTAGTTA TTGATTTACA	480
AAAAAAAGTG CCAATGAAAG TTGTGATGA AATACAAGAT TTAAAGTGC CTAAAGGTAT	540
TGAAGATCAT TTGTTTCAGAA TTACACAGGA AGCAATTTTCG AATACATTGC GTCATTCAAA	600
CGGTACAAAA GTGACAGTAG AATTGTTTTAA TAAAGACGAT TATTTATTGT TGAGAATTCA	660
AGATAATGGT AAAGGTTTTA ATGTTGATGA AAAATTAGAA CAAAGTTATG ECTTAAAAA	720
TATGCGTGAA AGAGCTTTGG AAATTGGTGC AACGTTCCAT ATTGTATCAT TGCCAGATTC	780
AGGTACACGT ATCGAGGTGA AAGCACCTTT AAATAAGGAG GATTCGTATG ACGATTAAAG	840
TATTGTTTGT GGATGATCAT GAAATGGTAC GTATAGGAAT TTCAAGTTAT CTATCAACGC	900
AAAGTGATAT TGAAGTAGTT GGTGAAGGCG CTTCTGGTAA AGAAGCAATT GCCAAAGCCC	960
ATGAGTTGAA GCCAGATTTA ATTTTAATGG ATTTACTTAT GGATGACATG GATGGTGTAG	1020
AAGCGACGAC TCAGATTAAA AAAGATTTAC CGCAAATTAA AGTATTAATG TTAAC TAGTT	1080
TTATTGAAGA TAAAGAGGTA TATCGTGCAT TAATG CAGG TGTCGATAGT TACATTTTAA	1140
AAACAACAAG TGCAAAAGAT ATCGCCGATG CAGTTCGTAA AacTTCTAGA GGAGAATCTG	1200

TTTTTGAACC GGAAGTTTTA GTGAAAATGC GTAACCGTAT GAAAAAGCGC GCAGAGTTAT	1260
ATGAAATGCT TACAGAACGA GAAATGGAAA TATTATTATT GATTGCGAAA GGTTACTCA	1320
ATCAAGAAAT TGCTAGTGCA TCGCATATTA CTATTAAAAC GGTTAAGACA CATGTGAGTA	1380
ACATTTTAAG TAAGTTAGAA GTGCAAGATA GAACACAAG	1419

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 608 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

ATGTnGGCGG ACGTAAAGGA CATGTTTATA CTGATGATCG AGCATTAGAT ATTGATATCG	60
TTCCGCGCTGC TCAAGCAGAT GGTAAAGCTA CTAACCCCGA ACAATTATTT GCAGCAGGTT	120
ATGCATCTTG CTTCAACGGT GCTTTCGACC TAATTTTAAA GCAAAACAAA GTGCGTGATG	180
CTCATCCAGA AGTAACACTA ACAGTGAGAC TAGAAGATGA TTCAGACTCA GAAAGTCCTA	240
AATTAAGTGT TTCAATTGAT GCGACAATTA AAAATGTAT ATCTCAAGAA GAAGCTGAAA	300
AATATTTACA AATGGCTCAT GAATTTTGTC CATATTCAAA AGCGACTCAA GGAAATATTA	360
ATGTCGATTT AAATGTAAAT GTTGTAGATT AGCATTAACT TAAAGAGATT ATTCAACGTT	420
ATTAATAAAA TTCACATAAA ATTCAAATt stCrAcCAA AATTTTGGT TGGyTATTTT	480
TTCTATTCGT GATTGAAATT TCTGGCAATA TTTAACTGAA AATGATTGTA CCTTAGTCAT	540
CATAAATGTG ACCGGTTCCA ATACTGGCTT GACTTCTTCG CATACCGTCT ACAAATAAAA	600
GTCCAGTG	608

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

CCTTTCAAtT TCTC C AAgA TTTACGCATG TCTGACCAAA TGTCAATACA ATACCTGAAT	60
AATGATTTCT GGAGTAATTG CGAAAAATAT TAAAAGTTG CTATAGATCA ATTTTCAAT	120
TATAGTATCT CATCTCAAGT TTCTAACTAT CATTTACAG TATTACTTGG AGATCGCCAA	180

AAACCACTTA TGTATCTAAA TAAAAATCGC GGTGGTGATGGTGGCATACC AGGTTATATT	240
ATGATTTATT TAGTGCCGAG TACAAGTACA ATTAATTCTA TGAAAAGCTT AATTGCACAT	300
GAAGTAAATC ATAATATGCG CTATCAATAT ATTGATTGGG ATGGCGGAAG TTTGATTGAA	360
TTGATTATTG CAGAAGGATT AGCTGAAAAC TATGTAGAAT CATTGTATGG TAAAGCGCAT	420
ATTGGACCGT GGGTAACAAA TACTAATTGA AGTCGTGATA ACGTAAAAAT TAAAAATACT	480
ATTTATAATC ATTTACATTT AAAGCATATA TTTGAATCGA tGCCTTATCT CTATGGTGAT	540
GATATTAATA AACTTCAAGG TAGGCCTATC GTTGGCTTAT CTCATGCTGC CGGGTATGCA	600
TGTGGCTATC ACTTGGTAAA ATACTTTTTTA CAAAAAACAA ACATACCTAT TGAAGTTGCT	660
ACAACACTTC CAGCACAAAA AA	682

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

ATCTTCTTTT AACATGACAA ATTGCAACAA AATATTAATG ACGCCAAAAG ACATTTTTTC	60
ACGTTCAATT AATTCTTCAA CCATTGTCTT TTGCGATATA GTGGTTCTG ATTCAGACCA	120
AGAAGCTAAC ATATCAATTG GACTCGTTTG TTCAAGTAAC TCAAACCATT CATCACTTTG	180
TGGCTTTGGA TTTCACTTCTG AAGATTTGCC CGCCGAAGAT GATGTAGCAG GAGATTTTAC	240
CTGTAATTTA GGCATTTGAT TTTTCGTGTTT CATTAAAGTAA TACGAGCGTG CTTGTTTACG	300
CATTTCTTCA AAGGATAACT GTTGTCCACT TGTAATTGAA TTTAAAATAA CATGCTTCAT	360
GCCATCTGCT GTTAAACCAT ATAAAGTCGC GAGTTGTGTA ATTAAACGCT TTGCATCTTT	420
GGTAACAATG TCTTGACTAA TAAAATGTTT ACCTAACATT TGTCTCAACA TTTCAAAGTC	480
AAAAGATTCA TTTGATAAAT CGATACCTTG GTACGGTTCA TTAATCGGaA TATCACTTGT	540
ATCGATATCT ATTTTTGTAG ACGGCACTTT AAAAACATCA GTAAATTGTC TTGTTACCTG	600
TTTAAATTCA CTCAAATCAA TTTGTTGATA CTCAAAGTAT TTCTTCAACT CATGAAATCG	660
ACGATGCTCG ACTTCACTAT ATAAAAAGAT TGACAACATT GGATCATTAATAAATAAATG	720
TGCTGAAGGG GtTGaATTAA TTGGTAAACA AATTGTGTTT CTTGTTTCATC ATGTTTGACA	780
AACGCCTTTA ACAATCCAAT CGCTTCAAGT AAGTCCATTT GTTGTCTAAA CTCTAGTAAA	840
TTAATTTTAA GTTCATTCAT AAAAATATAA TGAGAAAGAA TCAATGTTTC ATTATGACTT	900
TCTTTAACGA ATTGAGTCAT AAAATGATAT AAACCCACTG CTTGCGTTCC AATTAGCGGT	960

GTATACAGTC GATTCAATAC CTCTAAATGA TTCGTATTTA AATCAAAGTG TTGCATAACT	1020
TTGAATTGAT CCTTTGGTCT TAAGCCGAAT TCGAAGGCTT GTCGTCCCaT TTAAGCnATC	1080
ACTCCGTTTG TTTTCGCTTA AAATCCCTTG CnCGATGCT AACAATTGAT CAACATCTTT	1140
AAATTCTTTA TAGACTGATG CAAATCTAAC ATATGAAACT TGATCAACAT GCATTAACAA	1200
GTTCATAACG TGTTACCTA TATCTCGTGA AGACACTTCC GTATGACCTT CATCTCGTAA	1260
TTGCCATTCA ACCTTGTTAG TTATGTCTTC AAGTTGTTGA TATCTAACTG GTCGTTTTCC	1320
ACAAGAACGC ACAAGTCCAT TAAGTATCTT TTCTCTTGAA AACTGCTCTC TTGTGCCATC	1380
TTTTTTCACA ACTATAAGCT GACTAACTTC GATATGTTCA AATGTAGTGA AACGTGTTCC	1440
ACAATTTTCA CATTCTCTTC GTCTTCGAAT GGCATTTAAT TCATCGGCAT GCCTTGAATC	1500
TACAACTTTA GATGTGTAG AATTACATTT CGGGCATTTT ATTACATCAC CCTCTTTATT	1560
TTGATTATGC CTAATTATAC TATAAATCTA GAGATGAAAA AAGAATCCCT CAATTTAATT	1620
CATTTAACCA AATAATGAAA CAATAAAAAA CATTATATCG TTAATTATTA AGTAATTTGC	1680
ATGACAATAT TATTGTATTA AAAATAAAAA ACCTAACTCCGAAGTCAGAG TTAGGCTATA	1740
AATTAATTGT ATTAAGTTGC ACTTACAGTT TCTTTTGATG TCAAAAGTGC TCCAATTTGC	1800
TCAGCAACAT CTACAACTCT ATTTGAATAA CCCCATTCAT TATCATACCA AGCAATAACT	1860
TTTACTTTAT TCCCTGACAT GACCATTGTT GATTTTGCAT CAATAATAGC TGAATTTGGA	1920
TTAGTATTAA AATCAACAGA CACTAGTGGT TGATGTTTGA CTTCTATGAT ACCTTCTAAA	1980
CCTGCATTTT CAAAAGCTTG GTTTACTTCT TCTGCAGTTA CTTCTTTTTC TAAATCAACA	2040
ACTAAATCAA CGAGCGATAC ATTCTTTGTT GGTACACGTA ATGCCATGCC GTGTAATTTA	2100
CCTTCTAATT CTGGTAATAC TTCTTTTAAA GCTTTTCGCCG CACCAGTAGA AGTAGGAATA	2160
ATGCTTTTCAT TACATGAACG TGCACGTCTT AAATCTTTAT GTGGATTATC AATATTTTTT	2220
TGGTCATTTG TAATAGCGTG AACAGTAGTC ATTAACCAT TAACTATTCC AACTGATTA	2280
TTTAAACTT TTGCAACTGG ACCAATGCAA TTAGTAGTAC ATGAAGTT ACTAAAAATG	2340
TCAAATGCTT CTATATCTAA TTGGTTATCA TTTACGCCTT TAACTACCAT TTGAACATGT	2400
CCACCTTTTG nAGGACCAGT TAACAAAAsT TTTtTGGCAC CTGCTTTAAT ATGTGCGATG	2460
GCTTTATCAC CATGaTTAAA TTTACcAGTT GCATCTATAG CAATATCGAT ATCTAATTCT	2520
TTCCATGGCA AGTTTTcAGG ATTGCGATCA GCAACCAATT TAATTTTATG ATCT	2574

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

CAAGGTACCG GTTTAGGTTT GTTCATTTGT AAAATGATTA TCGAAGAGCA TGGTGGTTCC	60
ATAGATGTTA AAAGCGAATT AGGGAAAGGC ACAACATTTA TTATTAAACT ACCAAAACCA	120
GAATAAAATT GAATATAGTT ATTTGAGAAC GCATGTTATT GATTAGAGAC TCTAATTTAT	180
AGCATGCGTT TTTTGATTGA TGTGGGGAAT TTTGTATGTG GATTAGAACT TAGGGTTTTT	240
GCGAATATCA ACTATTAAAT ATATTACTAA TTTATACAAA AATATAAAGT TTGATAAAGT	300
TATTTATTTG ATTATAAAAA TAGGGTAAAA TATAGATATA TTGTATTAATTAAATTATTC	360
GAGGTGTCAT ATGAAAAAAT TCATTGGATC AGTTTTAGCT ACGACATTAA TTTTAGGGGG	420
ATGTTCCACG ATGGAAAATG AATCAAAAAA AGACACAAAA ACAGAAACAA AATCTGTACC	480
AGAAGAAATG GAAGCTTCAA AATATGTAGG CCAAGGCTTC CAACCGCCTG CAGAAAAAAA	540
TGCGATTGAA TTTGCGAAGA AGCATCGTAA AGAATTTGAA AAAGTAGGTG AACAATTCTT	600
TAAAGATAAC TTTGGACTAA AAGTTAAAGC TACAAATGTT GTAGGTAAAG ATGATGGTGT	660
AGAAGTTTAT GTGCATTGTG AAGATCATGG CATTGTATTT AATGCAAGTC TACCTTTGTA	720
CAAAGATGCC ATCCATCAAA AAGGATCAAT GCGAGTAAT GACAATGGTg ATGATATGAG	780
TATGATGGTG GGTACAGTGC TGAGTGCTT TGAATATCGA GCGCAAAAAG AAAAGTATGA	840
TAACTTATAT AAATTCTTCA AAGAAAATGA AAAGAAATAT CAATATACAG GCTTTACAAA	900
AGAGGCAATT AACAAGACAC AAAATGTCGG ATATAAAAAT GAATATTTTT ATATTATA	960
CTCTTCTAGA AGTTTAAAAG AATATCGAAA GTATTATGAA CCACTGATTC GAAAAAATGA	1020
TAAAGAATTT AAAGAAGGAA TGGAACGAGC AAGAAAAGAA GTGAATTACG CTGCAATAC	1080
AGATGCTGTT GCTACACTTT TTTCTACTAA GAAAACTTT ACTAAAGACA ATACAGTAGA	1140
TGATGTAATC GAACTAAGTG ATAAATTATA TAATTTAAAA AATAAACCAG ATAAATCTAC	1200
AATCACAATA CAAATAGGGA AACCCACTAT TAATACTAAG AAAGCCTTTT ATGATGATAA	1260
TCGTCCAATA GAATATGGGG TGCACAGTAA AGATGAATAA AATTAATGAT AGGGATTTAA	1320
CAGAATTAAG TAGTTACTGG GTTTATCAAA ATATTGATg AAAAAAAGAA TTAAAGTTA	1380
ATGGAAAAAG GTTTAAACAA GTAGACAGTT ATAATGATGA TAAGAATAGT AATTTGAATG	1440
GTGCTGCTGA TATTAAAATA TATGAGTTAT TAGATGATAA AAGTAAACCA ACTGGTCAAC	1500
AGACAATAAT TTATCAAGGA ACATCTAATG AGGCAATTAA TCCAAATAAT CCATTAAAT	1560
CATCGGGGTT TGGAGATGAT TGGCTCCAAA ATGCTAAATT AATGAATAAT GATAATGAAA	1620
GCACAGATTA TTAAAGCAA ACAGATCAAT TATCAAATCA ATATAAAATA AAGTTAGAAG	1680

ATGCAGATAG ATTATCAAAT AGTGATTTTT TAAAAAATA TAGAATGGAA TCAAGTAACT	1740
TCAAAAACAA AACCATTGTG GCGGATGGCG GTAATTCGGA AGGCGGTGCA GGAGCAAAAT	1800
ATCAAGGAGC GAAACATCCG AATGAAAAAG TTGTTGCTAC TGACTCAGCA ATGATTCCTT	1860
ATGCTGCTTG GCAGAAATTT GCTAGACCAC GCTTTGaTAA TATGATTAGT TTTAATAGTA	1920
CCAACGATTT ATTAACATGG TTACAAGATC CATTCaTCAA AGATAECCA GGAAAACGCG	1980
TTAACATTAA TGATGGTGTG CCCAGGTTAG ATACTTTAAT AGACAGCCAT GTAGGTTATA	2040
AAAGGAAGTT AAATAGAAAA GATAACACAT ACGATACTGT ACCACTAATC AAAATAAAGT	2100
CGGTAAAAGA TACAGAAATT AAAAATGGAA AAAAAGTAAA AAAGACTATT AACATAACAT	2160
TAGATATGGA TGGGCGAATT CCAATAAATG TTTGGACAGG AGATTCGATT GCACGTTCTG	2220
GAAGAGGAAC TTTAATTAAA CTTAATTTAG AAAATCTTGA TGCGTTGAGT AAAGTGATTA	2280
CTGGTGAAAC AAGTGGTATG TTAGCAGAAT GCGTAATCTT TTTAAATGAA AGTTTTAACA	2340
TCTCAGAAAA TGAAAATAAA AATTTTGAG ATAGAAAGAA ACAATTATCA GAAGGATTTA	2400
AGGATAAGAT TAACTTATTT CAGTTAGAAG AAATGGAAAG AACTTTAATT AGTAAATAA	2460
ACTCACTTGA AGAAGTTGCA GATGAAACAA TAGAAAGTAT TAGTGCTGTT AAACACTTAT	2520
TACCTGATTT TGCATTGGAT GCATTAAAAG AAAGAATTAA TGAGTTGTTT AAAGTATAA	2580
AATCTTTTAT AGAAAAAGTG TATGATAGTA TAGATAATGA AATTTTAGAA ATTTTCAAAA	2640
ATATAGATCA CGACTTCAGA GATGGAGTAT CTGAAGAAAT GATGAAACAT TTGAAAGTAG	2700
TGAAACAGAA TATAGACCAA ATAAAAAATC AAAATGATAT TTATGGTAGG CAAATTGCAG	2760
ATATTAGAAG TATTATGAAA CAACAAGATG CAACAATTTT AGATGGAAAT TTTCAAATTA	2820
ATTGTAGCGG CGAAAATATG GTACAGGGTC TAGTTATACC TTCTAATTAT TTAGGAAGAA	2880
AAATGAAAAT ATTAAAAGAC CATATCGATG ATGGTATTAA AAAAATAGCA GACTATGTTC	2940
AAGGTATATA TGATGAATAT GCA _T CGAAAA TTGTGATGT AATAAAATAT TTGATTAATA	3000
CAATTCCCAA AATACGTAAG AATTTAAGAC ATGCAATTGA AATGTTAAAT GTAAAAAAGA	3060
AAGAATTTTT GTCCCTGATT CCTAATGTAA CTTGTAATTA TATTAAAAC _T AAATTAGAAG	3120
AATTAGATAA TACTTTAGGC AAATGGGAGC CTTTTCTTAA TGATTTAAAA GCAGTGTCAC	3180
CAATTTTAGA TAACCATTTA GATGATATTG TTAAGAACAT GAAGCCTTTG ATTGTACAAA	3240
TGAyAtwTGA ACCATCACAT TATGaCGATA TGTTTAATTC aAGAAAAGCT TTAACGcCAG	3300
TGTTCTCAAG CGTTTTATAA AGGTTG	3326

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5301 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

ACCTATAGCT G	GCCCGTCAA	GTCTGAATC	ATATGTCGCT	ATAAACCCAG	TTGCATGCCC	60	
AGCAATCTCG	GTTTCAATTT	CAAAATCATG	CTCTTTCAAA	CGATCTATTA	AAGTTTCGAGA	120	
CGCAAATATT	TCTTCATTAC	CAAGTTCAGG	ACGTTTCATGA	ATTCTATGAC	TGATTTTCGAT	180	
ATAACTATAT	TTATTTGTTT	CTATATAATC	GAGAATT	ET	TGTTTTTCAC	TCATTTTTTA	240
CTATCTCCCT	TTTACCCTAC	ACTCATTTTA	ATCATCCACA	ATATTTTGTT	CTTTCAAAT	300	
GAATTATTAC	TTATTCTATC	GGTTTTATCT	CATGATGTCA	TCTAGTTTTT	CTTTATTTAC	360	
AAAATTTTCT	AATAACTAAA	aGCCTTTCAT	AAATTTATAA	AACAGTTTCA	AATTGTAAAA	420	
CATAAGCCCT	ATTGTTACAA	TTTAAGTATT	GTTAGAAACA	CAACTTACAA	CAAACCTAAG	480	
TTTTATAATG	CAACAAATCA	TAAGCGTTTT	ATAGTTTTGA	GTAGTTAATA	GGAGGAAATT	540	
CAAAATGACA	AAAATGAATG	TTGAAAAGTTT	cAATTTAGAT	CaTAcTAAGG	TGGTTGCCCC	600	
ATTTATTAGA	TTAGCGGGAA	CGATGGAAGG	ATTAAACGGA	GATGTCATTC	ACAAATACGA	660	
CATTTCGTTT	AAACAACCAA	ACAAAGAACA	TATGGATATG	cCCGGACTAC	ATTCATTAGA	720	
ACATTTAATG	GCTGAAAATA	TTAGAAATCA	TAGTGACAAA	GTTGTTGATT	TAAGTCCTAT	780	
GGGTTGCCAA	ACTGGTTTCT	ATGTATCATT	TATTAATCAT	GATA	ETATG	ATGATGTATT	840
AAATATTGTT	GAAGCAACTT	TAAATGATGT	GCTAAATGCT	ACTGAAGTGC	CTGCTTGTA	900	
TGAAGTACAA	TGTGGCTGGG	CAGCAAGTCA	TTCATTAGAA	GGTGCTAAAA	CTATCGCTCA	960	
AGCATTTCTA	GACAAACGAA	ACGAATGGCA	TGATGTTTTT	GGTACAGGAA	AATAAATCTT	1020	
AGTCAATCAA	GTTAATCAGA	AAaGCAGTCG	AACAATGATT	TTACAATCGC	CATTGTCCAA	1080	
CTGCTTTTTT	TTATGCTTCA	AAGTCAAAAA	ATCGAACAAA	TGAAAAAGTA	AAATCTTTAA	1140	
CATTTGTCCG	ATTTATTTGA	GAACCACTAT	AATTTCTTAA	TTAGTCCCAT	TAACACGAAC	1200	
TGCATAGGTA	ACCTTAAATA	TAGTTG	AT	GTTGGCAATT	GTTTATCTCC	TAAAGGTAAC	1260
TTTTTAACTG	CCATATAGAT	ATTAGCTGGG	AATACAGCTA	GCAAGAATAG	ATTGATTGTA	1320	
TTTTTCAAGC	ATTGAGATGG	TCTTTTAATT	AAAAGTGCAA	GTCCAAATAA	TATCTCAAAG	1380	
ATTCCTGTAA	CAAGAACCGC	TGTTTTTCGA	AGTGGCAAAC	ATTTCCGGTAT	G	AATTTCTA	1440
AATTGTCGTT	CTCGTGTA	AAA	ATGCAATACA	CCTATTACAC	TAAACCTAT	TCCTAATAAA	1500
TATCTTAGTA	TGTTCAATCA	GCTTCAACTC	CTATTCTGTA	ATGATTTTAT	GAATTAATGT	1560	
AGGCGATACA	ACATGaTCAG	CAATTGTTAT	GCTTGAATCT	AATTTTTTAA	CAACATCGTC	1620	

TACATCTTGG	CGATTACTGT	GAATCGTTAA	TAATGATTCT	CCTTCTTCTA	CTTTATCACC	1680
AATTTTTTTT	TTTAAAACAA	TACCAACCGC	TAAATCAATA	TCATCCTCTT	TTGTAAACG	1740
TCCCGCTCCT	AACATCATCG	AAGCGACACC	TATATCGTTA	GAGACTAATT	CAGTCACATA	1800
ACCTGATTTT	TTAGCTTTAT	ATTCAATTTG	ATATGAGCT	TGTGGCAAAC	GCTCTGGATG	1860
GTCAATAACA	GTTTCGTCGC	CACCTTGGTT	TTTAATAAAT	GTTTTGAATT	TTTCTAATGC	1920
TGCACCTGAA	TTAATTGCCT	CAATTAGCAA	CGCTCTCGCT	TCTTCAAGCG	TTTCAGCTTT	1980
GTTTGCAAGT	ACAACCATTT	GAGAACCTAA	TGTTAATACA	AGTTCTGTTA	AATCTTTCGG	2040
ACCTTGTCCT	TTCAACGTAT	CAATTGCTTC	TTGTAACTCA	AGCGCATTGC	CAATCGCACG	2100
TCCAAGTGGC	TGATTCATAT	CAGAAATAAT	CGCCATCGTA	TTACGTCCCA	CATTATTACC	2160
AATACGTACC	ATTGCGTGCG	CTAATGCTTC	AGCATCTTCT	AATGTTTTCA	TAAATGCACC	2220
GCTACCAGTT	TTTACATCTA	ATACAATTGC	ATCTGCACCA	GCAGCAATCT	TTTTACTCAT	2280
AATTGAAGAG	GCAATTAATG	GTATTGAATT	GACAGTACCA	GTAACATCCC	TTAAGGCATA	2340
TAATTTTTTG	TCTGCAGGAG	TTAAATTTCC	TGATTGTCCT	ACAACTGCCA	CTTTATTTTC	2400
ATTAACCAAT	TTCACAAATG	TTGCTTCATC	TATTTCAACA	TAATAACCAT	CAATTGCTTC	2460
TAATTTATCA	ATCGTACCAC	CTGTATGACC	TAATCCACGC	CCACTCATTT	TTGCAACAGG	2520
AACATCTACA	GCTGCTACTA	ATGGTGCTAA	AACCAATGTA	GTTGTATCTC	CTACACCACC	2580
TGTTGAGTGC	TTATCTACTT	TGACACCTTT	AATATCACTC	AAATCTATCA	TATCACCAGA	2640
ATTAACCATA	GCCATCGTTA	ATGCTGCACG	CTCATCATCA	TTCATATCTT	GGAAATAAAT	2700
CGCCATTGCT	AAACTTGATG	CTTGGAATC	AGGAATATCC	CCTTTAACAT	AGCCGCCAAT	2760
AAAGAAATTA	ATTTCTTCCG	TTGTTAGTGT	ATGACCGTCA	CGCTTTTTTCT	CAATAATGTC	2820
TATCATTTCT	ATTTTTATCA	TCCTTTTCTT	AAAAAGCTTA	GGACAAAGCA	TCTGCGCTTT	2880
CTCTAGTCCA	TTTTTAAAAG	CACAAGCGAA	AATTATTATA	GCAAGCTATC	GATTTCATTT	2940
TTAATATCAC	AATTTCAATG	CGATGTTATT	ATTCTTAAAT	AGATTGGTTA	TAACGTTAAA	3000
GTCCCTATTA	AATTATCTTA	GAATCATCAT	GGCATTTATG	ATGTCTTAA	GCTGATATCG	3060
ACATACTTAT	ATATGGTTAC	GATGTCCCAT	GCTTACATAT	TTTTATAAAA	TTAGTAATCT	3120
GAATCTGCTT	CTAAACCTTG	CATAATTTGa	ACGCCTGCGC	TCGCACCAAT	ACGTGTCGCA	3180
CCTGCTTCAA	CCATTTTATT	GAAATCTTCT	AAATTACGTA	CGCCACCTGA	TGCTTTTACT	3240
TCTATATCAG	CACCTACTGT	ATCTTTTATT	AATTTAACGT	CTTCTGCAGT	CGCACCGCCA	3300
CCTGCAAAAC	CTGTTGAAGT	TTTAACGAAG	TCCGCACCAG	CCGCTTTTGT	TAATTCACTC	3360
GCTTTTACAA	TTTCGTCATG	GTCCAACAAT	ACCGTCTCAA	TAATCACTTT	TACTGTGTGA	3420

CCTTTCGCAG	CTTTCACCAC	TGCTTCAATG	TCTTGTTGTA	CATCATCAAA	ACGTCCATCT	3480
TTTAATGCGC	CGATGTTGAT	GACCATGTCA	ATTTTCATCTG	CACCATTTTG	AATCGCATCT	3540
TCTGTTTCAA	ATGCTTTCGT	CGCAGTTGTC	GATGCACCTA	ATGGGAATCC	TATTACCGTA	3600
CAAACATAACA	CCTCTGAATC	AGCTAGTCGC	TCTGCTGCAT	ATTTAACATG	CGTTGATTC	3660
ACACATACAG	ATTTAAAATG	GATGCTTTC	GCTTCATCGA	TGATTTGATC	GATTTGCGTA	3720
CGTGTTGACT	CAGGCTTCAA	TAAAGTGTGA	TCAATCAATT	TTGCACTATT	CATTTTCTAT	3780
CTCCTCCTTT	ATGGTTGATT	ATAAAAATAC	GGTTGTAAAT	TAGTTGATTG	AGCGTCAGGT	3840
TCATTTAAAT	ATCAGGTTAG	ATGTTTCGCTT	TTTATGTAAC	CGCATACATA	TACTATTACA	3900
TTAATTCATT	TCCCATAAAC	AAACAATACA	ATTGAACGTG	ATATCTTCAT	TATGAACGAT	3960
GACTTGACAA	CAAGCTAATC	AGGATTATAT	TTTTATAATT	CTTTAATTCT	ATAGTACAAA	4020
AATTCGCAAA	AAAGGGAAAC	AAATGTTATC	TTAAAATAT	TAATGAATAT	TAAGGAGAAG	4080
ATAACAAATG	ACAAAAGGTA	CACCACATAT	TCAACCAAAT	GGAGTAAAAA	TTGCTAAAAC	4140
AGTATTAATG	CCTGGCGATC	CGCTACGTGC	AAAATATATT	GCTGATAATT	TTTTAGAAAA	4200
TGTTGAACAA	TTTAACGATG	TACGTAACAT	GTTTGGTTAC	ACTGGTACAT	ATAAAGGTAA	4260
AGAAGTTTCT	GTAATGGGTT	CTGGTATGGG	TATTCCAAGT	ATTGGTATTT	ACTCATATGA	4320
GTTATACAAC	TTCTTTGATG	TAGATACAAT	CATTTCGTATC	GGTTCTTGTTG	GCGCATTACA	4380
AGAAAATGTT	AACTTATACG	ATGTTATTAT	TGCACAAGCT	GCATCAACTA	ATTCAAATTA	4440
TGTAGATCAA	TACAATATTC	CAGGTCATTT	CGCGCCTATC	GCTGACTTCG	AGTTAGTAAC	4500
TAAAGCTAAA	AATGTCGCTG	ACCAAATCGG	TGCTACTACA	CACGTAGGTA	ACGTATTATC	4560
TTCTGATACA	TTTTACAATG	CCGATCCAAC	ATTCAATGAT	GCTTGAAAAA	AAATGGGTAT	4620
TTTAGGTATC	GAAATGGAAT	CAGCTGGTTT	ATATTTAAAT	GCGATCATG	CTGGTAAAAA	4680
AGCACTTGGT	ATTTTCACAG	TAAGTGATCA	TATTTTACGT	GACGAAGCTA	CTACACCTGA	4740
AGAACGTCAA	AATTCATTTA	CACAAATGAT	GGAAATCGCT	TTAGAAATCG	CAGAGTAACT	4800
TATTTAAATT	GACTTTAATT	GCTCTTTAAC	AATGCGATTA	AACTCAAAAA	GCCAACACAT	4860
TCTGGGCGTA	TCCCCATTTA	TGTGTTGGCT	TTTATTTATA	TTATTACTTA	TCTGTAGATT	4920
AGCTTAAGTA	AGATTTAAAC	ATCCAATTAT	GTTTATCTAC	TGATGTTTGC	ATACCTATAA	4980
ACATATCTTC	TGATACATCA	TCGCCAGCAT	TACCAGCAAT	TTCGATTGCG	TTTTCTAATT	5040
GTTTTGAGAT	ATTTGTGAAG	TCTTGTGATA	ATTCTTCAAC	CATTTGTTCT	GCAGAGTAAC	5100
CTTTCGCAGC	TTCTTTAACA	ATTGATTGCT	CTAAGCATTC	AGTTAATGTA	CCTACAGGGT	5160
TTCCTCCTAC	CGCTAAAATT	CTTTCAGCTA	ATTCGTCTAC	ATATTGGCTT	GCTTCATTAT	5220
ATAATTCTTC	AAATTTAACG	TGTAATGAGA	AGAAGTTAGG	CCCTTTCACA	TACAGTGGA	5280

AATTGTGTAG CTTTGTGTAA G

5301

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

GAAGATGAAA GCTATATTGA AGATGATGTT ACTAAAAAGG AAGCTATTTT AAGTATGCAA	60
ATTCCTAAAG GTTCTCTCA AAAATTAAAA GAGAACCGTT TAAAAGAAAC GATACAGTTA	120
TATGGTAGAG ATGACTTTAT AGGTGGTATT GCTGTAGAAA TTGTTAGTAG TTCATTATAT	180
GAGCAGCAAA TTCCTAACAT TATTTATGAA CACCTTGAGG ATATGAAACA GCATCAATCC	240
ATCGATGCTA TCAACAAGTC CTATCATAAA CATAACCTG AATCTAAAAT CAAATTTGTG	300
TCGCTTACTA AACAAGCACA ACACTCTAT TCAATTAGCT TAATCTTGC GGTGATTTTA	360
TTTGTTAGCG CTGTTCAAGT AGTACTTCAT TATCGTTTAA ACCAACAAGC AGCATTGCAA	420
CGATTATCAC AATATCATTT AAGCCGTTTC AAATATATA GTAATTATGT AATGACACAT	480
ACGATTTTGT TATTGTTGGT ACTATTGGCA GTTAGTCTAT ATTTGTCTCA ACCATCAGC	540
TTAATATTTT ACTTAAAATC ACTGTTACTT ATATTGATTT ATGAGATAGG TATCGTCTTT	600
ATCTTATTCC ATATTCAAAC AATAAGTCAT CGATTATTCA TGACATTTAT ATATGCACTT	660
GCTATGGGTA TCGTATACTT GATTATTTTC ATGTAAAGGA GCGTAACTGA TGATAGAAAT	720
TAATAACCTT TCAAAGCGTT ACCGTAACAA ACAGATTTTC AATCATTTAA CTATGTCCTT	780
TGATAGTAAT CGTTTAACCG TATTACTTGG TGATAATGGT GCTGGAAAAT CAACATTACT	840
TCGTATGATT GCTGGTATTG AAAAAGCTAA TGATGGAAC ATCAACTATT TCGGCGAAAA	900
ATGGAATCAA AGACaAATAC aAAATCACAT CGGTTAGTG CCACAAGACA TTGCGTTATT	960
TGAACACATG ACAGTGGCTG AAAACATTAA ATTTTTTAAA TCACTTTGTA AAAATCCAAT	1020
TAACGATACA ACTATCAACG AATATTTACA GCAATTAAAC TTTGATGATA CGTCTGCCAA	1080
AGTATCTACA TTGTCCGGTG GGAATAAACG TAAAATTAAT ATATTAGTAG GTTACTAGG	1140
TCAACCTCGA ATTCTCATTT TAGATGAACC GACAGTTGGT ATTGATTTAA AATCTAGACA	1200
TGACATCCAC CAACTACTTA ACATCATGAA ATCTAAATGT TTAATTATAT TAACTACCCA	1260
TCATTTAGAT GAAGTTGAAG CACTTGCAGA TGATATCAAG TTAATTGGCC AAGATCCTTT	1320
TTATCAACAT GTTTTAGAGG ACAAACAATG GACTTATACC TATyATTAAA ACGAAAAAAT	1380

CCCAAGCTGC	GTATGATATC	GCAACTTGGG	ATTTTCTGTA	TTATCTACTT	TGCAAGTATG	1440
ACGTTGGGTC	TACTGCATAT	TGATTACCGA	TGCCACCAGA	CATACGTTGG	AAGTGTACGT	1500
GAGGCGCTGT	TGAATTACCC	GTACTACCTG	AATATGCAAT	TTGTCACCA	GCTTTGACTT	1560
TATCACCAGC	TGAAACAGTT	AAACGATTAT	TATGCATATA	CCATTGGTAG	TTATTACTGT	1620
TCGCTTCTTT	AATCGTTACT	TGATTGCCGC	CACCATAGTT	ACTCCAACCT	GCTTGTTACTA	1680
CTGTACCATC	AGTTAATGAG	TAAACTGGTG	AATTTTCAGG	CATTGCATAG	TCGACACCGT	1740
AATGCGCACC	ACCACCGTGA	TATTGTCCAT	ATGGTTGTAG	TTGTTTACGA	CTTGTTAACC	1800
AGCTTGCGTC	TTTCGCATGA	CCACTAGcTG	TCGCTTTACT	TGCTGATCCA	CCATTTTGAT	1860
TAGATGTGCC	ATTAGGATAA	TTGACCTTTC	CATTACCATC	ATGGCTGTTA	TACGCTTGGT	1920
TGTTGTTACT	ATGTGAATAA	TAGCTGCGT	CTGGACCTAC	ATTTGATTGA	TAACCATATT	1980
GATTAATATG	CTGTTGGCTT	TGACTCGCTG	TGTAGTCATT	GTTATCTCCT	GCTGTTGCTG	2040
GATTCACATA	TGTTTGGCCG	CTTCCATTGG	CATTTGCATT	TTTTGGATAA	CAGTTATAAA	2100
AATAATGCGT	ATGTCCTTGA	GCATCTACGA	ATGTATAGCT	ATATTCTTTATTATCAAACA		2160
TTGCTTGATT	CCAGTTACCA	TCAGGTGTGT	GATGATAATC	CCCATTAGAA	TCAATTGTAT	2220
AATAAGTACC	ATAAGATACG	TCTTGTGATT	GTGTTGACAT	TTGTGTATGT	GCTTGTTGGG	2280
TGTTTGTCTG	TTCTGCTGCA	TCTGCTTGAT	GCGCCATTGT	AAATGTAGCG	AA s CCATCGT	2340
TGCAATCGCT	GCTGCTGTTA	ATTTTTTTCAT	GTATAAAACA	TCCTCCATTA	AAGTTAAAGT	2400
TAGTTTTCAA	TTAAACTGTA	CTGCACATAC	TAAAAGAATT	AGACAACTGA	GTAAAGGATT	2460
TAATTCTCAT	TTTCCAATA	TTTAATATTC	CCGAAATGTT	TTACTAAACT	CATTACATTG	2520
TCATTACAAA	ATAGCCATAC	ATTGATATTA	AATGACATC	TCTCACTGCA	TTCGTTTAAC	2580
CTTTTATAAA	TTTTCAAAT	TAACAACTAA	TCGTTTCGTCC	ATGTTTCGCGA	TTCAACGCTA	2640
ATGCATGATA	GTAATCATCC	ATCAAATCAT	ATCAACCAA	TTCCATTATC	AATCGCTATT	2700
GATTGTCATT	CAACTTTCTA	ATAGTGATAT	GCTTCTCAGG	CTTAAAAATC	GTCATAT TT	2760
TTCTATTAAT	TAAATCATCT	GTGAGCTTTA	ATGCTACTAA	TTCATTGCTG	CCATAATACT	2820
TAATATATAA	CGTTCTTGTA	GTTAAATTTA	TTACGGTCTG	ATACATCGTA	TAGTGATTGT	2880
CAGCATCATG	CGGACGTACA	ATTCCAATCG	GTATATTTAC	CGCATCTAAT	AAATAAAATG	2940
CATTCATTAA	ATCCATTTCT	TTATCATTGT	TTTGAGCAAT	GTTTGCTTTC	ATAAATGCCA	3000
TTCTCACAAA	GCGCTCAGTT	GAAGTAAATC	CACCTGGCAA	TCCAAATGTA	CCTGCTTCAT	3060
TGCCTAAAGG	TTCAATCGTT	ACACCTTCCA	ATAAATTTGC	TGTTGCTGGA	TAAGGAGAAA	3120
TATTGATATA	TTGTCTTAAA	TTACTATAAT	GCCAATTTAAGTCTGGATGA	TTTGTTAAGA		3180
CACCAATAGG	ATTATCTTTT	ATAACCACTT	CACCCTCTTT	AAATGAAACT	TCGACTGTAT	3240

GTCCAGTTGC	ATCGGAAACA	TGATAATGCA	ATGGCGGAAC	TTCACCGATG	TCATTTAAAT	3300
ATACAGCTAC	AACATGTATT	TGGGATGCTT	GTTGTTTCAT	ATCTTCAATG	CTTGTTGTAT	360
ATCCCAAAT	CCATGTCACA	ATTTCATTTT	GCGTAATATT	CATCGCGTCC	GCTTTGTGTG	3420
TTGATCCATA	TGAACTATAA	CCTCGGAAAT	ATTGTGTTGA	AATGGCAACG	CcATGTtCAT	3480
TAACACCATC	ACCATAAATA	AAACCTTCCA	TATCTGTTCC	TGTGCCAATA	AAGCCATATT	3540
GCGTTTGGCC	TGTCGTGCCA	GCGCAAGATT	TCCAACGATA	ATTTCTAGGC	GTCACTGCTG	3600
GCGAACCATC	TAATGGATAA	TCATAATCCA	TCGTGCGTCC	AAGAAGTACT	TGATTATTTA	3660
AAGTTTGTAT	TGTGAATCCT	GTGCACATTG	TTCTCACTCC	TCTGTACCTT	CATTTACTTT	3720
AATCACTTTC	AAATAAAGCT	GTTTCACTTA	AACATACTAT	AAAAAAATA	TTATACAAGC	3780
AATTAATTGA	TATTCATTCT	CAATAACTGT	GGTATGATAT	GTAAGGAAAT	CATGACTTAT	3840
GTGTGAGTGA	ACGATCATCT	ATACATCCGT	TCACTTCATC	TCATGACTTT	CTATATTTAA	3900
TTTTTACAAG	GAGTGACATC	TGTGAATAAC	ACACAATCTT	CACCACGCAG	TAATATTATT	3960
ATTGCGATTA	TGTTGTCTGC	ATTAACATAT	TGGTTGTTTG	CACAATCATT	TATTAATATA	4020
GGACCTCTCG	TTGGTCAAAC	ATATCAAACC	TCTCCTGCCG	TGTTAAATTT	ATCTATTAGT	4080
TTAACTTCCT	TCGCCACAGG	TATCTTCATG	GTGGCTGCAG	GTGATATTGC	TGATAAAATA	4140
GGACAACCTGA	GAATGACATA	CATGGGTCT	ATAATCAGTA	TGTTTGCATC	TCTTCTATTA	4200
ATTATATCGG	ACATCACTGC	ACTGCTCATC	ATCGGTAGAA	TTTTACAAGG	TCTATCAGCA	4260
GCTATCTTGT	TACCTTCAAC	AGTTGGCGTG	TTAAATAATC	AATTTAAAGG	AGAACATTTA	4320
AGACGAGCGA	TTAGTTATCT	AATGATTAGT	ACTGTTGGTG	GCATCGGCCT	AGCGTGTGT	4380
ATCGGCGGTT	TAATTGCCTC	AAATTTCGGA	TGGCAAACGA	ATTTTCATCAT	TAGTATAGTC	4440
ATTGCTTTCA	TTGCCATATT	GCTTCTAAAA	GGCACACCTG	AAAAAGTAAG	TCAACATAGC	4500
CACCGTCATC	CATTTCGATTA	CAAAGGTATG	TCGATTTTCG	CTGTTATGAT	TGGTAGCTTT	4560
ACATTATTGT	TAACACAAGG	ATTGAACAA	GGTTGGTTTA	GTACATTTTC	AATCATTTGT	4620
CTGAGCATTT	TTATCaTCAc	TACGTTGATA	TTCATCATCA	TCGAACGTCG	ACATGAAGTA	4680
CCTTTTATTG	ATTTCTCAGT	ATTACGCAAC	CGTCCGTTCA	TTGGTGCATT	TTTAAATAAC	4740
TTTGTTTTAA	ATAGCGGTCT	AGGCGTAACA	GTGGTtTTT	TCATATATGC	TCAAACACAC	4800
CTTGGTTTAt	CAgcTGCGCA	ATCTGGACTT	GTTACATTGC	CATATGCCAT	TGTGGCAGTT	4860
GCGATGATTC	GTTTAGGTGA	AAAAGCAACA	TTACGTTTCG	GTGGCAAATT	GATGCTCATC	4920
ATTGGTCCGT	TGTTCCCTGT	CATCGGCATC	ACTATTATTA	GCATGACTCA	ATTATTGGCA	4980
TCACAATATG	TCATTGCAGT	TATCATTGGT	TTCGTCATAT	GTGCGATAGG	TAATGGTTTA	5040

GTCGCAACAC	CTGGACTTAC	GATTGCAATT	TTCAGTATGC	CTAATGAAAA	AGTTGGTTTA	5100
GCTACAGGAT	TATATAAAAT	GAGTGGTACA	TTAGGTGGCT	CCTTTGGTAT	AGCACTAAGT	5160
ACTACAGTTT	TCAGTATGTT	ACAACATAAC	TATGCACCAA	GTGTAGCTGC	AACCGTAACA	5220
TTTATAGTCA	GCATTGTATT	GATGATCCTT	GGCTCATTGT	CTGCATACAT	GATCATTCCA	5280
AAAACAGTTA	AATCTTAAAT	ATAATAGAAG	AATTATGTTT	CGAAATATCT	TTATCACTTT	5340
AAAATGATAT	ACAAGAAATC	CAAGAAAAAT	AAGCGAACTG	AAATAATAA	GATTCAATTA	5400
ACGCATCAGT	ATTAGGATTC	ACTCTAAAAC	GATTAATAGT	TTTATAAGAA	GGTGTGTTGAT	5460
CTTGAGCTAA	CCACATCATT	CGAATACTGT	CATGAAGTAA	TTTCTCTATT	CTACGACCAG	5520
AAAATACAGA	TTGAGTATAT	GCATATAAGA	TGATTTTTAA	CATCATCTTT	GGATGATAGG	5580
ATGTTGCGcC	ACGATGATGT	CTGAATTCAT	CGAATTTGCT	ATCAGGTATC	GTTTCAACAA	5640
TTTCATTAAC	ATGTCGCGAA	ATATCATTTT	GAGGAATTCT	AACAGAAGTT	TTTATTGGTA	5700
GTGTAAGTTG	GGCAAAGTGT	CTTATTTTTT	TAAAGTATTT	CAAAGTAAAA	TTACATGTTA	5760
ATACGTAGTA	TTAATGGCGA	GACTCTGAG	GGAGCAGTGC	CAGTCGAAGA	CCGAGGCTGA	5820
GACGGCACCC	TAGGAAAGCG	AAGCCATTCA	ATACGAAGTA	TTGTATAAAT	AGAGAACAGC	5880
AGTAAGATAT	TTTCTAATTG	AAAATTATCT	TACTGCTGTT	TTTTAGGGAT	TTATGTCCCA	5940
GCCTCTTACT	CTAATTATAT	TCACTATCAA	TTAGACAAAA	TGGCCATTTTCAA	ATATCAC	6000
GCGTTGTTTC	TGACCTTGAA	TATATTTATT	ATAATTCTCT	TTTTGAAAAAT	CAGTTAACAT	6060
TAATTTAGAT	GTACCGTATT	TTAACACTTT	TTGCATTGTT	TCTATTCTCA	TTTTTCTAAA	6120
TAACCATCCA	TCTTTTAACA	CAATACGATT	AACAGCATCA	TATGATAATT	CTACTGTTTC	6180
TTTAATTTCA	AATGTCTTGA	ATGAAATAAT	CGTGCACATT	AAAAACGTAT	CACCAAAGTA	6240
ATAAACATCT	AAATCATCAC	GTTTATGTTG	TCCAACATAAC	AAACGACCAT	ATTCGAACCTC	6300
TTTTTCTGGA	TATTTCAATT	CTAAAAAACT	AATAATCTCT	TCTTCTTTTA	ATTTGAATTG	6360
CATTTAAAAA	CATCCTCTCT	TAAGTTTTAA	CAGCCTTAA	TTAAAAATTT	TTTCAATCAC	6420
ATAGTTCAAT	ATACATCATT	TCGTTATGTT	TTTTAATACT	TTGTTCAAAA	ACAAATATTT	6480
TATTCTTTAA	AATAATGACT	TTTGTATTTT	TAATCACAAT	AAACATTTTA	AAATTCCTGT	6540
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GTATACTTCA	GACGTCTGTT	TGTAGACAAT	AAAAGTCATT	CACGTCTTCA	TATGTCATCA	6660
AATGTTTATC	ATGATATGAT	GAATATAATA	ATCGGGTATA	TAAGTGTATG	ATTAATTACA	6720
CAATAAAGAG	AAGGAATATA	ATATGAAAAA	AGTGTCAATT	AAAGATGTTG	CTAGAGAAGC	6780
TGGTGTATCA	GTTCAACTG	TGTCACATAT	TTTAAATCAT	AATGATAGTC	GTTTTTCCGC	6840
AACAACGATA	AAAAACGTAC	ATGCTGTTTC	AGAACGTTTA	GGCTATGCCC	CTAATAAACA	6900

TGCAAAACAA	TTGCGCGGCA	GTAAAATTCA	AACTATTGGC	GTCATTTTGC	CTAGCTTAAC	6960
AAATCCGTTT	TTCTCAGCAC	TGATGCAAAG	TATTCATGACCATAA	ACCAT	CTGATGTTGA	7020
TTTATGCTTT	TTAACATCTA	CAGCAACTGA	TTTGTATGAC	AATATTAAAC	ATTTAATTGA	7080
TCGAGGTATT	GACGGATTAA	TTATCGCACA	ATACATATCA	TCCCCGGACG	CCCTAAATAA	7140
CTATCTAAAG	AAACATCATG	TACCTTATGT	CGTACTGGAT	CAAAATGACC	ATCAAGGCTA	7200
TACAGATTTT	GTTTCGGACAA	ATGAATATCA	AGGTGGACAA	CTTGCAGCAC	AACATTTAAT	7260
AGAACTCGGT	CACAACCATA	TGATAATTGT	TGCACCATAT	GACATGATGG	CGAATATGTC	7320
GACTCGTGTC	GCTGGATTTG	TCGATACTTT	GCGCGCGAAT	CAATTGCCAG	AACCACAAAT	7380
CGTCCATACT	GAATTATCTA	AGCGCGGTGG	GCTAACCATT	GTTGATGACA	TCATGGTTCA	7440
ATCTGCCACT	GCAATCTTCG	CTATTAACGA	TGAACTCGCT	ATTGGCATT	TACGAGGACT	7500
AATTGAACAT	GGCATCAGTA	TCCCCGAAAG	TATCTCATTA	ATAGGTTATG	ACGACATTGA	7560
TTATGCAGCG	TACGTCTCGC	CACCTTTAAC	TACTGTGGCA	CAACCTAAA	CTGATATTGG	7620
CAAAACATCT	TTAACCTTAT	TACTTCAACG	ATTACAGCAC	TTAGATAAAT	CCATTGATAT	7680
GATTGAATTA	CCAACGACTT	TAAAAATTCTG	TGCAACAAC	GGCTATCATC	TTTCAAAC	7740
ACTACGTATC	TTCCGAAATA	TACTCATCAT	TGTTAGGCC	TTAGCGTTGC	TTTAATGCTG	7800
AGGGTTTTTTA	ATCATAATTA	TTTTACTAAG	AAATTAAAAT	AATAATGTAT	GAATTTTTAA	7860
ATATGATTTA	AACGTTTTCA	GTTTTTATGA	AAACGCATGC	ATTTTACAAA	TAAAAATGGT	7920
ACGATGGCAC	TGGTAAAACG	TTTTACTAAA	AACAAATCAT	GAGGTGTATA	ACATGAGCAT	7980
TGTTGCATTA	CTTATCGGGT	TAGGCCCCCT	AATTGGCTGG	GGCTTCTTCC	CAACAGTCGC	8040
TTCAAAGTTT	GGTGGTAAAC	CTGTACATCA	AATTATCGGT	GCTACTGTAG	GTACGTTAAT	8100
CTTCGCTATT	TTATTAGCCG	TAGTCACATC	AAGTGGCTTC	CCTACTGGAA	CCAATTTGCT	8160
ATTCGCCTTA	TTATCAGGTG	CAGGATGGGG	ATTCGGACAA	ATCATTACAT	TTAAGCGTT	8220
CGAATTAGTC	GGCTCATCTC	GTGCCATGCC	AGTCACAACA	GCATTCCAAT	TATTAGGCGC	8280
ATCTTTATGG	GGTGTCTTTG	CATTAGGAAA	TTGGCCAGGC	ATTGGTCATA	AAATCATTGG	8340
ATTTACAGCT	TTAGTCGTTA	TTCTAATTGG	AGCGCGTATG	ACAGTTTGGA	GTGAACGCAA	8400
AGAAGCAAGT	AACGCCAAAA	ATTTACGTCG	TGCAGTGGTA	CTTCTGTTAA	TTGGTGAATT	8460
TGGATACTGG	TTATATTCAG	CTGCACCGCA	AGCAACTTCT	ATTGATGGCC	TAAGTGCCTT	8520
TTTACCTCAA	GCAATGGGTA	TGGTAATTGT	TGCAGTCATT	TATGGCTTTA	TGAATATGAA	8580
AGCAGAGAAT	CCATTCCGTA	ATAAAATTAC	GTGGTACAA	ATTATTTTCAG	GTTTCTTCTT	8640
TGCATTTGGT	GCTTTAACAT	ATCTTATTTT	AGCACAACCT	AATATGAATG	GTTTAGCAAC	8700

TGGATTTATT	CTTTCTCAAA	CATCCGTTGT	GCTTGCTACA	TTAACTGGTA	TTTATTTCTT	8760
AAAACAACAT	AAAACGTCAA	AAGAAATGGT	TATTACAATC	ATCGGCTTAG	TACTCATTTT	8820
AGTAGCCGCT	TCTGTTACAG	TATTTATAAA	ATAAGGAGTG	TAGATGTCAT	GAAAAAATCA	8880
GCTGTTTTAA	ATGAACATAT	TTCAAAAGCA	ATCGCGACAA	TTGGTCATTT	TGATTTATTA	8940
ACGATTAATG	ACGCTGGCAT	GCCAATTCCA	AATGATCATC	GTCGTATCGA	CCTAGCTGTA	9000
ACTAAAACT	TACCACGCTT	TATTGATGTC	TTAGCTACAG	TGTTAGAAGA	AATGGAAATC	9060
CAAAAAATAT	ACTTAGCAGA	AGAAATAAAA	GAACATAACC	CTACACAATT	GCAACAAATT	9120
AAACAATTGA	TTTCATCGGA	AATCGAAATC	ATTTTCATTC	CTCACGAAGA	AATGAAAAGT	9180
AACTTAGCTC	ACCCATTAAA	TAAAGGTAAT	ATTCGTACTG	GTAAaCAAC	GCCCTACTCT	9240
AATATTGCAT	TAGAATCGAA	TGTTACTTTT	TAAAAGTTAT	AACTTGAAAG	GAGCGTACAC	9300
ATGACCAACA	AAGTTGTTAT	TTTAGGTTCA	ACGAATGTCG	ATCAATTTTT	AACAGTTGAA	9360
AGATATGCAC	AACCAGGCGA	AACATTACAT	GTTGAAGAAG	CACAAAAAGC	ATTCGGCGGA	9420
GGTAAAGGTG	CCAACCAGGC	TATTGCCACT	GCACGCATGC	AAGCAGACAC	AACATTTATT	9480
ACTAAAATTG	GCACTGATGG	CGTTGCTGAT	TTCATCTTAG	AAGATTTTAA	AGTAGCTCAT	9540
ATTGATACAT	CATATATTAT	CAAAACAGCT	GAAGCAAAAA	CGGGCCAAGC	CTTTATCACT	9600
GTGAATGCAG	AAGGACAAAA	CACCATCTAT	GTTTATGGTG	GTGCGAATAT	GACGATGACA	9660
CCTGAAGATG	TTATTAACGC	AAAAGACGCT	ATAATCAATG	CAGACTTTGT	CGTGCACAA	9720
TTAGAAGTAC	CCATCCCGGC	TATTATATCT	GCATTTGAAA	TTGCCAAGGC	ACATGGTGTG	9780
ACGACAGTAT	TAAATCCTGC	ACCAGCGAAA	GCATTACCTA	ATGAATTATTATCATTAATC		9840
GATATTATTG	TGCCAAACGA	AACAGAAGCC	GAATTGTTAT	CTGGGATTAA	AGTAACTAAT	9900
GAACAATCTA	TGAAAGACAA	TGCCAATTAC	TTTTTATCTA	TAGGCATTAA	GACTGTTTTG	9960
ATTACGCTAG	GTAAGCAAGG	TACATATTTT	GCTACTAAAA	ATCAAAGCCA	ACACATCGAA	10020
GCTTATAAAG	TAAATGCGAT	TGATACAAC	GCTGCAGGCG	ACACATTTAT	TGGTGCATTT	10080
GTCAGTCGCT	TAAACAAGTC	GCAAGATAAC	TTAGCAGATG	CTATTGATTT	TGGTAATAAA	10140
GCGAGCTCAC	TCAGTGTACA	AAAACACGGC	GCGCAAGCAT	CTATTCCCTCT	ACTAGAAGAA	10200
GTAAATCAAG	TTTAAATGAA	TCAAACACAG	CTATGATATG	AAGGTTTAGC	ATATAACATG	10260
CAACATTCGT	ATATCATGGC	TGTGCTTTTT	TATCTTTATA	AAACATCATC	TATTAGAAAT	10320
AATTTTCCAC	TAAACCTATG	CTTGTTGACT	CATGTTTAGT	TATAAATGAA	GTGACAATTT	10380
TTTGTAATCT	TTTAACTTC	CAAATTaTCG	CATATAAATA	TGCTATATTA	ATGATAAA	10440
TTATCAATTA	AAAGGAGGTT	ATGCTATGTC	TAAAGAAGCT	GGTCATACAT	TTTTAGCTAA	10500
ATTAGGAAAA	ACTCGTCTAC	GCCCCGGTGG	TAAAGAAGCA	ACAGATTGGT	TAATACAACA	10560

AGGGGCATTT TCACAAGATA AACAAAGTGTT AGAAGTGGCA TGTAATATGT GCACAACATC	10620
TATTTATCTA GCTCATACAT ATGGCTGTCA CATTCAAGGC GTTGATATAA ATAAGAAAGC	10680
ATTAGAAAAA GCACAGGAAA ACATTTTCAGC AGCAGGTCTT GAATCATATA TTCAAGTTCA	10740
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AGCAATGTTA ACAATGTTAC CCATCGCCAT AAAGGAAAAAGCATTACGCG AGTACTACCG	10860
AGTCTTAAAG CCTGGGGGTA TCTTGTTAAC ACATGATATT GTCATCGTTA ATGAATCACA	10920
TGCCACACAT GTTGTTAAAT CATTATCTGC AGCAATTAAT GTCAATGTCT CACCGCAGAC	10980
GAAACTTGGC TGGTTAGATT TATATAATCA AGCTGGTTTT AATCATGTGC ATTATCATAC	11040
TGGTCCAATG AGTTTAATGA CACCAAAAAGG TTTAATTTAT GACGAAGGTA TTGTTGGAAC	11100
TATAAAGATT ATCAACAATG CTTTGAAAAA AGAAAATCGA CCAATGTTTT GTAAAATGTT	11160
TAAACGATG ACTAAATTGC GTAAAGATAT GAATTATATT ACTTTTGTCG CTAAAAAAGA	11220
GCACTAAATA TAATGCCACT AACTGTACTT TGTATCTATG TTTGACTATC ACTTTAATTT	11280
CTTTGTGACA CTAATCATCT ACTTAACAAT ATCGTTATCG TTGATTAGTA AGTCATCAAT	11340
TTTGGTTAAA GACTTTCATA AACACTCAAA CATTAACTACT ATACATAGTT AGTGGcATTA	11400
TTTTTTyCTn AAAATTTTAA CmTCmCGGGr TtGGGAmCrG AAaTGrAwT TcGCrmAAtT	11460
TAwTcT	11466

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2176 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

TTACATAGTT AACACTAGTT AATCTATTAG TTAACATTAG TTAATAATTA GTTAATTTCC	60
ATTTGTATTC TCATGTGATA AATTCTAAAA GCATACaATA AATTTAATAT GTAAAAAGAA	120
AGGGAATACA CATGAAAAAT AAATATATCT CGAAGTTGCT AGTTGGGGCA GCAACAATTA	180
CGTTAGCTAC AATGATTTCA AATGGGGAAG CAAAAGCGAG TGAAAACACG CAACAACTT	240
CAACTAAGCA CCAAACAACT CAAAACAACT ACGTAACAGA TCAACAAAAA GCTTTTTATC	300
AAGTATTACA TCTAAAAGGT ATCAGAGAAG AACACGTAA CCAATACATC AAAACATTAC	360
GCGAACACCC AGAACGTGCA CAAGAAGTAT TCTCTGAATC ACTTAAAGAC AGCAAGAnCC	420
CAGACCGACG TGTTGCACAA CAAAACGCTT TTTACAATGT TCTTAAAAAT GATAACTTAA	480

CTGAACAAGA	AAAAAATAAT	TACATTGCAC	AAATTAAAGA	AAACCCTGATAGa	AGCCAAC	540
AAGTTTGGGT	AGAATCAGTA	CAATCTTCTA	AAGCTAAAGA	ACGTCAAAAT	ATTGAAAATG	600
CGGATAAAGC	AATTAAAGAT	TTCCAAGATA	ACAAAGCACC	ACACGATAAA	TCAGCAGCAT	660
ATGAAGCTAA	CTCAAAATTA	CnTAAAGATT	TACGTGATAA	AAACAACCGC	TTTGTAGAAA	720
AAGTTTCAAT	TGAAAArGCA	ATCGTTCGTC	ATGATGAGCG	TGTGAAATCA	GCAAATGATG	780
CAATCTCAAA	ATTAAATGAA	AAAGATTCAA	TTGAAAACAG	ACGTTTAGCA	CAACGTGAAG	840
TTAACAAAGC	ACCTATGGAT	GTAAAAGAGC	ATTTACAGAA	ACAATTAGAC	GCATTAGTTG	900
CTCAAAAAGA	TGCTGAAAAG	AAAGTGGCGC	AAAAGTTGA	GGCTCCTCAA	ATTCAATCAC	960
CACAAATTGA	AAAACCTAAA	GTAGAATCAC	CAAAAGTTGA	AGTCCCTCAA	ATTCAATCAC	1020
CAAAAGTTGA	GGTTCCTCAA	TCTAAATTAT	TAGGTTACTA	CCAATCATTa	AAAGATTTCAT	1080
TTAACTATGG	TTACAAGTAT	TTAACAGATA	CTTATAAAAG	CTATAAAGa	AAATATATA	1140
CAGCAAAGTA	CTACTATAAT	ACGTACTATA	AATACCAAGG	TGCGATTGAT	CAAACAGTAT	1200
TAACAGTACT	AGGTAGTGGT	TCTAAATCTT	ACATCCAACC	ATTGAAAGTT	GATGATAAAA	1260
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CTGGTAAAGT	ATTATATACT	TTCTACCAA	ACCCAACATT	AGTAAAAACA	GCTATTAAAG	1380
CTCAAGAAAC	TGCATCATCA	ATCAAAAATA	CATTAAGTAA	TTTATTATCA	TTCTGGAAAT	1440
AATCAATCAA	AAATATCTTC	TCTAGTTTTA	CATCATTTTT	TAAATAATTT	TCGTAACAAA	1500
CCGTGATTAA	AAAGAACCGT	TGATTCTCAA	TCGAATCTE	GGTTCTTTTT	TCATTTTCCA	1560
TCAATTAAAT	GCTTCTTCGC	TATTTGTCAG	CCCACTTTTT	TACCTGCAAC	TTGTTAAATA	1620
ATCCTTACAT	CGTTAACGAA	TAGTTCATCA	TTTAGTTGAA	TCAGCTCAAC	TTTATTAACT	1680
TCATATTTTC	ACAAACTATT	GCGCAATCCA	TTCCTTTTCC	ACTACAAGCA	CCATAATTAA	1740
ACAACAATTC	AATAAAATAA	GACTTGCAA	GCATAGTTAT	GTAGCTATAT	AAACGCCTGC	1800
GACCAATAAA	TCTTTTAAAC	ATAACATAAT	GCAAAAACAT	CATTTAACAA	TGCTAAAAAT	1860
GTCTCTTCAA	TACATGTTGA	TAGTAATTAA	CTTTTAACGA	ACAGTTAATT	CGAAAACGCT	1920
TACAAATGGA	TTATTATATA	TATGAACTTA	AAATTAAATA	GAAAGAAAGT	GATTTCTATG	1980
ATTAAAAAtA	AAATATTAAC	AGCAACTTTA	GCAGTTGGTT	TAATAGCCCC	TTTAGCCAAT	2040
CCATTTATAG	AAATTTCTAA	AGCAGAAAAAT	AAGrTAGAaG	rTATCGGCCA	GGtGCaGAAt	2100
CmTyCAAArG	AcACaGACAT	TACTAGCCAA	CGATTTAGCT	ATnACTCAA	ACCTTCCATT	2160
GGATTTGGTA	AAGGnT					2176

(2) INFORMATION FOR SEQ ID NO: 446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

AAAAGCATGG CTTAAATGAA GTACGCTATA ACAAATTACA AGAACATGCT ATTGTTATGC	60
ATCCGGCACC TGTGAATAGA GGAGTAGAAA TACAAAGCGA TTTAGTAGAA GCTTCAAAAT	120
CAAGAATTTT TAAGCAAATG GAAAATGGCG TTTACTTAAG AATGGCAGTC ATTGATGAAT	180
TATTAAAATA GGTAAGGGGA CGAAAATGAT GAAATTAATT AAAAACGGTA AAGTATTACA	240
AAATGGCGAA TTACAACAAG CAGATATTTT AATTGATGGT AAGGTAATTA AACAAATTGC	300
ACCTGCAATT GAACCAAGCA ATGTGTTGA CATCATAGAT GCGAAAGGTC ACTTTGTGTC	360
ACCTGGATTT GTCGATGTTT ATGTTTCATTT ACGTGAACCT GGTGGTGAAT ATAAAGAGAC	420
AATTGAAACT GGTACTAAAG CTGCTGCTAG AGGCGGATTT ACAACTGTAT GTCCAATGCC	480
TAACACAAGA CCGGTACCAG ATTCTGTAGA ACATTTTGAA GCTTTACAA AATTAATCGA	540
TGACAATGCT CAAGTACGTG TATTACCTTA TGCTTCAATT ACAACACGTC AATTAGGTAA	600
AGAATTGGTT GATTTCCAG CACTAGTAAA AGAAGGTGCC TTTGCGTTTA CAGATGACGG	660
TGTAGGAGTA CAACTGCAA GCATGATGTA TGAAGGCATG ATTGAAGCTG CAAAGTAAA	720
CAAAGCCATC GTAGCACACT GTGAAGATAA TTCATTAATC TATGGTGGTG CAATGCATGA	780
AGGGAAACGC AGTAAAGAGT TAGGTATACC AGGTATTCCA AACATTTGTG AATCTGTTCA	840
AATCGCAAGA GATGTACTAT TaGCTGAAGC AGCAGGTTGT CATTATCATG TATGTCATGT	900
TTCTACTAAA GAAAGTGTTA GAGTCATTCG TGACGCTAAA CGCGCAGGCA TTCATGTTAC	960
AGCTGAAGTT ACACCACACC ATTTATTGTT AACAGAAGAT GATATTCCTG GTAATAATGC	1020
CATTTATAAA ATGAATCCAC CATTGAGAAG TACTGAAGAT AGAGAGGCTT TGTTAGAAGG	1080
GTTACTAGAC GGTACAATTG ACTGTATCGC AACAGAcCAT GCACCACATG CACGTATGA	1140
AAAAGCACAA CCAATGGAAA AAGCaCCATT CGGAATTGTT GGTAGTGAAA CAGCATTCCC	1200
ATTATTATAT ACGCATTTTG TAAAAAATGG TGATTGGACA TTACAACAAT TAGTAGATTA	1260
CTTAACAATT AAACCATGTG AGACATTTAA TTTAGAATAC GGCACATTAA AAGAAAATGG	1320
TTATGCAGAT TTAACAATCA TTGATTTAGA TAGTGAACAA GAAATTAAAG GAGAAGATTT	1380
CTTATCAAAA GCAGATAATA CACCATTTAT CGGCTATAAA GTTTATGGAA ATCCGATCTT	1440
AACAATGGTT GAAGGCGAAG TTAAATTTGa GGGGGATAAa TArTATGCAA gCAAACGTTA	1500
TCTAGTGTTA GAAGACGGTC TTTTACGAGG CTACCGTAg GTCTGATAAC TTAGTGA	1557

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

GCTAGAAATm TTGmATGaCA ATACAACCTCT GTTAAAaTGA TGGACGTAGA CAAATATGCG	60
TATTGACGCT TTATTTTAAA AATTaACATG CTTATAACAT GTTTATAGAA GGAGATTAAAC	120
CTATGAACTA TCaAGTTCTT TTATATTATA AATATATGAC GATTGATGAC CtGAACAGT	180
TGCTCAGGAT CACTTAGCCT TTTGTAAAGC ACACCATTTA AAAGGTAGAA TTCTTGTTTC	240
TACAGAAAGT ATTAACGGCA CATTATCTGG TACAAAAGAA GAAACCGAAC AATATATGGC	300
ACATATGCAT GCCGATGAAC GATTCAAAGA TATGGTGTTT AAAATTGATG AAGCTGAAGG	360
ACATGCTTTT AAGAAAATGC ATGTACGTCC TCGAAAAGAA ATCGTTGCTT TAGATTTAGA	420
AGATGACGTC GATCCAAGAC ACACAACCTGG CCAATATTTA TCACCTGTAG AATTTAGAAA	480
AGCTCTTGAA GATGATGACA CAGTCATTAT TGATGCACGT AATGATTATG AATTTGATTT	540
AGGTCATTTT CGAGGTGCAA TTCGTCCAAA TATCACACGTTTTAGAGATT TGCCTGACTG	600
GATTAAAGAG AATAAAGCGT TATTTGCAGA TAAAAAAGTG GTTACGTACT GTACTGGTGG	660
CATTCGATGC GAAAAATTTT CTGGATGGCT TTTAAAAGAA GGTTTCGAAG ATGTAGCTCA	720
ACTTCATGGC GGTATTGCTA CATATGGTAA AGATCCTGAA ACAAAGGTG AATATTGGGA	800
CGGTAAAATG TACGTATTTG ATGACCGTAT CAGTGTTGAT ATCAACCAAG TTGAAAAnAC	840
AATTATTGGT AAGGATTGGT TTGATGGCAA ACCATGTGAA CGTTATATTA ATTGCGCTAA	900
CCCAGAATGT AATAAACAAA TATTAGTTTC TGAAGAAAAC GAAACTAAAT ATTTAGGTGC	960
ATGCTCTTAT GAATGTGCTA AACATGAGCG TAATCGTTAT GTTCAAGCAA ATAATATTAG	1020
TGATAATGAG TGGCAACAAC GTTTAACAAA CTTTGATGAT TTACATCAAC ATGCTTAGTT	1080
TTAATTAAAT ACCTTTCAAA ACACGCTTTG AAAATCCGAT TTATAAAGGT TTTTCAAGGC	1140
TGTTTTTTTAT GCGCATACAT AACCTGATAT GTTTTTAATT ATGCGCGGT TATACTAAAT	1200
TAAATTTTAA TACTGCGGGG TGTCTTAAAA TGCACATTTT AGTAACAGGG TTTGCGCCTT	1260
TTGACAATCA AAATATCAAT CCCTCATGGG AAGCTGTGAC TCAACTAGAA GATATTATTG	1320
GCACACATAC AATCGATAAA TTAAACTAC CAACCTCTT TAAGAAAGTA GATAATATTA	1380
TAAATAAAAC GTTGGCATCT AATCATTATG ATGTTGTAAT AGCTATAGGA CAAGCTGGTG	1440
GTAGAAATGC CATTACCCCA GAACGTGTCTG CCATTAATAT TGATGATGCA CGTATTCCAG	1500

ATAATGATGA TTTTCAACCT ATTGATCAAG CCATTCACTT AGACGGTGCG CCAGCTTATT	1560
TTTCAAATTT ACCaGTTAAA GCAATGACTCAAAGTATTAT TAATCAAGGA CTTCTGGAG	1620
CACTTTCAAA TAGCGCAGGT ACATTTGTTT GTAATCACAC ACTTTATcAC TTAGGTTATT	1680
TACAAGATAA GCATTACCCT CACCTACGAT TCGGATTTAT TCaTGTGCCA TACATACCAG	1740
AGCAGGTcAT TGGTAAACCC GATACACCAT CTCATGnCCA TTGAGGAAAA GATnATTG	1799

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

ACTTGGTTTT TTATTGTTTA TAAATAAAAC TCACTTAATA ATGTTTTCAT AATCTTCTTC	60
GACTACTTAA TTCTTTAAGA TATTCGTGAA AAGAGACATT AACTAGTTA ATTTTCAAAC	120
AATACAAAAA GCGTCTACCT CCTACATATA ATTGTAGCGG AGATAGACGC TTAATATTTA	180
TTTAAAAATT ATTTTAAACC ACCGAATGTC ATAACATCAC GGGCAATCAT ACTTTCTTCA	240
TCTGTTGGAA TAACGACAAC TTAACTGGT GAATGAGGAT AGTTAATAAA TCCTTCTTTA	300
CCACGTAGTA AGTTTTCACT TTTCTTAGGA TCCCAGTAAA CACCCATAAA TTCTAAGCCT	360
TCAAGAACTT TCGCACGAAT TTCTACTGAG TTTCACCGA TACCTGCTGT AAATACGATA	420
ACATCAACAC CATGCATTCT CGCAGCATAT GATCCAATAT ATTTGTGAAT TTTAGAAGCA	480
AATACATCTA AAGCCATTTG TGAACGTGCT TTACCTGATT CAGCTTCTTC TGATAAGTCA	540
CGTAAATCAC TAGATGTACC TGATAATCCT AATAAACCTG ATTCTTTGTT TAAGATTTC	600
AATACTTGTT CAGCAGTTTT ACCTGTTTTT TCCATAATAA ATGGAATTAA AGCAGGGTCA	660
ATATTACCAG AACGAGTACC CATTGTTACA CCAGCAAGTG GTGTGAAGCC aTTGATGTAT	720
CAATAGATTT ACCGCCATCG ATAGCTGCAA TTGATGCTCC ATTACCAATG TGACATGAAA	780
TAATACGTAA ATCTTCAATT GGCTTATCTA ACATTTCTGC CGCTCTTTGT GATACAAATT	840
TATGGCTTGT ACCATGGAAA CCATACTTAC GAATGCCATA ATCTTTATAA TAATGATATG	900
GCAAGCTATA TAGATATGCT TTTTCAGGCA TTGTTTGATG GAATGCTGTA TCAAAAATTG	960
CCACATGAGG GATATTTGGT AATAATTTAC GGAAAGCACGAATACCCAtC AAGTTaGCTG	1020
GGTTGTGaAG CGGTGCTAAT TcGCTTAATT CTTCAATTTC CTTTTCAACC TCATCAGTAA	1080
TAGCTACTGA TTCAGGGAAT TTTTCACCAC CATGTACAAC ACGGTGACCT GTTCCATCGA	1140

TATCGTTAAT ATCATTAATA ATATTGTGCG CTTTAAAAGC ATCCAACATG ATATCAACTG	200
CCTCAACGTG ATCCTTGATA TCTTGTACTG TTTTAACTTT TTCCCCGTTG ACTTCAATTG	1260
TAAAAATTGA ATCCTTCAAT CCGATTCTTT CTAATAAACC TTTTGTTACT AATTCCTCTT	1320
CAGGCATTCT AATTAATTGA A	1341

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

TTTTGAAGAT ACTACCGATG AAAATAGACA AAAGATTTTT CAATATTTAT CACCTGAAGa	60
AGTTGCAAAT TTCTTTGATC AATTAGATAT TGATGACGAT GAATATGAGT TGCTATTTGA	120
TAAGATGAAT GCGACATACG CAAGTCACAT ATTAGAAGAA ATGTCATACG ACAATGCAGT	180
AGATATTTTA AATGAGTTGA CTAAACCAAA AGTTGCTAGT CTTTAACAT TGATGAATAA	240
AGATGACGCG AATGAAATCA AAGCATTACT TCACTATGAT GAGGATACGG CCGGCGGTAT	300
TATGACGACG GAaTATTTAT CACTTAAAGC GCATACGCCT GTTAAAGAAG CATTATTATT	360
GGTCAAAGCG CAaGCACCAG ACGCAGAAAC AATATATGTT ATATTTGTCG TTGATGATGA	420
TGGTAAATTA GTAGGTGTTT TATCGCTAAG AGATTTAATT GTAGCTGAAA ATGATGCTTA	480
TATTGAAGAT ATTATGAATG AACGTGTCAT TAGTGTGAAT GTAGCAGACG ACCAAGAAGA	540
TGTTGCTCAA GTTATGAGAG ACTATGATTT CATGGCTGTA CCTGTTATAG ATTACCAAGA	600
ACATTTGCTT GGTATCATCA CGATTGATGA TATTTTAGAC GTTATGGATG AAGAGGCTAG	660
TGAAGACTAC TCTCGTTTAG CCGGGGTATC AGATATCGAT TCGACTAATG ATTCAATCAT	720
TAAACAGCA TTAAACGTT TACCATGGTT GATTATTTTA ACATTTTATG GAATGATTAC	780
TGCGACAATT TTAGGGAGAT TCGAAAAAAC ATTAGAAAAT GTAGCGCTACTCGCAGCGTT	840
TATTCCTATT ATTAGTGGTA TGTCAGGAAA TTCAGGTACA CAATCTTTAG CCGTTTCAGT	900
TCGTAACATT ACGAcAGGGG AAATTAATGA GCAAAGTAAA TTTAGAATTG CATTAAGAGA	960
AGCAGGAAGT GGTGTATTAT CGGGTGTTGT ATGTTCAACA ATATTATTTA CAATTATTGT	1020
TGCAATATAT CATCAGCCAC TTTTAGCATT AATCGTTGCA GGAAGTTTAA CTTGTGCGAT	1080
GACGGTGGGG ACGTTTGTAG GTTCGATGAT TCCATTATTG ATGAATAAAT TAAATATCGA	1140
TCCAGCAGTG GCTAGTGGAC CATTTATTAC AACAATTAAT GATATTATTA GTATGTTGAT	1200
TTATTTTGGT TTAGCTACAT CATTTATGGC TACTTAATT TAAGGAGGAG TTATGGAGTT	1260

TTTATCTTTA GTTATTGTTG TTTTAGCAGC GTTTTTAACT CCAATAATTG TCAATCGATT	1320
AAATATTAAT TTCTTGCCAG TTGTTGTTGC AGAAATTTTG ATGGGGATTG TGATTGGAAA	1380
TTCATTTCTA AATATAGTAG AAAGGGATTC AATTCTAAAT ATTTTATCAA CGTTAGGTT	1440
TATCTTTTTTA ATGTTTTTAA GTGGTTTAGA AATTGATTTT AAAGCTTTTA AAAAAGATAA	1500
ACGCGCACGT CAAGGACAAA ATGATGATG	1529

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

TTCTGGAAAC CAAAGTATTG TCATCTTCTA CTAGTAGTAT nGGCATCCAT ATCACCCAAT	60
ATCATTTAGT ATATTTTATA TTTTCTCCTG ATTTTAATCG ACTTTGAAAA TCTTTAATCC	120
GGCAGTCAAC TTCAAAGCCA TGAATCATCA TTTTTTG CAT TGGTGCTTGT ATAAAGTAAT	180
AAATCGGCCA AAATAATCGA GGGATATAAT CGTATAGATG TATATAAACG ACTGCCGACT	240
CTTTGATTAA TCTAAATTCT AACTTCCCTT GATTAAGTGT ATATTTTTTC ACTAAACTTC	300
CACTCAATAA AATTAAAGTT ATTATTCCAT CAGCTGTTTC TTCTATTTTA AATACTGCGA	360
GCGGTCGCAC CTTATTCTTA ATATATATCT TAAATTGATC ATGTGATTTT TCTGTTTTCA	420
CAAAAGTTCC TTTAGTGTA CCCATCCATG CAATAAAATG GTTTACAACG TTCTTTAATG	480
TCCATCCCTT TGGTAAACT ACCTTCATCG TTGATCTAAC ATCATCATAC TTTGAAACTT	540
GTAATTCTAC ATTAATAAA GAACGTTTAA AACTAAATT TGTTGTTTCT ACAGGTGTAC	600
CATATGCACC TAGGCGTTCA ATTGTTTCAT TATCATAACG ACTCCCAGGT ATGTAGATTA	660
CTTTTTTTTAC TTGATTGATA GCCGCTGCTC GACCAAAATT ATCTGCTGCG ATTAATGTTA	720
AATCTCTTGC TGATGATTGT GTTATTTTGG CAGAATTCTT TGTTGGGTCG ATAAAGAATA	780
CAGCAATATC TATTTGATTC ATTGCTGCAA CAACCTGTTT GTAATGAAAT ATATCACACT	840
GAATCCAAGT CATTTCAACA TCATCTGTTT kTTTATTGTC EGATATTTT GATATAGCAA	900
AAAGTTCAGC ATCATTTTCA ATCACTTCAC TTAAATACTT ACCAATATAT CCTGTTCCAC	960
CTGCTAATAA AACTTTAGGT TTCATCTAAA ATACTCCTTT AACTGTAAAC CAAAAACAT	1020
ATTACTCCAC CTTTGTAGTTA CATATATATT ATAATAGTAG CAAATGTTTT AAAATTTCAA	1080
AATACTGGAG GCTTTTTATG GCCCATATTA TACGTAGAGT TAGTATCAAA GATGTAGAAA	1140

ATTTTCATTTTC AATGTTAGCG AACATATACG ACGAATCTCC GTATATGTTC TACACACCAG	1200
GAGAATATGA TCCTAGCGTC ACATCGGCTA GTAAACAATT AGAAGAATAT ATCACTTCTC	1260
CGCATAAAGT CATCTTCGTT GCTGAAAGTG ATGAACAACCT CGTTGGCTTT GCCTTTGTTA	1320
ATACGACACC ATTTCAACGC ATTAAACATG TTGCTAAAAT TGATTTAGGT GTAAAGAAAT	1380
TATATCAACA TCGTGGAATT GGCCAAGCAC TTCTTGATGC CATTATGGCT TGGTGTTTAA	1440
ACAATCAAAT ACACCGAATT GAAGCAAATG TACCACTCAA TAACCAACT GCCCTCGAGC	1500
TTTTTAAAAG TGCCGATTTT CAAATCGAAG GCGTTTTTAA AGATAAGTTA TTTATCGATG	1560
GTAAATATTA TGATGACTAT ATGATGGCTA AAATTCTTAA TTAAAGCTAT TTTATCATAA	1620
TCTTGTATCA GAATCGTATA ACAACGAATT TAATGGTTAC CTAATACATT ACTCATACTT	1680
ATCAATGTTA TCTAATCTCA AATAAATACG TACACTCTTA TTCATTTATC AAATTTAAAT	1740
TCAAATAnA ACACCACTAA TGTGTAATTG ATTAACATC AACTACGATT AGTGGTGCTT	1800
TATATATGTG GTTAGTTTTT CTnACTA	1827

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 616 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

ATATAGATTA ATGTTTGTTA TTTGTACTGT GTTTGCCAGT GACATTTATT ATAAAACATA	60
TGACGTTATT CTATGktGTA CTCATTtTCT ATATTGTAGG TTTATTAACG ATTAGAAGTA	120
TTATTTAAAAA GTTGAAATAT CAGGAAACAT TATTACGAGA CTAAAAAACT TCCATTGGCA	180
TGTATGTTGT AAAGGTGCAT GTAATGTTGA ACGCCAAATG ATACGGCGTT CkATTACAT	240
TAGCATCTAT ACGTTAACAG CATAACCAAT GGAAGTTTTT TTCGAATCTA TTCTTTTATT	300
GGGTATAGAT ATCTTTCAAA ATAACCTGAA TGTTGTCCGC TTGAACCAAA GTAATGACTT	360
AATGCGTCTT TTGAAAAATG GTCATTAAAG GCATCAGATT GCTTAAAGTC TTCGTATGCA	420
TGTCGATCAG CAAATCCGAA ATAAATTTTG TATGTTGTAC CTTTAGCAGG TCTTAACAAA	480
CGATAGCTTT TAAAGCCACC AAAGTTTCTG AAATTATCGT CTACACTAAT CAGTTTCTTT	540
TCAAGTTGAT ATGCATGATC TTCTGTTGAT GGaATGAAGa TTGCACaATA GAAATGaTGT	600
TCACtGAATT CACCAA	616

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 944 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

GCACGAGTGA TTAAACGGTT AATCAATGAA ACATTTGATG CAAATTACAT TGAAGTTATT	60
GAGGGAGGAA TTGAAGAAAC GCAAACGTTA ATTCACCTAC CTTTGTACTA TGTCTTCTTT	120
ACAGGAAGTG nAAATGTAGG CAAAATCGTT TATCAAGCTG CCAGCGAAAA TTAGTCCT	180
GTGACATTAG AAATGGGCgG TAAAtCTCCa GTCaTCGtTG ATGAAACAGC GAATATTAAA	240
gTTGCTAGTG AGCGCATTTG TTTTGGGAAA TTCACTAATG CCgGCCaAAC ATGTGTTGCa	300
CCAGATTACA TTTTAGTACA CGAATCTGTA AAAGATGATT TAATCACAGC CCTATCAAAA	360
ACGTTGCGTG AATTTTATGG TCAAAATATA CAACAAAGTC CAGATTATGG CCGCATTGTA	420
AACCTTAAAC ATTATCATCG TCTGACTTCA TTACTIONA GTGCACAAAT GAATATTGTA	480
TTTGGTGGTC ATAGTGATGA GGATGAACGT TATATAGAAC CAACATTGTT AGATCACGTT	540
ACAAGTGATT CAGCAATTAT GCAAGAAGAA ATTTTTGtC CTATCTTACC GATTTTAAACG	600
TATCAGTCAT TGGATGAAGC AATAGCCTTT ATTCACCAA GACCAAAACC TTTGAGTTTA	660
TATTTATTTA GCGAAGATGA AAATGCTACA CAACGTGTAA TAAACGAGCT ATCATTGCGC	720
GGCGGCGCTA TTAATGATAC ATTGATGCAC CTAGCGAATC CTAAATTACC ATTTGGTGGT	780
GTTGGTGCCT CAGGTATGGG ACGCTATCAT GGTAAATATT CATTCGACAC TTTTACACAT	840
GAAAAAAGCT ACATTTTCAA ATCnACACGA TTAGAATCAG GTGTCCATTT ACCACCATAT	900
AAAGGTAAAT TTAAATrCAT CAAAGCTTtC tTTAAAnATT AATT	944

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

TCTCCAGTAG ACCTTGtGTA TGAACAGTTT CTTTCATATG AATGAACATC GTTTTTAAAG	60
TTTGTTTCAA CTCAGCCTTA TCAGGATAAT ATCTAGAGAC AGTCGTCTCT GGCATCTCCA	120
TTGTATGATA TTAAACCTTA TGCAGCGACC CATGATTTTC GTTATAAACA AATGTATGAT	180
TCACTTCATC GAAATCATGA TCTTCTCCTG CAATCCAAAAAACTGGTACT ACTTGTTGCT	240

TATGTGTATC CGTTAATTCC TTAGATAAAG TAATGATTGa AAATATTTTA TGGAATGTAT	300
ACAATGGTCC CCCGAAAAGC CCTGCTTGTT GTCCACCAAT CACAACTTTT GAACCATTAG	360
CTAAATGTTG TATGTTTAAAT TCTTGTTTAC TTGAAAGCTT GAAAGCTTTA AATCACTCAT	240
ATATTCACGA ATAACATTCT CTAATGCCGC TTCTCTTCCA TTATTTTCTT TAGACATCCT	480
TTTTTCAAAA CTAGTTTGTT GAGCTGCATC ATATTGAAAT AATCCTGTTA TTACAGGGTC	540
ACTGCTCTTT ATTTTGGTA TAAACTGATC TTTTTCATTT AAACCTAATA CTTTACAGTC	600
CATGTTTTTT CTCCTTAAGT AGCGATTAC AAACCTATAGT ATAAAGTCTA TACCGGTGAT	660
TGACAATTTT ACGGCTTGAA AATCAATTTA ATCATGGAAA ATTTATAATA TTCATTGTTT	720
TACATTTTCA AATCAATGAA AAACACAAGT GGTTTAATGT ATAATAATAG TAGTAAACAA	780
ATAAGGGGTA GATAAATATG AGTGAAATCA AACGTCTTGA AATTAATTC AAAACTGACG	840
AATTATTCGA AAACCTTAGA GCGTTTGGCA ACAAAGACTT ATACATGGTC AATGAGTTAA	900
ACGGTCAAAT GATTGATGCA AGTTCAGATT CACCATTTTA TGGCATATTT GTCGaGATCA	960
ATTAGGAGCT AGAATGGCAT TACTAAAAAA AGGTGATGTC GAAGAAATCT ACTTCCCAGA	1020
TTTTGAAGAT TATATATTAT TATGGAAGTT AGAAGTATTA CCAAAATATC AAAACAGAGG	1080
GTACGCTTCA GAATTGATTG ATTTTGCAAA GAGTTTCAAT ATGCCAATTA AAGCCATTGG	1140
CAGAAATGAT TCTAAGGATT TCTTTTTTACA TCATGGATTT ACAGATGTGG AAGCTAAAAA	1200
TATAGAGGGA CATGATGTCT TATTGTGGAA ACCATAAGAT AATAATATTC GACACTACGA	1260
GCATGAAAAAT GCATCTTTTC GTAGTGTCTT TTTTACAATT ACTTTCTTAA GCTAATATAA	1320
GTaAATCATT TTCAAATTAT TTGTCTTAAC GTACAATATC ATTTAGTTGT TTCCATGrAT	1380
TAATTTTATA ATCAGGTATA ATTCCTGGAT TATGATCAAA TCCTCTAAAa TTAAACAGC	1440
AAGTAGCTAT ACCcGCATTG ATTCCACCTA GAATGTCAGA TGTTAnAGAA TCTCCaACTA	1500
TAATCGAGTG CTGtCTTTCA TCCTCACCAA TATCATTAAC AACATAATTA AAAAATTCCG	1560
GATTAGGTTT TTGATATCCT GTTTCTTCAG ATATAAATAT CTTTTTAATA TATTTATGCA	1620
ACGGCGTCTG ATTTAACCTT CTCTTTTGCG TTTCGGTTAC ACCATTAGTA ACAATATATA	1680
AATCATGTCT TTTCGATAAT TCGACAATTG TTTCTAATGT TTGATCAAAG TATTTAACTT	1740
TAGCTTCTGC TAATCCATTT CTAAATAACA CATCTGCACG ATGCCCATCA ACTTCCATTT	1800
GATGATGTTT GAAGTAATTC ACAAATCGTT CTGATAAAC TTCAGACTTC GkTAATTTAT	1860
TTTGkTGAAA AGCTTCCCAA TGTTGGTGaT TGaTTTTTTTT AAATGkTAAA AAATCATCCy	1920
TTGTTGCTTT ATGATTAAAA ACATTGCGCA TATAGTGAAh CGCCCATTCT TCTGcATCAT	1980
AAAAATCAAC AATTGTATCA TCAAAGTCTA TCAAATATT TTTATATCCC AATTTCCCCA	2040
TCTCCTATAT TGTCTATGTA TCTAAATCTT AACAGAGGCT CAAATTTCTG CAAATAAAAT	2100

AAACTGAGTG CATAACATTA AAGTATGCTC ACCCAGTTTA TTTTAAAGAA TATTAGTTAT	2160
TATATTAGAA TCCAAATAAT TTACCTAGTA AACCCACACC GTTAGCAACG ATGTCTACGA	2220
TACTTGTGCC TAATTTCAOA CTATCATGTT GTTGTGCAGC TTGCACAGTA TTTGCGATTG	2280
CTTCTGCTAG TCCAGTCATT TAAATCTCTC CCTCACCTTT GAAATAATAC TGATTACTTA	2340
CATAACATAT TGAAATTAGA ATCCGAATAA TTTACCTAAT AAACCTACGC CATTTTCAAC	2400
GATGCTCACA ATGCTTGTGC CTAATTTTGC GCCATCATT TTA A MTGCTG CAGTTACGGT	2460
ATCTTTAATT GCGTTAAATA AACCTTCCAT TGAAAACACT CCTTAAAATT TAAATTTGAA	2520
GATAACAAAA ACGTGCGTA _g yTTTTAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT	2580
GTTGTTATTT TAAAATAAAT TTGATGCAAT TAGTTTGTTT ATCCGCACAA CATCTTATAA	2640
TGTACTTAAC TGTATTTTAA AGAGAAAAGA AATACAGTTA GGCATTCAAA ACTGTATTTA	2700
ACACAATTAA GTTGCCTGAA TTCGTATTTA AGTCTTATTG AACCTTTTTA GATAAATAGC	2760
TCTATAATAG TGAAAAATAT AAACATTTTT TATTTACAAG GTATTGCTAA TTTAAGTTCA	2820
TTTAGATATA ATAATTCTTG TGTTGTAAA CGTGTCTGG TAGCTCAGCT GGATAGAGCA	2880
ATGGCCTTCT AAGCCATCGG TCGGGGGTTC GAATCCCTCC CAGGACGTTT ATAGGTATTT	2940
TTATACGCAT TACCAAACAA AAGAGTTCCG TGATTACGGG GCTCTTTTTG TTTTGAATTT	3000
CAGTAATATA GTATGATGCG TCACCAAAAC GTCCCCGCA TAAGCCCCGA A AACAGTA	3060
ATTAAAACAA GCATGCTTAT TCGTTATAGA ATTTTTTGAC ACACAATTGA CACGCGTCTG	3120
ACACTTGTTT ATACATTTTT AATTAAGTAA TTTTGTGCTC AAATTTCATC TATACTGCAC	3180
CTGAACTACA CCAACACTAC ACCAAGATTT TTAACACTCA CCATTTGCAT GCGTAGAGAT	3240
TTTTATTATT ATATTATTCC TATAGATTTT GATACTATTC AAAATTTTAG GGACTTTTCA	3300
GGGGCCCGAA ATCCTATAAT TATAATTATA TACATCTAAA AAAAATAACC ACGTCCATCG	3360
AGACGTGGTT TTTTAATTAT TTAACTCACT AATTATTCTT CTTAATTTTC ATTGCTAAAT	3420
ATACTATTGG CAAATTTATA AAGTAGTTCA GC T TTTTTCA ATGACATATT GTCTAATGAT	3480
CTTTCATTTT TTCTCATTCT GTGTATTGTG CTTTGTGGAA CTCCTGTTTG TTTCGATATA	3540
TGTAAACTGC TCAAATCACT GTCTAATAGT TTTTGAATTT GATTTCTCAT TTTGTACACC	3600
CCCTTGTA AA TCTTCAATCA TCATTTAAAT TAAATAATTA CTTTTCCACA TATTCCA AT	3660
TTTAGGTTGC AAAGCATACC TCAAATATCA TTAATTTTGA GATTTAAATG TCAATTATGT	3720
GTCTATCAAT CCAATATACA TACTCTAATA ACGTAATAGT ACACACTCTT CTTATTAATT	3780
GGCCATAGCT ATCATGATAT AATTAGTGAA GAAAATCACA TAAGAAAGGT TGTAATCAT	3840
GAGACTTCAA AAAGCACCTC TAGTAACGTC AGGACTAGTC TTAGGATTAT TAGGCCTGGG	3900

TAATCTATTA AAAGACTTAT CTCTTACTTT AAACGCTGTT TGC GGAATCT TTGCTTTCTT	3960
GATTTGGATT CACCTTTTAT GTACTATGAT CAAATATTTT AATAATGTGA AAGAACAATT	4020
AAACAGTCCT CTAGTTTCAT CAGTGTTTAC AACATTTTTCATGTCTGGCT TTTTAGGTAC	4080
TACTTATTTA AATACATTTT TTAGTAACAT AACTTTTATC AATAGCTTAA TAACGCCTAT	4140
TTGGATTTTA TGCCTTGTGG GAATTATGAC GCATATGATT ATTTTTTCAA TAAAATATTT	4200
AAAAGATTTT TCACTTGAAA ATGTTTATCC TTCGTGGACT GTACTTTTTA TTGGTATTGn	460
TATCGCAGGA TTGACGGCAC CCGTTAGCGG ATATTTTTTC ATAGGTCAAT TAACAGTAAT	4320
ATATGGCTTT GTAGCTACTT GTATTGTCTT ACCTATAGTT TTCAAGCGAT TAAAGCATT	4380
TCCATTGCAG ACGTCAATCA AACCGAACAC ATCGACAATT TGTGCACCAT TTTCTTTAGy	4440
CGCTGCAGCA TATGTTATAG CTTTCCTAA GGCGAATGCT TTTATCGTAA TTATATTTTT	4500
ACTATTAGCT CAAATATTTT ATTTTTATAT CATTATACAA TTGCCTAAAT TACTAAAAGA	4560
ACCTTTTTTCG CCCGTATTTT CAGCTTTCAC ATTCCCTTTA GTAATCTCAG CAACTGCTTT	4620
AAAGAACAGT TTGCCTGTAC TTATGTkTCC AGACATTtGG AAAGGkCTT TGTTTATCGA	4680
AGTGTTATTA GCCACTGTAA TAGTACTTAG AGTCTTTATA GGATATCTTC ACTTCTTTTT	4740
AAAAAAGGAA AAACAAGATA AATTTCTnCG TAATGCGTCT CAGTAACACT ATTACCAAGA	4800
ATTAACACGT ATATTTAATA	4820

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

ATTTGGATCT TTAATATCAC CAATATTTTT AATATCTTCC GGATTCAATC CATATACTTG	60
TACTGTATCT GAGTATTTAA TTGTGAAATA ATCACCTGAT TTAACCTTGT CATCAACTGT	120
AATTTGTGAT TTTAATGATA AATAATCTTG GGCTGGTACG ATTTTATTGT TTTTATCTGC	180
ATCAACGACA GTtAATGTTG TATTtGATGT GATTAAATCA TTAACATTTT TAGCCTCTGT	240
TGATGATGGC TGTACTGCTG CTATACGCAT TCTTGTATTC AAACGTTTAG GTGCTGTACT	300
TTTTGGCAAA ATGATATCTG CATTATTTTC ATTATTTGAA TTACTATTGT TATCAACAAG	360
AGTTTCATCA TTACTCTTGA TAGCATCACT TTTAACATTT AATGTAGTTGATTCAGTTTT	420
GGCATCTACC TTTTGTGTTTT CCTCATTAGT TG GTTGAACA TTTACCACTG ATTTATTCTC	480
TTGCAAATCA GGTGTAAACG CTTCTTGATT ACTTATAGTT TGTTTAGTGT TTAAATCTTC	540

ATTCGTAGAT	TTTGGTGAAG	CTTGCTCATC	TGATTTGGCA	GTTGAAACTT	CAACTTTATT	600
TCCAGTGGTA	GATTGTACAC	TTTCTTTTTT	TATTAATTTA	TTCCCATTG	AAGTCGTTTC	660
ATTACCTTGa	GATGATACCA	TTTCTTTTTG	ATTATCATTT	TTAGTATTGT	CTTCTTGATT	720
TAGTTGCTGC	ATATCAACTT	TATCACTCGA	TTGATTATCA	CTTGCTGAAG	TTGTCGCTcG	780
TTCAATTCTT	TATTAGTACT	TTCTGCAGCC	TTGCTTCTT	GGTTCCCCAG	ACCAAAAATT	840
AATGTTGTAC	CTACTAAAAT	TGATGCTGTT	CCCACTGTGT	ACTTTCTAAT	CGAAAATTTA	900
TTTAATCGAT	TGGATACCAT	GCCTTTCCTT	GTTATTGCCG	TTTTATTTTC	TCTGTTTAGC	960
ATTAGATTAC	TCCTAATTCA	TCAAATTTTT	AAATAATACA	ATTGTTTTAA	ATACAAAAT	1020
GTATATCAAT	ATAGTATTAC	ATTTTTAGAT	AAAGCACAAT	ACTTTAATTA	TTTTTCTTTA	1080
TCGTAAAACG	TTATTTAACA	TTTGTGTTTA	AATAAAAGTT	TTTATGAGTt	TTGTAATCTT	1140
TATTTAATCA	TCATAAAAAA	TAGTATTATT	TGCCCTTGAA	ATTAATATCT	TAGCTTTTCT	1200
AATTCATAGA	CAATTACATT	TCTGTAACAA	ATTAAATTGT	ATCTATTCCT	TAAAGATTTT	1260
TTGTTTTATA	TCTGGGAATT	TCTAAACAGA	AAAAACCAGG	CCACATGGAC	CTGGTTAAGT	1320
TAATCATATT	ATTTATTTTG	TTTTTTACGA	CGACCGAATA	ACAATAATGA	TCCTAATGCC	1380
GCGAATAATC	CACCGAATAA	TGTGCCATTA	TTTGAATTATT	TTTTTCACT	ACCTGTTTCT	1440
GGTAATGCTT	TAGCTGTTTT	ATGCTGATCT	TTAACCGTAC	TCATTGGTTT	AGCCGGAGTA	1500
TGTTTACCTG	CATCTGAATC	TGAATCGCTA	TCTGAATCTG	AGTCGTTGTC	TGAGTCCGAA	1560
TCGCTATCTG	AATCTGAGTC	GCTGTCTGAA	TCTGAATCGC	TATCCGAGTC	TGAGTCGCTA	620
TCTGAGTCTG	AGTCGCTATC	TGAATCTGAA	TCGCTGTCTG	AGTCTGAATC	GCTATCTGAG	1680
TCTGAATCGC	TGTCGAATC	TGAGTCGCTA	TCTGAATCTG	AATCGCTATC	TGAATCTGAG	1740
TCGTTGTCTG	AGTCCGAATC	GCTATCTGAA	TCTGAGTCGC	TATCTGAGTC	TGAGTCGCTA	1800
TCTGAATCTG	AGTCGCTGTC	TGAATCTGAA	TCACTGTCTG	AGTCTGAGTC	GCTGTCTGAG	1860
TCTGAATCGC	TGTCAGAATC	TGAGTCGCTA	TCTGAGTCTG	AATCTGAATC	ACTGTCTGAG	1920
TCCGAATCGC	TATCTGAATC	TGAATCGCTA	TCTGAGTCTG	AGTCGCTATC	CGAATCTGAG	1980
TCGCTATCTG	AGTCTGAGTC	GCTATCCGAG	TCTGAATCGC	TGTCTGATC	TGAGTCGCTG	2040
TCTGAATCTG	AATCGCTATC	TGAGTCTGAG	TCGCTGTCTG	AATCGCTGTC	TGAATCTGAG	2100
TCGCTATCTG	AATCTGAGTC	GCTATCTGAG	TCTGAATCGC	TGTCAGAATC	TGAGTCGCTA	2160
TCTGATGTTT	CTTCTTCGTA	GTAGCCATTA	TCAAGTGTGA	AATCATCATG	ATCCGTAATT	2220
GTTACATCAA	CTTCGCCACC	ATCGGCATCT	TTATCATCTT	CAGTTGTATT	TGTACCTGTT	2280
TGAGTTAAGC	CAGCAGGTTT	TTCAAAGATA	ACTTTGTATT	TACCACTATC	TAAATTATCA	2340

AAGCGGTATT TACCATTTTC ATCTGtYtCA GTTGTACCAA TTA	2400
CTTTCAGTCG AATCTTGTTT ACCATCTTTA	2460
TTACTGTCGT ACCAAACATA ATCACCTAAA CTATATTTTG GTGTTT	2520
GTGAATCCACTA TCTAATGTCA TGTTGTCAGC GTCTTTAATG	2580
ACACCTGTTG TAGTTAGTCC ATCAGAATCT	2640
ACAGCATCAT CTGTACCTAC ATTTGCAGTT GTCGGTGTAT AACCGGCTGG	2700
TGTGAAAAC TCTACACTAT AAGTTCCATT GCTTAAACCA GTGA	2760
ACTGAT ATTTACCATT TTCATCTGTT	2820
GTCGTACGAT CTAATTCTTT ACCGTTACTA TCTTTAAGAA TGACATAAAC	2880
ACCTTTAATC CCTTTTTTCAT TGGCATCTTG TTTACCATCT TTATTTGTAT	2940
CTTCCCATAC ATAGTCACCT AGATTATATT TCTTTTGGTC GCCATTAGCA	3000
GTTGATGAGC CATTACACATT TGAATAACTA TTTGACCAAC	3060
TATATTTAGT TTTGTCAGTG TCTAAAGTAT AATCAATTTT TCCATTATCT	3120
GTTGAACTAT TATCTGGATA AGCAACTTGT TGAATGATGT ATTGTTTATT	3180
GCTGCTTGTT TGGCCTTTCA TTAAATCGAC TGTAGCTGTT TTATTACAT	3240
TACTATAAAT AACATCGAAT TGATCAGTAA CATCTTTAAG TTTTGAAGTA	3300
TCAGGGGTGA AACTATCCAC AAATTGATTT TGATCTGtCA CTtCGTAAAT	3360
TTTGAAGTTT TTTGCATTTG GATTAAATTT ATATCCAGTT	3420
AAATTAGTAA CAAACGTTTG TTTAGTATAT GTATTTT	3480
TTAG GTTGATTAC ATATGCAGTC ATATTACGCG ATAAATCTTC	3540
ATTGTTAATA TAGTTTGTAC TTGAAATAAG CGGTTGTGCT	3600
TTTTTATTAC CATAATCGAC AATGATTTCT TCGCTATATG TATCATTACC	3660
TAAAGTTACT TCCATTTTAT AAGCTGTTTT ATCAGTTGTT GCATTTT	3720
TAC GTTTTCGCAA TGCAACTTGT TCAAAGCTAC CTCTAACtT	3780
TGTATATTGA TCTACATAGT TCGTAAAAGT ATATGTTGTT	3840
GTGTTTGTTG TACTATCATA AATACCTTTT GCAATAATAT TACCTTGGGC	3900
ATTATATAAA TTTTGAGTTT GTGAAGGTAA TCTTACTGAT CCTGGACGGA	3960
AATATTGACC ATATTTAAAA GTAAATGTAT CGCCCTCTTT AACAGAATCA	4020
TCGATTGTGT AATTGCTTT TAATTTTAAA ACATCACTTG AAGTTGCCCA	4080
AAATTTCAGTT TTACCAGTAG TCTGATTAAAC ATGTCCTTTA	4140
TCAATCGCAA TGTCAATATT TGAAAAATGT ACTTTATCAT TAACATTTGT	4200
TCCTTGTTGT GGAGCTGCAA CAGTATTCAC TGCCATGCGA TTTAAAGTTC	
TTGGTTTAAT AGTCGTTGTT TTAGGTGTAG TTGAAACATC TTTTGCTTGT	
GTAAATTAC TTTTATCAGT TTCATTACTA TATGTAGTTG ATGATTTATC	
ATTTGTTGTT ACATTGCTAG TTTTGTAGT AGATTGATTA	
GCTGTAGCGT TTTGTGGTGA TTGCATGTTA CTACTAGTTT CTTTAACTGT	
TGCACTATCA CTCATTGTCA CTTTAGGCTG ATCTCAGTT GCAGTTTGCG	
TATTGTCTTT TAGTTGACGA CTATCAACTT TTTTAGTTGT TTTATTCTCA	
CTTGGGGCTG TCGTTTCATT TTTTGATTGA TTTAATTCTC	
CATTCGTATG TTCTGCCGCT TTAGCTTCAT GACCACTTAA CCCAAAAATC	

AATGTTGTCC CTACTAAAAT TGAAGCAGTA CCTACAGAAT ACTTTCTTATCGAAAATTTG	4260
TTTAATCGAT TTGGTATCAT GCCTTTnCTA TTTGTnGCTG TCTTTTTATA ATTCATTTAA	4320
TAATACTCCT TTAAAATATC AAAATTTGAT AAATATAA	4358

(2) INFORMATION FOR SEQ ID NO: 455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1060 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

TTGACTTCTT AATTCAGCAT TTTCTGCACT TAATGCTTTG TTCTTTTAA TAAGTTGCTT	60
TCTTGCATAA ACTTCGGTAT CTATTTTACT AFTACTATAC CTTTGATTTA AAATAATAT	120
ACCAATTAAT GCTACAATGA TAATGATAAG TACAACATAA AAAGACATTT TTTCACCAAT	180
CCTTTTTGAC TTCTTTAACT TTGTATACAA TAATAATTAA TAAAGATTAA TTGTTATTCA	240
ATTTCCCACA TTTTATTAG TTGATTTAG TTCATCATTG TTATAATCAA ATTATAAACT	300
GACAGATATT GATGTTCAAT GAATATGACG TGAAAGATTC GTGAATTCAA GTTTATGTCTG	360
AATTTATGTT ATAACGGTCA TTTAAATGAC AGAATTAGGT CACTCATAGT ATTTTGAAGA	420
TTGAATTCAT TAATTTTAA ATGTATAATG ATATTTGTGA AAGCGCTTGC TTAGAGGTG	480
TATTTGAGAG TGAATGAAAT GAATGCTAAA GAACAATTAG TGGACAATTT AATGAAAACA	540
TCATCGCAAT TATTTAAATT TCACGGTGAA GTTGCCATGC AGCTTTTCTT AAATGATGAA	600
TTAAAATTAC CTTCTATTGT TGAAATATGC GTGGAACGTA AGCGTTTAAG TGATATTGTG	660
AAAGTTATTC CGCAATCATA TCGGTTACTA TACATAGATA AGCAAGATCA AGCAATAGCT	720
AAAGAAGATT TATCACTTTC AAAAATTGCA AAAGTTTATG TGCAATATGA TGATACAACA	780
ATAATGAGTA TTTTCGTTTA TGATGTAGTA AACGATGAAT GGATTTTATG ATTGGATCCG	840
AATATACGTA TACCTAAGAG TAACATATAC TTCCATAGTT TAAATTGGGA TGTGGATATA	900
TTAAACCGGA GtCGTCTAAT GTATGTCTAA TGCaCACCAT CAGaTCATCA TtATCCATTA	960
TAAcGrGCAT AGTGCATAAn yACTwCAtTT TaTTaaATTG AGaGGgGCAC GATAGGTGCA	1020
TCAGGACATA ATATAGGAAG CATCAACGCG TGAnCAGGTC	1060

(2) INFORMATION FOR SEQ ID NO: 456:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

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ATAATnACTA AATACnAAAG TTAACTGTC TTAATAATA TGACTATGTT ATAATTTTAA      60
AAGTGATATT TTGGGTAATC GCTATATTAT ATAGAGGAAA GTCCATGCTC ACACAGTCTG      120
AGATGATTGT AGTGTTTCGTG CTTGATGAAA CAATAAATCA AGGCATTAAT TTGACGGCAA      180
TGAAATATCC TAAGTCTTTC GATATGGATA GAGTAATTTG AAAGTGCCAC AGTGACGTAG      240
CTTTTATAGA AATATAAAAG GTGGAACGCG GTAAACCCCT CGAGTGAGCA ATCCAAATTT      300
GGTAGGAGCA CTTGTTTAAC GGAATTCAAC GTATAAACGA GACACACTTC GCGAAATGAA      360
GTGGTGTAGA CAGATGGTTA TCACCTGAGT ACCAGTGGA CTAGTGCACG TGATGAGTAC      420
GATGGAACAG AACATGGCTT ATAGAAATAT CACTACTAGT TTAGCTCTCC TAGATGATGG      480
AGAGCTTTTT TCATGAAAAG AACACTTAAA ATTAACGCCy TGTCTTGaTA tAATGACaT      540
GCcTTGTTTT AAAATAGTAA GCGGATGCgT TAATGTATCA GCGATTAAAT TTGTTGGAAA      600
TGTATAAAAA ACACAAGCTA AGAATAAAAT ACCTGTATAA AAGGAGAATC ATATATGTTT      660
CAATTACTTG CAGTTTGTCC GATGGGATTA GAAGCTGTTG TTGCTAGGGA AATTCAAGAA      720
TTAGGCTATG AAACAAATGT TGAAAATGGT CGTATATTTT TTGAaGGAGA CGCAAGTGCA      780
ATTGTAAAGG CAAATTTATG GTTGCGCACA GCAGACCGAA TCAAAaTTGT TGTTGGACGT      840
TTTAACGCAA CAACGTTTGA CGAATTATTC GAACAAACCA AAGCGCTCCC TTGGGAATCT      900
ATAATTGATA AAGAGGGTAA CTTCCCAGTT CAAGGTAGAA GCGTTAAATC AACACTACAT      960
AGTGTGCCAG ATTGTCAGGC GATAACTAAG AAAGCTATTG TTGAaGATT ACGTCGCGCA      1020
TATAACGAAA AAGGTTGGTT AAATGAATCA GGTGCCAAAT ACCCTGTTGA AGTTGCCATT      1080
TTAAAAGATA ATGTATTATT GACTATCGAC ACATCAGGTT CTGGTTTGAA CAGACGTGGT      1140
TATAGATTAG CACAAGGTGA AGCACCAATT AAAGAAACGT TGGCAGCAAG TTTAATCCGT      1200
CTTGCCAAAC TGGGAAAGGT GATTACACCT TTAATTGGT CCCATTTGCG GTTCnGGTTA      1260
CA                                                                    1262
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(2) INFORMATION FOR SEQ ID NO: 457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

CCTGGCTGCT TTATCAGCAT CTACTACTTT AAAACCGAAT ACGGATAAGA GTTCTGATAC	60
TGTTGATTTT CCTGAGGCGA TTCACCTGT TAGACCAATA ACTTTCGGCA TAATTTCACT	120
CTTTCTTTAT TTTTGACATA CTGGACAATA ATGACTATTT CTTGTCGCGA TGATTTTTGT	180
TTCAATTTGA CTTCCACACA CTTTGCATAC CGGCTGCTTA TATACATTAA GATGCAATTG	240
CATCTCACCA GTTTTTCCAT CAGCATGACG ATAATCTGAA ATACTTGAC CGCCATATTT	300
AATACCTTCT TCTAGTACTT CTCTAACATA ATAAAAACC ATTTCTTGTT GTTGGTGTGT	360
TAAGTCTTTT ACTTTTTTAT CTGGTAAAAC ACCTGCACGA AACAACGCTT CACATGCGTA	420
AATATTTCCA CAACCTGCGA TTACTTTATG ATCCAAAATC ACTTGTTTGA TTGGTTTATT	480
CTTATTAGAC TGTTGATGAA TTCGATTTAA ATAATACGTC AATGCTTCAT TTGAAAAGG	540
TTCAGGCGCT ATTTCTAAAA ATGAAGGATA AGATGCTACA GACGCAACAT TTCTAATTTT	600
TCCAAAACGA CGTATATCTG AATAAATTAA CTTTTGTCA TTTGACAACT CAAAATAAC	660
ATGCCAATGC TTACGATAAT TAGGTATCATAAATATCTTCA AGTTCATCTA CAATGAAAAA	720
ACCGCCCGCC ATACCTAAAT GACTAATTAA TGTACGTTGT TCTCGTTTAT TATCTAGCTG	780
AAAAACGATA TATTTACTTC TTCGTTCTAC ATTTGTAATG GTATAGCCTT CCGATAAAGT	840
TTTAAAAGTA TCTAATTCAA TTCCTTTTAT AATTGTTTCC TTGCCTTGAG CTTTACTTC	900
GATTACTTTA TCCGAAAATA TAACGTGTTC AATTTTTTGA TTTATAACGT AGGGTTCAAT	960
TCCTCTTTTT ACATGTTCTA CTTCTGGTAA TTCGGGCATA CCATTAACCT CACTTTATTT	1020
TGCATCATAC CAGGTTGCAC CATAACTTGA GTCTACTTTT AATGGAACAT CTArTTGCAA	1080
TGCATTTTCC ATTAKCTCTt CTACAAATTC ACTAAATGAA TCTACTTCTG ACTTAGGTAC	1140
TT	1142

(2) INFORMATION FOR SEQ ID NO: 458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

CCTTTAGTAA ACAATCCTTC TTTAGTTTTA GTACGTTGTT CCAATCCAAA TAATTTGTAT	60
TTCATTGCCT CGCCCGATTG AGTGCCGCTA AATTATCAT CTTTCATGTT AGGCGTGTTG	120
GTAAACATGT GTATATCACT GTTTAAACGG TCTTTATAAG CTTCGGTACC TTGTACATCG	180
TATTGCTTAT AAATATAACC ACCATCAACA GAGCCTTCTG TTTCTCTACC TTCGCTATCA	240

GCATAAACAG TCGGTTCTAA AAACAACACG TTAGCTTCCT TTTGTTTTCT AACTTCTAA	300
GGATCTAAAT TTAAATTACC TTTAATAAGT AACATAGCGT CATTTAAATC ACTCATATAG	360
TTAGCAsymy CTGATTACAG ATTATCATAC AAATCAATTA AAGTGATTAC TTTCTCATAA	420
TCCCCTTTTC TTCTTTCGTT GTTGCTAAAT TCTGTAATAG GCATACGTTT GAAAGAGTGT	480
GATTCAAAAC CGTTTTACAG TGGTGTGAGC TTCAATCCAT TTGTTCTACT GGTAAGATAT	540
CTATAAACAC CGTGTGAAGT GAATAAATCA ACTGTAAACA CTTCATCTTC GTCAGTCTTG	600
TCTATTGGTT TAGTTCTTAA ATATCTAACG CCTGCGATAC TATTACGTTT AATTGTATTG	660
TCGTATATGA CAAAAGTACT CATTGCATCA CTCTTGATAAACGCGTTTC ATCATCTTGG	720
TTTCTAATCA TTAAGTCATA AGCTTTGCCA TAAATTGACA AATCTAATCC TAAAGATCTA	780
TTGTGTGACT CAACATCATT TAAATCATTG AACGCCTCAA TAACTTCTAA TACATCTTTG	840
TCATCATCTT GATATTGAAT TGGATTACCC AAGAAATAGC CGTTGATAAA ATCGCTAATA	900
TAAGATGCGT AATCATGCGC TACACGGTTA TCTGCCATGT ACTCTTCTTT GCGTCGTGTT	960
AACTCAACTA AGTTCTTAGT TTTACCTTCG TAATAATCAC TTAACACTTT CAATCTAGGT	1020
CGTTGGTAAT CCATGTGATG TTCAATGTAT TTAATTACTT CATTAACGTT TTGTAATAAA	1080
TCGGATTCCG TCCCGTCATA TGTGTAAACA ACATTGGCTT CATCATTAAT TAAGTAATTT	1140
ATGTTTCCCC GTAGATCTGT ATCTGTTTCA AATTCGTTTA CTTTTAACAT TTGTTCCCTC	1200
CTATAATCCT AGAGATTTTA TTGTGTCAAC TTTGCAACTG AGATTTGTGC GTTTtCTAAC	1260
CGGTCTGTAG AATCGTTCCA CTGAATAACG CAACGAATCG ATACAAGAT TGTATGTATC	1320
TACTGGTTCA TTGGTATATT CACCTGTATC TTTGTCCTTT TGCCATGTGT AGTTGTCAAA	1380
CTCTTCAATA GTCTTGAAAC AACGTTTCATC AACAATGATT TCAAATTGCA TTAAGAATTG	1440
TAACCCTTGT ACAACCGAGC CCTTCCCTTT TTTGGTTGGT AAAATCCTTT TAAGCCCTAG	1500
ATTCCTTAAT TCAGCTATAC TTTTTTGTTT TGCATATCT GCTGTAATTT CTTCTTTAGC	1560
ATAACCAAGT TGCTTTATGA CATTAGCTAT TTCATCATTC AGCATACCTT GTTTAACATA	1620
CTCTTCAATG ATGTATAACT TCTTTTTCTT TACATCTATT TTAGAATGTA TAAAGCACT	1680
AGGATCATTA ACGTAGCCAA AGTCCAATC AAAATAAGAA GGTAATGTC TTAATCATC	1740
TTTATTTATT AAACGTTTTT CATACTTAGG GAAAACCAAT TTGTCTAGTG TAGCAAATTC	1800
ACCTAACGCA TAAA	1814

(2) INFORMATION FOR SEQ ID NO: 459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 686 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

AATTnAGATT ATTACCCTCC TTAAAAATA TTTGTTTCAC AATTTTTTATTACCTATTTA	60
CTGGTTTCAT GTCTTATGGG GCATTTTACT TGTTGGTATT TGAAAATGTG CAAAATTTAA	120
TCTTATATGT TTCTTGGCTT TTCATGACTA TGCTATTTAT GTTTATGAAT ATGCATTCAA	180
TTATAGATAA AAAAGTACAT ATATTCTTAA AGTCTAATAA ATAGTTACAA ATTTAGTTAG	240
TTTTCAATTG TTAATTAGGG GTGGTAAACA GTGCTTTGTG AATCTAGACA AATTTATAAA	300
AATCCTAAAT ATCGAGTTAT TAGATATAAT AATGAATATT TCATGGTCGA TTTAGTAAGT	360
ACTTGGATTA CTTATTTTTT CCCTATGATT AATTGGTTTT TGCCCAAAAA ATACGCAAAA	420
ATTAGCGAAA ATGAATTTGA AAGGTTAAAT AAGTCGAGC CTGTTAAAAA TAATGTTTTT	480
TGGCCGGTTG CAGGAAGTTC AGTTCTATTT GGAATTATAT TGAGAAAGTA CGGTAAGTTC	540
TTTAATGTTT AGTTTGAAAA ACAACTAGCA ATCACTGTAT TTTTATCAT GTTAATAGGG	600
ATGTTAATTT TTTATTTTTA TCTAAATAAA AAATTAACAT TAAAAATTTT TAATACCA	660
GTGGGTAATA AGAATAGGAG TTGTAT	686

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

ATCTGCAATT ATGGGCACAC CCAAGCTnAT GCAAGTAACT AAAGGAGAAG TACTTTTAGA	60
CGGTGTAAAT ATTTTAGAaT TAGAAGTTGA TGAAAGAGCA AAAGCAGGAT TATTCTTGGC	120
AATGCAATAT CCATCAGAAA TTACAGGTGT TACAAATGCT GATTTTCATGC GTTCAGCAAT	180
CAATGCGAAA CGTGAAGAAG GACAAGAAAT CAACTTAATG CAATTTATTA AGAAATTAGA	240
TAAAAACATG GATTTTCTAG ACATAGATAA AGACATGGCA CAACGTTATT TAAATGAAGG	300
TTTCTCAGGT GGAGAGAAGA AACGTAACGA AATCTACAA TTAATGATGT TAGAACCTAA	360
GTTTGCaATC TTAGATGAAA TCGATTGAGG GTTAGACATC GATGCATTAA AAGTTGTATC	420
TAAAGGTATT AACCAAATGC GTGGGGAAAA CTTTGGTGCA TTAATGATTA CACACTATCA	480
ACGATTATTA AATTACATTA CTCCTGATAA AGTACATGTA ATGTATGCTG GTAAAGTCGT	540
TAAATCTGGT GGTCCAGAAT TAGCAAAACG TCTTGAAGAA GAAGGATATG AATGGGTAA	600

AGAAGAGTTC GGTTCAGCTG AATAATCTTA TTAATACAGT ATCCATGAGA TGTTTCATCTA	660
TATATGATGA AAATGAACAT TTATACGAAA TAGTAAATTT CATCAAGTAG GAGGAAAAAG	720
TTATGACAAC TGATATTTTG rACaTTyCTG AAGAACAAC TGTGATTAT TCTAAAGCCC	780
ACAATGAACC TTCTTGGATG ACAGAATTAC GTAAAAAAGC TTTGAAATTA ACAGAAACTT	840
TAGAAATGCC AAAACCTGAT AAAACAAAAT TAAGAAAATG GGATTTTGAT TCTTTTAAAC	900
AACACGATGT AAAAGGTGAT GTTTATCAAT CTTTATCACA ATACCTGAG TCAGTAAGAG	960
AAATTATTGA CGTAGATCAT TCTAAAAACT TAGTAATTCA ACATAATAAT ACGATTGCGT	1020
ACACACAAGT TGATGATAAT GCATCGAAAG ATGGCGTTAT CGTTGAAGGT TTAGCAGACG	1080
CTCTTATGAA CCATAGTGAT TTAGTACAAA AGTACTTTAT GAAAGATGCA GTAACAGTAG	1140
ATGAACATCG TATCACAGCG CTACACACGG CATTAGTTAA TGGTGCGTA TTTGTTTATG	1200
TTCCTAAAAA TGTAGTTGTA GAACATCCAG TACAATACGT TGTGTTGCAC GACGACGAAA	1260
ATGCAAGCTT TTATAACCAT GTTATCATCG TTACTIONAAGA	1300

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

GACAGCAAAT TCAAGATACA TTAAATAAAG ATATTGTCAT AAAGCATATT CTTGTTTCGAG	60
ATAAATCTAA AAAGAGACCG CTAAATATTA GCCAATATCA TTAACTGAA GATGTTAATG	120
AAATTTTAAA TGATGATTCA TTAGATATTA TCGTTGAAGT CATGGGAGGA ATTGAACCAA	180
CTGTAGATTG GTTAAGAACA GCACTTAAAA ATAAAAACA TGTTTATACC GCAAATAAAG	240
ATTTATTAGC AGTACATCTT AAACTTTATG AAGATTTAGC AGAAGAAAAT GGTGTAGCTT	300
TAAAGTTTGA AGCGAGTGTA GCAGGTGGTA TTCCGATCGT AAATGCCATA AATAATGGTT	360
TGAATGCGAA TAATATTTCA AAATTTATGG GAATTTTAAA TGGTACCTCT AATTTTATTT	420
TATCTAAAAT GACTAAAGAG CAAACGACAT TTGAGGAAGC ACTTGATGAA GCGAAAAGAC	480
TTGGTTTTGC TGAAGCGGAT CCAACTGATG ATGTAGAAGG GGTAGATGCA GCGCGTAAAG	540
TTGTCATTAC ATCATATTTA TCATTTAACC AAGTCATTAA ATTAAACGAC GTTAAACGAA	600
GAGGAATTAG TGGCGTAACT TTAACCTATA TTAATGTAGC CGATCAACTG GGGTATAAAA	660
TTAAATTGAT TGGTAAGGGA ATATATGAAA ATGGCAAAGT TAATGCATCG GTAGAACCAA	720
CGTTAATTGA TAAAAAGCAT CAATTAGCAG CTGTAGAGGA TGAATATAAC GCGATTTATG	780

TTATTGGTGA TGCCGTTGGT GACACGATGT TTTATGGAAA AGGAGCAGGC AATTAGCAA	840
CAGGTAGTGC CGTTGTCAGT GATTTATTGA ATGTAGCATT ATTCTTTGAA TCAGATTTAC	900
ACACATTGCC ACCACATTTT GAATTAAAGA CAGATAAAAC ACGGGAAATG ATGGATTTCAG	960
ATGCAGAAAT TAATATTAAA GAAAAATCCA ATTTCTTTGT AGTAGTGAAT CATGTCAAAG	1020
GTTCAATTGA AAATTTTGAA AATGAGTTAA AGGCAATATT ACCATTTTAC CGATCATTA	1080
GAGTTGCAAA TTACGATAAT CAATCATATG CCGCTGTTAT AGTTGGATTG GAATCATCAC	1140
CGGAAGAATT AATCACTAAG CATGGATACG AATTGACAAA GTATACCCAG TAGAAGGAGT	1200
TTAATTATAA TGAGAAGATG GCAAGGATTA GTAAGAGAGT TTAAAGCACA TTTACCAGTA	1260
AATGAAAATA CACCAAAATT AACATTGAAC GAGGGAAATA CACCACTCAT TCATTGTGAA	1320
AATATGTCTA AAATACTAGG CATAGATTTA TATGTGAAGT ATGAAGGTGC CAATCCGACA	1380
GTTCAATTTAA AGATCGCGGT ATGGTAATGG CTGTGACAAA AGCAAAAGAG CAAGGTAAGA	1440
AAATTGTAAT ATGCGCTTCG ACTGGAAATA CATCAGCGTC TGCAGCAGCA TATGCAGCGA	1500
GAGCAGGTTT AAAAGCTATC GTCGTAATAC CAGAAGGTAA AATTGCATTA GGTAATTGT	1560
CGCAAGCAGT AATGTATGGT GCAGAAATCG TTTCTATTGA AGGAACTTT GATGAAGCTT	1620
TAGAAATTGT AAAAGAAATT GCAAAAAGTG GCGAAATCGA GCTTGTAAC TCTGTCAATC	1680
CATTTAGAAAT CGAAGGACAA AAGACAGGCT CATTTGAAAT TGTACAACAA TTAGACGGTG	1740
AAGCACCTGA TATTTTAGCG ATTCCTGTAG GTAATGCAGG TAATATTACT GCATATTGGA	1800
AAGGCTTTAA AGAATATCAT GAAGCTAAAG GATCACAATT GCGAAAATG TTTGGCTTCC	1860
AAGCTGAAGG CGCATCACCA ATTGTTCAAA ATAAAGTCAT TAAAAATCCT GAAACGATTG	1920
CAACTGCTAT TCGAATTGGT AATCCTGCTA GTTGGGATAA GGCGACTAAT GCTCTTAAAG	1980
AATCAAATGG ATTAATAGAT AGTGTTACTG ATGATGAAAT TCTAGAAGCA TATCAGTTAA	2040
TGACAACTAA AGAAGGTGTC TTTAGTGAAC CAGCGAGTAA TGCTTCTATT GCAGGTTTAA	2100
TTAAATTGCA TAGACAAGGT AAATTACCTC AAGGTAAAAA AGTAGTTGCT ATTTTAACTG	2160
GTAATGGATT AAAAGATCCT GATACTGCTA TTTCACTACT AGATAATCCG ATAAAGCCAT	2220
TGCCAAATGA TAAAGATAGC ATTATCGATT ATATTAAAGG AGCTTTATAA CATGTCGAAT	2280
GTTTTGGAGT TAACAATTCC TGCATCAACA GCCAACCTTG GAGTTGGCTT TGATTCTATA	2340
GGTATGGCTT TAGATAAATT TTTGCATCTG TCTGTAAAGG AAACATCAGG GACAAAATGG	2400
GAATATATTT TCCATGATGA TGCATCTAAG CAATTGCCTA CTGACGAA AACTTTTATT	2460
TATCATGTAG CACAACAAGT TGCTTCTAAA TATAGTGTTG ACTTGCTTAA TTTATGTATC	2520
GAAATGAGAA GTGATATTCC ATTGGCAAGA GGGTTAGGTT CGTCAGCTTC TGCTTTAGTA	2580

GGAGCTATAT ATATCGCAAA TTATTTTGGT GATATCCAAC TGTCTAAACA TGAGGTATTA	2640
CAATTAGCGA CTGAAATCGA AGGACATCCT GATAATGTTG CGCCGACCAT TTATGGTGGT	2700
TTAATCGCTG GATATTATAA TGATGTCTCG AAAGAAACGT CaGtGCACA TATCGACATA	2760
CCAGACGTGG ATGTGATTGT AACGATACCA ACTTATGAAC TAAAAACAGA AGCATCAAGA	2820
CGTGCTTTAC CACAAAATT AACACATAGT GAAGCGGTTA AAAGTAGTGC AATTAGTAAT	2880
ACAATGATTT tGgCATTAGC ACAGCACAAT TATGAATTAG CAGGTAACT CATGCAACAA	2940
GATGGCTTTC ATGAACCGTA TCGTCAGCAT TTAATTGCTG AATTTGATGA AGTGAAAACA	3000
ATTGCTAGTC AACATAATGC CTATGCAACT GTAATTAGTG GTGCTGGACC AACTATTTA	3060
ATATTTAGTC GTAAAGAAAA TAGTGGGGAA TTGGTTCGCT CTTTAAATAG TCAGGTAGTA	3120
TCATGCCATT CTGAA	3135

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

AACAATTAAA ACTGAACTTG ACTTACGAGG CTATCGTTAT GAGGATGCTT TAATTGAACT	60
AGnTCAATAT TTAGATCAAG CCGTTTTAAG TAATTACGAA CAAGTTTATA TCATTCATGG	120
TAAAGGTACA GGTGCACTTC AAAAAGGTGT ACAACAACAT TTGAAAAAGC ATAAAAGTGT	180
TAGTGACTTT AGAGGTGGTA TGCCAAGCGA AGGTGGATTT GGC GTTACCG TTGCAACACT	240
AAAATAAATT ATAATTTGAT AAATTAAATA GCTCAGTTA AAATAATGTA AAGCAACAAG	300
AATACATTTT AAACATGTTA TTTGAAATAA GCATAAAAAT TGAGCAAATA GAAATACATG	360
AAGCATGTTA TCTGATATAA TTTGAACATC ATAATAATAA TTAAGGAGGA TTGGCATTTA	420
TGGCAATCGT AAAAGTAACA GATGCAGATT TTGATTCAA AGTAGAATCT GGTGTACAA	480
TAGTAGATTT TTGGGCAACA TGGTGTGGTC CATGTAAAT GATCGCTCCG GTATTAGAAG	540
AATTAGCAGC TGA CTATGAA GGTAAAGCTG ACATTTTAAA ATTAGATGTT GATGAAAATC	600
CATCAACTGC AGCTAAATAT GAAGTGATGA GTATTCCAAC ATTAATCGTC TTTAAAGACG	660
GTCAACCAGT TGATAAAGTT GTTGGTTTCC AACCAAAAGA AAATTAGCT GAAGTTTTAG	720
ATAAACATTT ATAAGTTACA ACCAATGACG ACTGGGGCAT TTCTTTAATG AATTGCTCCA	780
GTTTTTGTTT GTGTTTTTAA TATAAAAAGT TGAATGATAA GTCATCATAT TGTTTACGAC	840
TTGAGAATGG TGGGATTAAT AAATCTATGA ACGTTAAATGATAATCTAGC ATGCTGATAG	900

ATTTGTAGCA GTTGGTTTGA TAAAACCATG TTCAATATTA CATGATGTGC ATGAAAAGTC	960
ATACTCGAAG ATGTTGATTA TTAAC TAGAA TTAGTGGTGA TAAATTTGAA GCACTTTTGT	1020
AGCATCATTC ATTTTAAAT TAGAAGGGGG GATATTTTTG GAAGACTATA AGCAACGAAT	1800
TAAAAATAAA TTAAATGTCG TACCTATGGA ACCAGGATGC TATTTAATGA AAGATCGTAA	1140
TGATCAAGTG ATATATGTTG GCAAAGCTAA AAAGCTAAGA AATCGATTGC GATCATATTT	1200
TCACGGGTG	1209

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

AGTTCAACAC GACGAATTTT ACCTGAGTTT GTTTTTGGTA AGTCGTCAAC GAATTCATC	60
TCTCTCGGAT ATTTATATGG TGCAACTTCA TTTTAAACAA ATTGTTGTAG TTCTTTAACT	120
AACGTATCAT CACCCGCAGT ATGGTCCTGT AAAATAACGA ATGCTTTAAC AATATTTCTT	180
CGTATATCAT GAGGTTTTGC TACTACAGCA CATTCTTTAA CGGTGGATG ATTCGTTAAC	240
GCATCTTCAA CTTCAAAAGG CCAATCGTA TAGCCTGAAC TAATAATAAT GTCATCTCGA	300
CGTCCTTCAA ACCAGAAATA ACCATCATCA TCTACATGAG CTAAGTCACC AGTGATGTAG	360
TATTtAqCTG TTTGCGCTTT CGCCGTACGT tCTGGCTCTT tATAATACCC TTTGAAAAGT	420
GCTGGCAAAT CAAGTGGTAC TGCAATATTC CCTTTCGTAT TAGCAGGTAC GCTATTCCCC	480
TCATCATCTA CTACAGTGAC CGAACTACCC GGAATGCCTT TACCCATTGA TCCAATCCTC	540
TGTGGTGTAT CTTTTAAAA GCCTATAAGC AAGGTACTTT CAGTCTGGCC ATATCCATCT	600
CTTACAGTTA AATTAAAGTA TTTCTGAAT TGTTCAACTA CTTCTCGATT TAGTGGCTCA	660
CCTGCAGAAA CGGCACTATG TAAATGCGTT AAGTCATAAT CATTTAAGTT CTGTAATTTA	720
GCCATCATAC GATATTCTGT CGGTGTACAA CATAAAACAT TAATTTGATA TTTTGAAGC	780
AATTCTAAGT ATGTTTCAGG ACTGAACCTT CCATTAAATA CAAAAGCAGTTGCACCTGAA	840
CCTAATACAG ATAAGAAAGG ACTCCATACC CATTTTTGCC AACCTGGTGc TGCTGTTGCC	900
CAAAC TAAGT CATCTTCATT aATACATaAC CAATGTTTTG GTGCCATTTG TaAATGTGcA	960
AATCCCCaTC CATGACAATG TGTAACGGCT TTAGGATTGC CAGTTGTACC AGATGTATAT	1020
GACAGAATCG CCATATCATC ACGCGTCGTA TCTGCCATTT CTAGTTTGTT ACTTGCGTTT	1080

TCTTTTTCAG CTTCAAGTGA AATCCATCCA TCTTTTGTGAC CGGCAATAAC AAATTTAGTT	1140
AACGCATCAT ATTCTTTAAT TTTTTCAAAT TCAACTGTGA ATGGCTCTAG TGCAATAACT	1200
GCATTAATTT CACCATGTGT GATACGGTAT TCAAATCTT TAGTTCTTAG CATTTTCAGAA	1260
CATGGAATGA TTGCAACACC TAATTTTAAA GCAGCAATAT ATAATTCATA CGTCGCAATA	1320
GATCGTGGCA TCATAATGAG TACTTTATCG CCTTTAGATA AACCGTGCGA TGCTAAAACA	1380
TTACCTACTT TATTAGACTG TTCAATGAGC TGTGGTAAG TGAATGATAT ATCTTCGCT	1440
TCAGTATTAT GATATAAAAT TGCCTTTTTA TCTGGTATGT GGCTATATTT TTCGATTTC	1500
GAAATAATGT TATATTTTTC AGGCGCGAAT AGAGCTGACT TTTGCATAAC TAACCTCCTT	1560
TCATACATCC ACTTTTCCTG TGATGAACAT TGTAATTTTA TAAATGAATT ATATACATCA	1620
TACGCCTATC TTTACAGAAT TTTCAATTAA ATAGGGTTAA ATACCAAAGT CCTCGACACT	1680
ACACTTTGAC ATGACGTAGC ATTCAAGGAC TTTCAAATGA TTGAGGGTTG ATATCTCGGG	1740
CTAGACCATA TCAGCTAATT CAATACGAAT ATTGTATGAT AATTCACGAT TAATTATTTT	1800
TACATCTGCA CCTTTCGAAG TGCCACGATG CTTGTGTGTATGCTTGTACT CAGCTGAATT	1860
TTGCCAATGA TAAATGCTT GCCTATTTTC CCACAGCGTA ATAATGATAT AGTGTCTACC	1920
AGCTGTTCTA GGTCTTAAAA ACCTTAATGC TTTAAATCCA TCAACGTTTT TTAAATGCTT	1980
ATTACGTCGC AAAAATTTTT GCTCGAATGT TTCTTCTTGT CCTTCGTTAA TATATAAATG	2040
ATTTAACACA CATAATGAAT CATTTGATAA ATCATTTATC GCTTCTAGCA CATCGTAATA	2100
TGCAGTGTCA TTATTTTTTT GTATTGTGAG ACAATCATCC AGTTCTTCTA TTACATAACT	2160
TCTATATTCA TCATAAATTT TCATAATAAA TGCCTTCATT TCATTTATAT TTTTGGTCAT	2220
ATTACTkTAT ATCTATTACT AetkCATTCC CGTATTTATT AATTACAATC ATAGTTTGGC	2280
TyCTTTTTTAA AAGATAAGAC TTTGTAAAAA GTATTAATAT TTCATGCAAA TGGGGGACAG	2340
GAGTCGCCCA CTATTTTTGT GTCTTCAATT TCATGATCAT TATTTAACAT TAGTCATGAA	2400
AATAGCCGAC	2410

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

TTTATTAATT GTAAAAAATT GAGTAAATTA TCTTTACATT CTAATTAGT CTTAACTACA	60
ACTAGTATCC TAATAATTAT AGGAGCTATT ACATTCTTTT TATTAGAACA GTTTAATACT	120

ATGCAACATA TGGGACTAGT TGAAAAAATC GGAAATTCTT TTTTCCAATC AGTAACAACA	180
CGAACAGCGG GTTTTAACAG TATAGATATA GCAAGCATTa rCAAAATCTAC CGCATtAaTG	240
TTAATGCTAC TTATGTTTAT TGGTGGTGCC CCTCTCAGTG CAGCTGGAGG AATTAAAATA	300
ACTACTTTTG CAGTTGCGTT TATTTTTGTA CTAAATTATA kACGTAAAGA AAATAATGTT	360
TCAGTATTCA ATAAAGAAAT ATCTGACAAA CATATAAAAC TATCTATTGT TACCATTAAT	420
ATCTCATTTT TATTTATCAG CATCATTACT TTTATATTAT CGATAATTAA TCCGAACATA	480
TCATTAATCA AGTTATTATT CGAAGTGGTT TCTGCATTCT GAACAGTAGG GTTAAGTATG	540
AACCTTACCA CAGAATATCA TGGTATTACT AAAATAATTA TTATATTCGT	590

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

ATCTAACTCT GTATGTTGCT CAATATGCGA TArATCTAAC AGATCTGTTA CTAAAGATTC	60
TATTTCGATTT GAnTCTTTTA AAATTATGTT TAAAAACATG TCTAATGATT CCGCATCATT	120
TTTTGCACCA TCAATAAGCG TTTCAGcAAA CCCCTTAATT GAAGTAATAG GTGTTTTTAA	180
TTCATGTGAA ACATTTGCTA CAAATTCACG TCTTAGATTT TCAAGTTGTT TCAGATTTGT	240
TATATCATGC ATCACaACTA AAATCCctTG CAAACTTTTT TGAGACCTAG TTAAAATCGG	300
AACGCATGAA ATATCAAAGT ACTTGGCATG GACTTGGTTT ATTGCAACTT CCAATTGTTC	360
ATAAATAGGT TTTTCAACTT TAAAACTTt TAAAATTAAT TGCTCAATTT CAGTATTAAC	420
ATAGCCGTGA TAGCCTACTT GTTCAATATT ATGCGAGATG TTGAACTGTT CATAATACGC	480
TTTATTTGCA ACAACGATTT TTCCATTTCTG ATCTATCATT AAAATAGCAC TTGGAATATT	540
TTCAATCGTT GTTTTTAAAC GGTTGGATTG AATTTTTTGC TCATTATTAA GCTTTGAAG	600
GCGTCGTGCT AAATCATTGG TAGACACAAA AAGCGCTTTA GTTTCTACAA CATTACTTTC	660
AGGTACACGT ATGTGATAAT AACCATTtGC CAACAATTGT GTTGCATAAG TAACTTCTTG	720
AATGGGACGG ATTAATGTAC GCTTAAAACT ACGGCTTGCA AAATACAGAC AAATGAGTAC	780
AACTAAACAT GTCAAAATAA GATATTTCCA CAACGTCCAA TGCATTTCTG TAATATCGTT	840
ATTGTAACCT TTAATCCATA CATGATAACC GTTAACCTTC TTATtAAAAA TAAAAACGTC	900
CCTTT	905

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

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TTTGGTTAGC CCATAAAAGA AAAAAACAAG AGTCATTTT TAAACAACAT ATCAAGTCTA      60
CCCAAGAAAT ACGTTTTTGAC AAAGCGAAAG TGCTTGAACA CAAAGATGAA ATAGCAAATT      120
TTATTTCTTT CGAACCACAA AGTTTTGAAT TTTATTATTT TACAGAATCG GAATTTTCAG      180
AAGAACAATT AAATGAAGTT TCGCCAATTA GAATTAAATT CAATGTTATA AGACACAAA      240
AAGATTTGaT AAAGCATATG CCGAATATAT TTTTGGcTAG ACTTATTTCA GAAGATAATG      300
ATAAAAGAC ATATATGTTT TATAACGCA AAGTATTAAC CGATAACTTT TTAGATAAAT      360
ATATGCAGAA ATTTTCACCG GCAACATACA CAATAATATT TGTAATGTC TTAATATGGT      420
TATGTATGAT TTTATATTTA AATAATTTTT CGGATGTAAA ATTATTAGAT GTTGGCGGGT      480
TAGTGCATTT TAATGTCGTA CATGGTGAAT GGTATCGAAT TGTTACATCG ATGTTTTTAC      540
ATTTTAGTTT TGAACATATA CTTATGAATA TGCTTTCATT ATTTATTTTT GTTAAATAG      600
TCGAAGCAAT TATTGGTTCA TGGCGGATGT TAACTGTAA CTTTATTGCA GGGTTGTTTG      660
GAAACTTTGT ATCACTATCA TTTAATACGA CTACAATTTT AGTTGGGGCT AGTGGTGCTA      720
TATTTGGTCT GATTGGATCA ATTTTTGCGA TGATGTATGT TTCAAAAACA TTTAACAAAA      780
AAATGTTAGG ACAGTTATTA ATTGCATTAG TGATATTAGT TGGTGTTTCT CTGTTTATGT      840
CAAATATAAA TATTGTGGCG CATATTGGAG GATTCATTGG TGGTTTATTA ATAACTTTAA      900
TTGGCTATTA CTATAAAGTG AATCGtAATA TTTTTTGGaT TTaCtAATTG GTATGCtTGt      960
tATATTTAwT GCACyTCmAA TTAgtTTTT ACmATTAAAG AAGATAATAw TTATAA      1016
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(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

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AACTTTAAAT TTAGACATCT TAAAACCTC TCTTAAACCA TGCCTATATC TCAAGATGAT      60
ATTTCAAATG AACAATACTA TTGCTTGAGA CCATTAATGA ATGATCATAA ATATTTCTTT      120
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CTATAAAATT AGCTTTCCAA TAACTGTGTT GTTGCATAAT ATCATT CACA AGTACACCAT	180
TTTCGGAAGT ATGATTATCT TTATCTATAC TTAAACAAT TTTTAGTT TTAGCATGGC	240
TAAATTGTTG AAGACCCTTA CACGATAAAC GTATAGCGTC TGAATTCTCA TTTAACAATG	300
CGGCTGGgCA AACAAATGAC ACATTGTACT TCATGTTTGA ACTTCGTTAC AATCaTCGTG	360
kCatTTTGat AAATAACAAT CCCTCGTAAT kGATTAAGTA TATTAT	406

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

AGATAATACA CTTGAAGTTG GAATGGTTTG TGACGGTTAT TTAATGCGAA TTGAAACTT	60
AACACCATCA AATTTCTTCA ACTCAGCAAG TGAAGATACG ATTACTAAAA TTAAATTAAA	120
TGCATTGAGA GAACAACGTC GCATTTTACG TGAGTTGATT GATACAGATG AAGTATCAGA	180
AGGTACAGCG TTAAAACTAA GAGAAGCCAT CAATTATGAT GAAATGGTTA TTGTAGATAG	240
TATGACGTAG TTCCTAATTA TGCKAAAAGG GATTGATGAA AAAGTGAAGG GCTTTTCATC	300
AATCCCTTTT ATTTTAGGGG AATTGAATAG ATAGTTTAA ACTATACGAA TTATTAATAT	360
TTGAGATTTA ATTGAAATAA GTTTTAAAAA TTGGAGGAGA TAGATAAGC GAAGTCATTT	420
AAAGGTGAAG TTAAGTGTAT TCACAAAAAn TAGCCACACT CATATGACAT CGGATGAGTG	480
TGGCTTAAGG ATCTATGGGG GGAGGAAnCC ATAGATGTTT ACTTTGATAG GCCAGATTAA	540
ATATCAAAGT ATGCGATTAT TTATAGCTTG ATGCAAAAGT GGTATGCCTA TTAAAAGTTA	600
CTGCACATAG CTTTTAATAT TCCGTTCAAA GGAAAGGGGC ATACAATTGA ACAATCTGTA	660
ATAGTACTTT TAACCAGCTA TGCTAAAAGT CTAGTAGGGA GAACAGTTGT CCAATCACAT	720
AAGAACCTCT AACTTCGTTA GTACGATTAA GAAAAGCTTT TTAGTTAGTA TGTAATACAA	780
TTTATTGACG CGCGTGAATC TCTTTTATAA GAGTGTGTAG GGAATGGCGT TGTATAAATT	840
GTATTAGAAG AACTTCTAAC GCATCTCTGT GGTAAAAGA GATGAAGGGA ACGACAGTTT	900
aATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTCTCGT TCAAAGAGAA GCAGcTGTTc	960
GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AAGTGATAA	1020
ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAgAG	1080
AAGCAGCTGT TCGCAgTTTA ATCAAAACCA CATAAAGCTT TTAACTTTAC TCTTTGATTT	1140

AAAGAGTGAC AAATGTTTAC AGTTTAATTA AAAC T GCATA AGAACTTCTA GCTTTTCTCT	1200
TTCGTTCAAA GAGAAGTTCT AATACCACCA TATCGTGCGA TCGGGAACGG TATATATATT	1260
AATAGGAGGG TAATATATAT TTAACGCACG ATATGGGACT ATTAGCCTTC GACTTTGTTA	1320
TGTTGATGTG TGGCCTAAAA TATTGGAGAT ACCAATATTT TAGGTTGCAT CAACATCA	1378

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

TCCCAACCAA TAATCGTGGC AAAAATACGG ATATTGGTAT GGCTTAACAA ATTGCAAATA	60
TCGTTTAATC ATACATCCCC CCTAATCTAT TGCCCTATCC TATTCaTAAG CATAAAAATG	120
AATAGAGGTT GGATACATAA TTTGTAGATG TAAATTCTTC TTACAATTTA CATTTTTTAA	180
ATTAAGATAT CTCAACCTCT GTCATATTCA TGTGATTAAA TACGTTGTCT TATTGTATG	240
TTATATTCTA TTCAATTTAA TCTATGGATA CTGTGTCCCC ACACGACAGC AAAAGTTATC	300
ATACTTCTTT ACATCACTAA GTCAATATAA ATGATTTAAT CAGTATTTAC ACTTTATTTG	360
CTTAATACTG TCTAATTTTT TTGTAACGTT CTTTCCAAAC TTTGATAAAA TCTGGCGCGA	420
ATGGGCCCTT CTTCTGTTCT ATCCATTGTT GAAGAATGTC CACGTTGCGT CTAAAATAA	480
TATCAATATC ATGCGGATAA TTCATTTGAT TCATATGTTG CTCATATTCA TCTTCATCTA	540
ATAAATGATA CTTTCCGTTT GGATATACTT TAATATCTAA ATCATAGTCT ATATATTTTA	600
ATGCCTCTTC ATCACAAACA AATGGTGATG ACAAAT E CA ATAGTAATAA ATTCCATCTT	660
CTCTAAACAT GCAGATAACA TTaAACCAAT ATTCTGAGTG AAAGTaAACA ATTGCCGTT	720
CACGTGTTAT CCAAGTTCTT CCGTCACTTT CAGTCACTAA CGTATGATCA TTTCCACCAA	780
TGACAACATG ATCAGTACCC TTTAATATTG TTGTTTCAGA CCAAACGCGA TGAATCTTAC	840
CATCATGTTT ATA A CTCTGA ATTTTAATGT TTTCCCCTTC TTTAGGTATG GATTCTCTGA	900
CCATACTCCA CACCACCTTC TGTTAATTTA ACCATTATAA ATTATAGCAT ATTTCAGAAA	960
TAGTATTATA TAAATACATA TTTTACGAA ATAAGATTTT ACTACTTAAT AATTAACTC	1020
GGTAATATTG CTAAGTACT A CAACAGAGAT TTACATGTCC CATTTAAAGT ATATAAAATC	1080
ATCACTTTTA TATATCAACA CTTTAACTTT TTGACATTGT TATTCTATGA GATTTAAAGA	1140
TATCATTTAT ACTTTTTTAA ATTAATGTCA CTATGTTTTT CGATAATATT ACCAATCATC	1200
GAATGTTACC CATTTATAAA TTGATAAAATs TTTGACATAG GTAA G GGGAA TGTATATTGA	1260

TCTCGATCAC	TTAAATCAAA	CCAAATCATG	TCATCTGGTA	ATGTTTCAAT	GTTAATTGCT	1320
CCTGAAACGG	CGTATACTTT	AATCTTCCAT	GTTAAATGAG	TAAATTGATG	CTTCAACTCA	1380
AAAATAGGTG	TTTCTACTGG	TTGAATGTCA	TGACCGATTT	TTTCAGTCAT	TTTACGTCTA	1440
GCATGCTCAC	TTTCAAACAT	AGGAAATTGC	CACATACCAT	GCAATAATTT	TTCGCTACGC	1500
TTTTGCAACA	GATATTGACC	TTGATTATTT	CTAATTAAAA	AGACGGATTG	CTCAATTACT	1560
TTTTTACTTA	CATTTTTAGA	TTTAACAGGT	AACTTTTCAA	ATGTACCTTT	ATCAAATGCC	1620
TCACAGTTTT	CTTGAAGTGG	ACAAAATAAG	CATAATGGAT	TTTTTGGTGT	ACAAAATTAAC	1680
GCCCCTAATT	CCATCATAGC	TTGATTAAAC	GTTCCAGCTT	CTGTAGTAAC	ATACGGTAAT	1740
AATTCTTGTT	CGTACGATTT	CCTCGTCGAT	TGTAATTTAA	TATCTCGATA	GTCATCATTC	1800
AATCTAGACC	ATACTCGAAA	AACATTTCCG	TCTACAGTTG	CTAGTGGTAC	ATATATGCA	1860
ATGCTCATTA	CTGCAGCTTG	TGTGTATGGG	CCAACACCTT	TTAACGCTTT	AAATTGATCA	1920
GGATCTTTGG	GAACATAAGCC	TTCATATTTA	TCATGAAGTT	CTTTAATCGC	CGTATGAAAA	1980
TTTCGAGCTC	TACTATAATA	TCCTAAGCCT	TCCCAATACT	TTAACACTTC	ATCTTCCGAA	2040
GCTTGaCTCA	AAACTTCCAC	AGTTGGAAAT	CGTTCAACAA	AACGATGATA	ATAGTCAATA	2100
ACTGTTTTTA	CTTGTGTCTG	TTGTAACATG	ACCTCACTTA	ACCAAATATA	GTACGGATTG	2160
GTCGTTTGTC	GCCATGGCAT	TTCTCTTTGA	TTTTTCATCA	ACCAGTGTAT	CAAATTTTCT	2220
TTAAAACTAG	ACTGCTGATA	CATTTATAAA	ACCTTTTCCT	CACCAAATTT	AATTGTCTTT	2280
ACTCATAATG	TTTTTATTGT	ACATTAAAAAT	CATGGTTAGT	ATGTAAGTTA	ATTTAGTTAT	2340
TTGCGAAATT	GGATTATAAT	AGTATATATA	ATATTATGAA	ATGAGTGAAC	TGATATGGAC	2400
ACTGCAACAC	ATATCGCAAT	TGGGGTGGGC	CTTACAGCAC	TTGCAACTCA	AGATCCAGC	2460
ATGGCTTCTA	CGTTTGGTGC	AACAGCTACA	ACCCTTATCG	TTGGTTCATT	AATTCCTGAT	2520
GGGGATACTG	TTCTTAAATT	AAAGGACAAT	GCAACATATA	TTTCGCATCA	TAGAGGTATC	2580
ACGCATTCCA	TCCCTTTCAC	AATACTATGG	CCAATTTTAA	TTACATTTTT	AATATTCACG	2640
TTCTTTAGTG	GAACCAACCC	ATTTTCATGT	TGGATGTGGG	CTCAGCTCGC	AGTATTTTTA	2700
CATGTCTTTG	TAGATATATT	CAATTCTTAT	GGTACACAAG	CGCTTAGACC	TATCACAAC	2760
AAATGGATTTC	AATTAAGTGT	GATTAACACA	TTTGACCCTA	TTATTTTCAC	AGTTCTTTGT	2820
ATTGGTATTG	TATTATGGGT	TATAGGCTTG	CATCCATTTG	CAGTCTTCTT	TCCTATAATC	2880
GCTTTACTAA	TCATTTATTA	CATGATTTCG	TTTAAAATGA	GAGCCGTAAT	TAAGCAACAA	2940
GCTTTAAAAG	CAATTCAACA	AGAGCATCAC	CCTGTAAAG	TATTTGTTGC	GCCAACAATA	3000
AAATTTATGG	AATGGCGTGT	CGCGATACAA	ACTGATGCAC	ATGACTATGT	TGGAAAAGCA	3060

TATGGTAGGA ATGTGGTGT TAGTGATAAA GTGGAACGTC AAACATTATC AACAGACTCC	3120
ATTTTATGGA AAGTCAAAGG TAATAAAGAT ATACGTACTT TTTTAACTT TTCATCAATC	3180
TATCGTTGGC AAACAACAAC GTTAGCAGAT GGTTCCTACTG AAATTCGTTT GATTGATTTG	3240
CGTTATTTAA AAAATGATCA TTATTCATTT GTGGCAATTG CACATGTAAC AAACGATAAT	3300
GTCATAGACC ACTCTTATAT TGGCTGGGTA TTTACAGAAG ATAAGTTACA ACGTAAACTG	3360
TATGCTAAAT AATTTCAAGT TATTATTCAC TAAAGTTAAT CTATAAAAAA TGAACAACCG	3420
GGCAGAAATGA AAATCAAAAC GATTTTTTACT CTGTCCGGTT TTTTAATGA AACTATGAA	3480
TGCTTTTACA AAATCTAAAA TTTATATTGT TGCTAACAAA CTACCTTTAA TGACTCGAAA	3540
TATCAAAATC AGTATAGGAA AACAATATCT AGATGATATT CTAATTGTTT CTGATTCTCA	3600
CAGATTAATT TACACAACAG GTCAGCTAAA CATCATGAAG AAGTATCCGC CTCGTCTGTA	3660
CTATCATTTG AAACATCCTG TTGATTATCa GTTTGTGTCA CTTTAGATGT TTTATTaTAA	3720
ATTGCGTGTG TCGTATACCT TGCTAATACG AAATTTACTG CAGCTATTAA ACATAAGAAT	3780
AAAATAAAGT AAAAATGATA TGGAATGTTT TCCATACTTG ATATACCAA TATGATAGAT	3840
TGTGCTATAC CATTAACAAT GTAATACATT GGATTTAGCA TTAGGATGTG ATTGATAAAT	3900
ACATGATTTG GATTTGGTAT GAAAATAATT GGTAACAATA AGAAACACAA TACACAAACC	3960
CCATAAAATA TGATATTTAT TTTTTCAGwT AACAGTCGAA TAAGACCAA AGTAACGGAT	4020
ATTAATCCTA CAAAATAGT TGCCATCACA ATAAATAGA ATAGCGCTAT ATATSTGTT	4080
TCGAAGTTTA CTGGTTTAAAC CAATGCACTA ATCATCGTCA AAATGACTAG CATAATAAAA	4140
CTTAAATAG ACATAATAAC TACTGGCGTC G	4171

(2) INFORMATION FOR SEQ ID NO: 470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9821 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

TGGTTGAAGT AGCAGTTAAT TCAAAATCTG CAACAGTTTC AGCAGAATaG GGGCTTTCAA	60
AATAAtCAAA GGAGAATAAT TTATGACTAA AACTTTAAAG GTTTATAAAG GAGACGACGT	120
CGTAGCTTCT GAACAAGGTG AAGGCAAAGT GTCAGTAACT TTATCTAATT TAGAAGCGGA	180
TACAACTTAT CAAAAGGTA CTTACCAAGT GGCATGGGAA GAAAATGGTA AAGAATCTAG	240
TAAAGTTGAT GTACCTCAAT TCAAAACCAA TCAATTCTA GTCTCAGGCG TATCATTTAC	300
ACCAGAAACT AAATCAATTA TGGTAAATAC CGATGACAAT GTTGAGCCAA ACATTGCACC	360

AAGCACAGCA	ACGAATAAAA	TATTGAAATA	TACAAGTGAA	CATCCAGAAT	TTGTTACTGT	420
AGATGAAAAT	ACAGGAGCAA	TTCACGGTGT	AGCTGAAGGT	ACTTCAGTAA	TCACTGCTC	480
GTCTACTGAT	GGAAGCGATA	AGTCAGGACA	AATTTTCAGTG	ACAGTAACAA	ACGGATAGGG	540
ATTTAAGGCG	CAGTATATCT	GCGTCTTTTT	TATTTGAATA	AAAGGAGCTA	ATACAATGAT	600
TAAATTTGAA	ATTAAAGATC	GTAAACAGG	AAAAACAGAG	AGCTATACAA	AAGAAGATGT	660
AACAATGGGC	GAACAGAAAA	ATGCTATGAG	TATTTAGAAT	TAGTAAATCA	AGAGAATAAA	720
AAAGAAGCAC	CTAACGCAAC	AAAAATGAGA	CAAAAAGAGC	GACAGTTATT	AGTAGATTTA	780
TTTAAAGATG	AAGGATTGAC	TGAAGAAGAT	GTTCTGAACA	AGATGAGTAC	TAAAACTTAT	840
ACAAAAGCCT	TACAAGATAT	ATTTTCGAGAA	ATCAATGGTGAAGATGAAGA	AGATTCAGAA		900
ACTGAACCAG	AAGAGATGGG	AAAGACAGAA	GAACAATCTC	AATAAAAGAC	ATTTTATCGA	960
ACATTAAGAA	AATACAACGT	TTCTGTATGG	AGCAGTATGG	GTGGACATTA	ACTGAAGTCA	1020
GAAAACAGCC	GTATGTAAAA	CTTTTAGAAA	TACTTAATGA	AGAGAATAAA	GAAGAGACTG	1080
AAGAAAAACA	AAGTGAACAA	AAAGTCATTA	CAGGTACGGA	TTTAAGAAAA	CTTTTTGGAA	1140
GCTAGAAAGG	AGGTTAATAT	GAATGAAAAA	GTAGAAGGCA	TGACCTTGGG	GCTGAAATTA	1200
GACCATTTAG	GTGTCCAAGA	AGGCATGAAA	GGTTTAAAGC	GACAATTAGG	TGTTGTTAAT	1260
AGTGAAATGA	AAGCTAATCT	GCAGCATTTT	GATAAGTCTG	AAAAATCAAT	GGAAAAATAT	1320
CAGGCGAGAA	TTAAGGGGTT	AAATGATAGG	CTTAAAGTTC	AAAAAAAGAT	GTATTCTCAA	1380
GTAGAAGATG	AGCTTAAACA	AGTTAACGCT	AATTACCAA	AAGCTAAATC	CAGTGTAAAA	1440
GATGTTGAGA	AAGCATATTT	AAAGTTAGTA	GAAGCCAATA	AAAAAGAAA	ATTAGCTCTT	1500
GATAAATCTA	AAGAAGCCTT	AAAATCATCG	AATACAGAAC	TTAAAAAAGC	TGAAAATCAA	1560
TATAAACGTA	CAAATCAACG	TAAACAAGAT	GCGTATCAAA	AACTTAAACA	GTTGAGAGAT	1620
GCAGAACAAA	AGCTTaaGAA	TAGTAACCAA	GCTACTACTG	CACAACTAAA	AAGAGCAAGT	1680
GACGCrtACA	GAAGCAGTCC	GCTAAGCATA	AAGCACTTGT	TGAACAATAT	AAACAAGAAG	1740
GCAATCAAGT	TCAAAAACATA	AAAGTGCAAA	ATGACAATCT	TTCAAAATCA	AATGATAAAA	1800
TTGAAAGTTC	TTACGCTAAA	ACTAATACTA	AATTAAGCA	AACAGAAAAA	GAATTTAATG	1860
ATTTAAACAA	TACTATTAAG	AATCATAGG	CTAATGTGCG	AAAAGCTGAA	ACAGCTGTTA	1920
ATAAAGAAAA	AGCTGCTTTA	AATAATTTGG	AGCGTTCAAT	AGATAAAGCT	TCATCCGAAA	1980
TGAAGACTTT	TAACAAAGAA	CAAATGATAG	CTCAAAGTCA	TTTCGGTAAA	CTTGCAAGTC	2040
AAGCGGATGT	CATGTCAAAG	AAATTTAGTT	CTATTGGAGA	CAAAATGACT	TCCTGGGAC	2100
GTACAATGAC	GATGGGCGTA	TCTACACCGA	TTACTTTAGG	TTTAGGTGCA	GCATTAAAAA	2160

CGAGTGCAGA	CTTTGAAGGG	CAAATGTCTC	GAGTTGGAGC	GATTGCACAA	GCAAGCAGTA	2220
AAGACTTAAA	AAGCATGTCT	AATCAAGCGG	TTGACTTAGG	AGCTAAAACA	AGTAAAAGTG	2280
CTAACGaAGT	TGCTAAAGGT	ATGGAAGAAT	TGGCAGCTTT	AGGCTTTAAT	GCCAAACAAA	2340
CAATGGAGGC	TATGCCAGGT	GTTATCAGCG	CAGcAGaAGC	AAGTGGTGCA	GAAATGGCTA	2400
CAACTGCAAC	TGTAATGGCT	TCAGCGATTA	ACTCTTTCGG	TTTAAAAGCA	TCTGATGCAA	2460
ATCATGTTGC	TGATTTACTT	GCGAGATCAG	CAAATaTAG	TGCTGCAGAT	ATTCAATATA	2520
TGGGAGATGC	ATTAAAATAT	GCAGGTACTC	CAGCAAAAGC	ATTAGGAGTT	TCAATAGAGG	2580
ACACTTCTGC	AGCAATTGAA	GTTTTATCTA	ACTCAGGTTT	AGAGGGGTCT	CAAGCAGGTA	2640
CTGCATTAAG	AGCTTCGTTT	ATTAGGCTAG	CTAATCCAAG	TAAAAGTACA	GCTAAGGAAA	2700
TGAAAAAATT	AGGTATTCAT	TTGTCTGATG	CTAAAGGTGA	GTTTGTTGGA	ATGGGCGAAT	2760
TGATTAGACA	GTTCCAAGAT	AACATGAAAG	GCATGACGAG	AGAACAAAAA	TTAGCAACAG	2820
TGGCTACAAT	AGTTGGCACT	GAAGCAGCAA	GTGGATTTTT	AGCCTTGATT	GAAGCGGGTC	2880
CAGATAAAAT	TAATAGCTAT	AGCAAATCAT	TGAAGAACTC	TAATGGTGAA	AGTAAAAAAG	2940
CAGCTGATTT	GATGAAAGAT	AACCTCAAAG	GTGCTCTGGA	ACAATTAGGT	GGCGCTTTTG	3000
AATCGTTAGC	AATTGAAGTT	GGTAAAGATT	TAACGCCTAT	GATTAGAGCA	GGTGCGGAAG	3060
GATTAACAAA	ATTAGTTGAT	GGATTTACAC	ATCTTCCTGG	TTGGTTAGA	AAGGCTTCGG	3120
TAGGCTTAGC	AATTTTTGGT	GCATCTATTG	GTCCTGCTGT	TCTTGCTGGT	GGCTTATTAA	3180
TACGTGCAGT	TGGGAGCGCG	GCTAAAGGCT	ATGCATCATT	AAATAGACGC	ATTGCTGAAA	3240
ATACAATTCT	TTCTAATACC	AATTCAAAAG	CAATGAAATC	TTTAGGTCTT	CAAACATTAT	3300
TTCTTG GTTC	TACAACAGGA	AAAACGTCAA	AAGGCTTTAA	AGGATTAGCC	GGAGCTATGT	3360
TGTTTAATTT	AAAACCTATA	AATGTTTTGA	AAAATTCTGC	AAAGCTAGCA	ATTTTACCGT	3420
TCAAAC TTTT	GAAAAACGGT	TTAGGATTAG	CCGCAAAATC	CTTATTTGCA	GTAAGTGGAG	3480
GCGCAAGATT	TGCTGGTGTA	GCCTTAAAGT	TTTTAACAGG	ACCTATAGGT	GCTACAATAA	3540
CTGCTATTAC	AATTGCATAT	AAAGTTTTTA	AAACCGCATA	TGATCGTGTG	GAATGGTTCA	3600
GAAACGGTAT	TAACGGTTTA	GGAGAAACTA	TAAAGTTTTT	TGGTGGCAAA	ATTATTGGCG	3660
GTGCTGTTAG	GAAGCTAGGA	GAGTTTAAAA	ATTATCTTGG	AAGTATAGGCAAAAGCTTCA		3720
AAGAAAAGTT	TTCAAAGGAT	ATGAAAGATG	GTTATAAATC	TTTGAGTGAC	GATGACCTTC	3780
TGAAAGTAGG	AGTCAACAAG	TTTAAAGGAT	TTATGCAAAC	CATGGGCACA	GCTTCTAAAA	3840
AAGCATCTGA	TACTGTAAAA	GTGTTGGGGA	AAGGTGTTTC	AAAAGAAACA	GAAAAAGCTT	3900
TAGAAAAATA	CGTACACTAT	TCTGAAGAGA	ACAACAGAAT	CATGGAAAAA	GTACGTTTAA	3960
ACTCGGGTCA	AATAACAGAA	GACAAAGCAA	AAAAACTTTT	GAAAATTGAA	GCGGATTTAT	4020

CTAATAACCT TATAGCTGAA ATAGAAAAAA GAAATAAAAA GGAACCTCGAA AAAACTCAAG	4080
AACTTATTGA TAAGTATAGT GCATTTCGATG AKAAGAAAA GCAAAACATT TTAAC TAGAA	4140
CTAAAGAAAA AAATGACTTG CGAATTAAAA AAGAGCAAGA ACTCAATCAG AAAATCAAAG	4200
AATTGAAAGA AAAAGCTTTA AGTGATGGTC AGATTTCAGA AAATGAAAGA AAAGAAATTG	4260
AAAAGCTTGA AAATCAAAGA CGTGACATCA CTGTTAAAGA ATTGAGTAAG ACTGAAAAG	4320
AGCAAGAGCG TATTTTAGTA AGAATGCAAA GAAACAGAAA TGCTTATTCA ATAGACGAAG	4380
CGAGCAAAGC AATTAAAGAA GCAGAAAAAG CAAGAAAAGC AAGAAAAAAA GAAGTGGATA	4440
AGCAGTATGA AGATGATGTC ATTGCTATAA AAAATAACGT CAACCTTTCT AAGTCTGAAA	4500
AAGATAAATT GTTAGCTATT GCTGATCAAA GACATAAGGA TGAAGTAAGA AAGGCAAAAT	4560
CTAAAAAAGA TGCTGTAGTA GACGTTGTTA AAAAGCAAAA TAAAGATATT GATAAAGAAA	4620
TGGATTTATC CAGTGGACGT GTATATAAAA ATACTGAAAA GTGGTGGAAAT GGTCTTAAAA	4680
GTTGGTGGTC TAACTTTAGA GAAGACCAAA AGAAGAAAAGTGATAAATAC GCTAAAGAAC	4740
AAGAAGAAAC AGCTCGTAGA AACAGAGAAA ATATAAAGAA ATGGTTTGA AATGCTTGGG	4800
ACGGCGTAAA AACTAAAAC TGGTGAAGCCT TTAGTAAAAT GGGCAGAAAT GCTAATCATT	4860
TTGGCGGCGA AATGAAAAAA ATGTGGAGTG GAATCAAAGG AATTCCAAGC AAATTAAGTT	4920
CAAGTTGGAG CTCAGCCAAA AGTTCTGTAG GATATCACAC TAAGGCTATA GCTAATAGTA	4980
CTGGTAAATG GTTTGGAAAA GCTTGGCAAT CTGTTAAATC GACTACAGGA AGTATTTACA	5040
ATCAAATAA GCAAAAGTAT TCAGATGCCT CAGATAAAGC TTGGGCGCAT TCAAAATCTA	5100
TTTGGAGAGG CACATCAAAA TGGTTTAGCA ACGCATATAA AAGTGCAAAG GGTGGCTAA	5160
TAGATATGGC TAATAAATCG CGCTCGAAAT GGGATAATAT TTCTAGTACA GCATGGTCGA	5220
ATGCAAAATC CGTTTGGAAA GGAACATCGA AATGGTTTAG TAACTCATAC AAATCTTTAA	5280
AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACGATCG TTTTGATCA ATTTCAAGTT	5340
CGGCATGGTC TAACGCTAAA TCAGTATTTA ATGGTTTTAG AAAATGGCTA TCAAAAACAT	5400
ATGATTGGAT TAGAGATATT GGTAAAGACA TGGGAAGAGC TGCGGCTGAT TTAGGTAAAA	5460
ATGTTGCTAA TAAAGCTATT GGCGGTTTGA ATAGCATGAT TGGCGGTATT AATAAAATAT	5520
CTAAAGCCAT TACTGATAAA AATCTCATCA AGCCAATACC TACATTGTCT ACTGGTACTT	5580
TAGCAGGAAA GGGTGTAGCT ACCGATAATT CAGGAGCATT AACGCAACCG ACATTTGCTG	5640
TATTAAATGA TAGAGTTCT GGAAACGCCC CAGGTGGTGG AGTTCAAGAA ATAATCACA	5700
GGGCTGACGG AACATTCCAT GCACCCCAAG GACGAGATGT GGTTGTTCCA CTAGGAGTTG	5760
GAGATAGTGT AATAAATGCC AATGACACTC TGAAGTTACA GCGGATGGGT GTTTTGCCAA	5820

AATTCCATGG TGGTACGAAA AAGAAAAAAT GGATGGAACA AGTTACTGAA AATCTTGGTA	5880
AAAAAGCAGG GGACTTCGGT TCTAAAGCTA AAAACACAGC TCATAATATC AAAAAGGTG	5940
CAGAAGAAAT GGTGGAAGCG GCAGGCGATA AAATCAAAGA TGGTGCATCT TGGTTAGGCG	6000
ATAAAATCGG CGATGTGTGG GATTATGTAC AACATCCAGG GAAACTAGTA AATAAAGTAA	6060
TGTCAGGTTT AAATATTAAT TTTGGAGGCG GACTAACGCT ACAGTAAAAA TTGCTAAAGG	6120
CGCGTACTCA TTGCTCAAAA AGAAATTAGT AGACAAAGTA AAATCGTGGT TTGAAGATTT	6180
TGGTGGCGGA GGCGATGGAA GCTATCTATT TGACCATCCA ATTTGGCAAA GGTTCGGAG	6240
TTACACAGGT GGACTTAACT TTAATGGCGG TCGTCACTAT GGTATCGACT TTGGTATGCC	6300
TACAGGAACG AACATTTATG CTGTTAAAGG CGGTAAAGCT GATAAAGTAT GGACTGATTA	6360
CGGTGGCGGT AATTCTATAC AAATTAAGAC CGGTGCTAAC GAATGGAACT GGTATATGCA	6420
TTTATCTAAG CAATTAGCAA GACAAGGCCA ACGTATTAAA GCTGGTCAAC TGATAGGGAA	6480
ATCAGGTGCT ACAGGTAATT TCGTTAGAGG AGCACACTTA CATTTCCAAT TGATGCAAGG	6540
GTGCGATCCA GGAATGATA CAGCTAAAGA TCCAGAAAAA TGGTTGAAGT CACTTAAAGG	6600
TAGTGGCGTT CGAAGTGGTT CAGGTGTTAA TAAGGCTGCA TCTGCTTGGG CAGGCGATAT	6660
ACGTGCTGCA GCAAAACGAA TGGGTGTTAA TGTTACTTCG GCTGACGTAG GAAATATCAT	6720
TAGCTTGATT CAACACGAAT CAGGAGGAAA TGCAGGTATA ACTCAATCTA GTTCGCTTAG	6780
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AGCGTTCTTT AACAACAGAT ATTGGCGCTC ACAGTTTAAAC CCAGAGGTG GTTGGTCTCC	6960
AAGTGGTCCA AGAAGATATG CGAATGGTGG TTTGATTACA AAGCATCAAC TTGCTGAAGT	7020
GGGTGAAGGA GATAAACAGG AGATGGTTAT CCCTTTAACT AGACGTAAAC GAGCAATTCA	7080
ATTAAC TGAA CAGGTTATGC GCATCATCGG TATGGATGGC AAGCCAAATA ACATCACTGT	7140
AAATAATGAT ACTTCTACAG TTGAAAAATT GTTGAAACAA ATTGTTATGT TAAGTGATAA	7200
AGGAAATAAA TTAACAGATG CGTTGATTCA AACTGTTTCT TCTCAGGATA ATAACCTAGG	7260
TTCTAATGAT GCAATTAGAG GTTTAGAAAA AATATTGTCA AAACAAAGTG GGCATAGAGC	7320
AAATGCAAAT AATTATATGG GAGGTTGAC TAATTAATGC AATCTTTTGT AAAAATCATA	7380
GATGGTTACA AGGAAGAAGT AATAACAGAT TTTAATCAGC TTATATTTTT AGATGCAAGG	7440
GCTGAAAGTC CAAACACCAA TGATAACAGT GTAAC TATTA ACGGAGTAGA TGGTATTTTA	7500
CCGGGCGCAA TTAGTTTTGC GCCTTTTTCA TTAGTATTAA GGTTTGGCTATGATGGTATA	7560
GATGTTATAG ATTTAAATTT ATTTGAGCAT TGGTTTAGAT CTGTGTTTAA TCGCAGACAT	7620
CCTTATTATG TTATTACTTC TCAAATGCCT GGTGTTAAAT ATGCAGTGAA TACAGCTAAT	7680

GTTACATCTA	ATTTAAAAGA	TGGTTCTTCA	ACTGAAATTG	AAGTAAGTTT	AAATGTTTAT	7740
AAAGGGTATT	CTGAATCAGT	TAATTGGACC	GATAGCGAGT	TCTTATTCGA	CTCTAATTGG	7800
ATGTTTGAAA	ATGGAATTCC	TCTTGATTTC	ACACCTAAAT	ATACTCATAC	ATCAAATCAA	7860
TTTACTATTT	GGAACGGTTC	TACTGATACG	ATAAATCCAC	GATTCAAGCA	CGATTTGAAA	7920
ATATTAATTA	ATTTAAATGC	GAGTGGAGGA	TTGAACTGG	TTAATTATAC	AACAGGTGAT	7980
ATTTTTAAGT	ACAACAAAAG	TATAGATAAA	AACACTGATT	TTGTTTTAGA	TGGTGTGTAT	8040
GCATATCGAG	ATATAAACAG	AGTGGGAATT	GATACAAATA	GAGGCATTAT	AACATTAGCG	8100
CCAGGTAAAA	ATGAATTTAA	GATTaAAGGA	GACGTCAGTG	ATATTTAAAC	TACATTTAG	8160
TTTCCTTTTA	TTTATAGGTA	GGTGATTTAA	TGGATTATCA	TGATCATTTA	TCAGTAATGG	8220
ATTTTAATGA	ATTGATTTGT	GAAAATTTAC	TAGATGTAGA	TTACGGTTCT	TTTAAAGAAT	8280
ATTATGAACT	GAATGAAGCT	AGGTACATCA	CCTTTACAGT	TTATAGAACT	ACTCATAATA	8340
GTTTTGTTTT	TGATTTATTG	ATTTGTGAAA	ACTTCATAAT	TTATCATGGT	GAAAAATACA	8400
CAATTAAGCA	GACAGCGCCA	AAGGTTGAAG	GTGATAAAGT	TTTTATTGAA	GTTACGGCAT	8460
ATCACATAAT	GTATGAATTT	CAAAATCACT	CAGTGGAAATC	AAATAAGCTT	GATGACGACA	8520
GTAGCGAAAC	TGGTAAAACG	CCAGAATACT	CTTTAGATGAGTACTTAAGA	TATGGATTTG		8580
CAAATCAAAA	AACGTCAGTC	AAGATGACCT	ATAAAATAAT	TGGAGATTTT	AAAAGAAAAA	8640
TACCAATTGA	TGAATTAGGT	AATAAAAATG	GCTTAGAATA	TTGTAAAGAA	GCAGTAGATT	8700
TGTTTGTTTG	TATTATTTAT	CCAAATGATA	CGGAGATATG	TTTTTTATTCT	CCTGAAACAT	8760
TCTATCAAAG	AAGCGAAAAA	GTAATAAGGT	ATCAATATAA	TACTGATACT	GTGTCTGCTA	8820
CTGTCAGTAC	GTTGGAATTA	AGAACAGCTA	TAAAAGTTTT	TGGGAAAAAG	TACACAGCCG	8880
AGGAAAAGAA	AAATTATAAT	CCTATTAGAA	CAACTGACAT	TAAATATTCA	AATGGTTTTA	8940
TAAAAGAAGG	TACTTATCGT	ACGCAACAA	TTGGGTCTAA	AGCTACTATT	AACTTTGATT	9000
GCAAGTATGG	TAATGAAACA	GTTAGATTTA	CAATAAAaAA	GGGCTCTCaA	GGTGGAAATAT	9060
ATAAGTTGAT	TTTAGACGGC	AAGCaAATTA	AGCaAATTTT	TTGTTTTGCT	AAGTCGGTTC	9120
AGTCTGAmAC	AATAGATTTA	ATAaAAAAATA	TTGATAAAGG	CAAGCAGTT	TTAGAAATGA	9180
TATTTTTTrGG	AGArGrCCCC	AAAAATAGAA	TTGATATATC	TTCAAATAAA	AAAGCTAAGC	9240
CTTGTATGTA	TGTTGGAAC	GAAAAATCAA	CAGTCTTAAA	TTTAATTGCT	GACAACTCAG	9300
GTCGCAATCA	ATACAAAGCA	ATTGTTGaCT	ACGTCGCAGA	TAGTGCAAAG	CAGTTTGGGA	9360
TTGCATATGC	TAATACGCAA	ACAAATGAAG	ATATCGAAAC	ACAGGATAAG	CTGTTAGAAT	9420
TTGCAAAAAA	GCAAATAAAT	GATACTCCTA	AGACTGAATT	AGATGTTAAT	TATATAGGTT	9480

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CTGAATTAAA GGTTGTTAAA CTTGATAGT CACATCCATT TGTAACGCA ATAGATGAAG	9600
TGTCTTTCAG CAATGAAATA AAGGATATGG TACAAATTCA ACAAGCGCTT AACAGACGAG	9660
TTATTGCACA AGATAATAGA TATAACTATC AAGCAAATCG TATAAATCAT TTATACACTA	9720
GTACTTTGAA TTCTCCTTTC GAGACAATGG ATATAGGGAG TGTATTAATA TAAGGCAAC	9780
AGAAGAAGTT AAAATCAAAG CGCTACTTGA AAACGATAAA C	9821

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

TTATTGTTTT CCAAATGGTC TTCTCGGTTA TTTAACCATC GGTTTCAATC CTACGTGCTT	60
CACTTTCTAT CtATTAATTC AaTTTCAGCT TGACCACCCG CTGTATAAAG GGTCAAAGTT	120
GCTAATCGAT AGCGTCTCAT TATAGGACCA ACATCGATAT CAATATTTTG AATACGAAAA	180
TATGGTATTA CCTTTTCATC CAAAAATAAA ATGCCGTTTC GTACACGCAA ATGGTGTTTT	240
TCAAATGCAT ATCTGCAGTG CTTATATCGA TAGACTGGCG CTATAACAAG CGTGAAAACA	300
GCAACAAGTA ATATTATAAT CACACTACTA CAATGGATA AATGGTTATC TAAAATCTCC	360
CAAAATAGCC AGTTCAAAT ATTAATGCG ATTAAGTA CAAGCGCTAT GGGTATCCAA	420
AACAGCACAG CACTTAACCT CATCACTTTT TTAGCGTGTG GTGACATAAA ATTATAATCC	480
CTCATCATTT TCACCTCTTA AATACCATGA TTTCAATTTA TTTGCATCTT CACTTCTGC	540
GTATTTTAAG TTAATCGATT GGGCTCCCAC ACCTTTAGCA ACAATAAAGC TAAATTATT	600
TAAATTGTTG CGTTTAAGTA ATGTATGTTG CCAAGTGTCA AATCCTATAA TGTGATGCGC	660
TTTAAAATAA TAAATATTTT GTTTCAATAG CTCGAAATTC TGGATAGTAA TTTGTTCTTC	720
TGTCATTTTA AAACCCGCAT GTTTGACATA AAGATATCCT TTGATCACAA ATAAACCAAT	780
AATGACTATT GTTATAATCG TAAATAACAA TAATAATTGA TTCCAAAAAT AACAGCCTAT	840
ACCTGCCATA GCTATGACAA TAATACTAGG TATTAAAAG TGTCTGTGGA AACCTGACAA	900
AGGCATACCT TCATTAACCT GTTGATAAGA TAAATCTGT ACTAAATTCT GGATAATTTG	960
ATATGCTTTG TCTCGTTTAA TAAACGGCaA TATCGGCACA CTACCTGAAT CATTGTC	1017

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

TAGGATTGAT TAATCCTTTC TTCAAAATGA TGAATGTGTA ATGTTAAATA TATAATTTCA	60
GACTCACTGA TATTAACATC AAATTGTTTT TGTATCATAG TTAAAATTTT ATATGCTGTG	120
TTATAGCAAA TCGGATAGTG ATTTTAAATC ATAGACACAA AATCATCTTG TGCATGTATA	180
TATTCTTTTC TTCTTAATCG GCGAATTAAA AATTGTACGT GCCTTATAAA ACGTTGGTAT	240
TGTAATGATT CCTTATCAAC AGTTGTCACA AGGTCTGATT CAATGATATC TATACCTTTT	300
TTAATAACAT TATTnGATCA AGGTCATCTC ATGCATAGAT AAATCTTCTG TATTaGATGC	360
AATATGTAAT GCAATAAATC CTATCTCATC TTCAGGaAAA TGTAaCATCTA ATGCTGCATT	420
TAACTGATCA ATCACCTGTT TAGCAATATG ATATGCATCA CTATATAACT GCATAGTTTC	480
CATAACAAAT GGATTGCTAA TAACTTGATT TTGTTTTAAG GTTTATAAG CAAATATAAT	540
ATGATCCGTT AATGAAACTA CAAGTTGTTT TGAATCAACA TTCATCGCAG TATTAGAAAT	600
AAAATTCAAC GAATCAATAA TTAATTGTAA TACATTATCA TCAGCGATTT CAACTAACT	660
TTTATAATGT GCTTTTTGTT GCTCACTTTC TAATTTATAA ATTTTCTCTA TTGTAATAGT	720
TTGGTCGTTT AACGCCATTC CCTCTTTTTT GTTAAAACCA ATACCTTTAC CGATTAAAT	780
AACTTCTTGA TCATTATTAG TACATACTAC GACATTGTTG TTCAATGTTT TAGTAACAAT	840
ATATTCTCCC ATTATCATCA CCTATTTTTT TATTATTAAG ATTATATATC GGAAATGTCT	900
AACTTGAAAG TATAATAATT TAATACTTG TGTTCTATTA CACGCCTATC CTATATGATA	960
TATCTTAATT TAATTTGAT GTCTCTCAAA GTGGAATAAC TATAATAAAA AAATCTGACT	1020
CCCATATTTA CAAATAATTC TATTTATTTA TATATTATCT GAATTAATAC TCAATACAA	1080
CTAAAACGTA CTATTAAATT GTGCAAAGCT AAAACAAATT TATATTCAE TATCCAACAA	1140
TATGTCTTAT CAATGGTATA GTCTTTGCAC ACCAATGGAG GAAATAAATC TCAACCTTAC	1200
TATATTAATA TATAATCAAA TCTTAGATTA ACTAGTGTA TGATACAGAT GATAATTGAG	1260
TACAAATTTA AAACCCTGAG ATTTTCGCTT TAATTTGAAA ACCTCAGGGT TTATTTGATT	1320
TTTATATAAT GAATCGTTAC ATTAAAAATA TTTATTTATC AGAGTTCTTA TATTTGTTAG	1380
CGCCCCAAGC ACTAATTCCA AATAAGTTAA TTTCTAAGTT TTCAGGTTTA AAGACAGGGT	1440
TCTTGCCCTC TTTTCTGCTC TTTTGATAAT CTTTCATCAA TGCAAAAGCT ACATTGGACA	1500
GTCCTATAAT GGAAATAATG TTTACAATTG CCATTAAGCC CATAAATAAG TCTGCCGTAT	1560

TCCATACTGT	TTCTGTTTTT	ACAACTGCAC	CGACAAAGAC	AAGTACTACA	ACAAGACATC	1620
TAAAGATAAA	TAATATTACA	CGGTTTGTG	ATAAAAATTC	AATATTAGAT	TGACCGTAAT	1680
AGTAATTACC	TACAACAGAT	GAAAATGCAA	ACAGTGTAAC	tGCTaTTGTT	AAGAAATAC	1740
CTCCAGCAGA	ACCTAAATGC	TCATTAAGTG	CTGATTGAGT	AACTGCAACA	CCTTGAGGTG	1800
CGTTATCACC	AAATTTTCAGT	CCTGAATATA	GTAAAATCAT	GATTGCAGTT	GCTGTACAAA	1860
CCAACATTGT	ATCAAAGAAC	ACACCTAATG	ATTGGATTAA	ACCTTGCTTA	ACAGGGTGTG	1920
GTACGGCAGC	AGTTGCCGCT	GCATTTCGGCG	CAGAACCCAT	ACCAGCTTCG	TTAGAGAATA	1980
AACCACGTTT	GATACCTTGA	AGAACCGCAG	CACCTACAGC	GCCACCAGTT	ACTTGTTCTGA	2040
TACCAAATGC	ACTTTTAATA	ATCGTACCTA	TCATAGGAAC	AATTTGATCT	AAATTAAATA	2100
GCAATATTAC	TAAAACCATA	CCAATGTAAA	TGATAGC&T	AATCGGTACA	ATTAACGAAG	2160
ATAACGTAGC	AATACTACGT	ACACCACCAA	ATATAATAAT	AGCTGTTACG	ATTGCTAAAA	2220
TAATACCTGT	GATTACTGGA	CTAATATTAT	ATTGCGTATT	TAACGACTCC	GCAATTGTAT	2280
TAGATTGCAC	TGTGTTAAAT	ACAAATGCAA	ATGTAATTGT	AATTAAAATC	GCAAATACGA	2340
TACCTAGCCA	TTTTTGATTT	AAACCTTTAG	TAATATAGTA	AGCTGGACCA	CCACGGAATC	2400
CACCATCTTT	ATCATGTACT	TTATAAACCT	GAGCCAAAGT	CGCTTCTATA	AATGCACTCG	2460
CTGCACCTAT	AAATGCAATA	ACCCACATCC	AAAATACTGC	ACCTGGACCG	CCTAAAACAA	2520
TCGCAGTCGC	AACACCAGCA	ATATTACCAG	TACCAACTCT	CGAACCAGCA	CTAATCGCAA	2580
ATGCTTGGAA	TGGCGAAATA	CCCTTCTTAC	CATCTTCTAA	AGTTTCTGGA	CGTTCTACTA	2640
AAGCTCTAAA	CATTTTCAGGT	AACATTCGTA	ATTGAACGAA	TTTAGAACTA	ATCGTAAAGA	2700
AGAATCCAGC	TGTCAATAAT	AGACCAATTA	AATATTGAGA	CCAT&TAAA	TCGGTACCAA	2760
CATGGACAAA	TTCTTTAAAC	CATCCAGGTA	TTAAACTATC	GAAATCTTTC	AAAATAAACC	2820
CCTCGCATCC	TCTACATGAA	TCATGTACCT	TCTATAAAAT	TAGACCGAAT	TGAACCTTCA	2880
GTAAATATAG	AGATACATCA	TCATTTCTTA	TACAATACAA	GAGATTTATA	TTAGTTTGGT	2940
CAAAGTATAT	CGCTAATTTA	ACGATAAGTA	CTTGGTCAGC	ATTTAATATA	AATCCCTTGA	3000
ATTTAGTCAA	AATTTAACAT	TACTGTATTT	TATCATTTAA	TTTCGTGATT	GCATATAGTT	3060
TTTAGCTAAT	ATACATGTCT	ATTACTTCAC	CAAAATCATC	TGTATCTACA	ATGAATGAGC	3120
CATTTGTATA	TTGTTTCAGAT	TTATGA&TAT	CATTAATTAA	ACCATGTTCT	TCATTTGATT	3180
TTGAATATAA	TGTATATTGA	CTATGTTTAC	CTGTCACTAC	ATGTGCAGCT	ACAATACGAT	3240
GTGGATTTTT	CTTTAATTCT	TTTAATAAAG	TTATTCCaCG	TTGTGCTCTT	TTAGCAACTT	3300
GTAAGATTTT	AAAACATAA	CGTTTTAACG	AGCCGCGTTG	TGTGGCCATC	A&ATAGTAT	3360
CATTTTCAGA	AACACCTTCT	GTCATAACAA	CGAAATCTTC	AGCTTTAAGA	TTTATTGATT	3420

TAACACCAGC	TGCCCTTAAT	CCGGTATCTG	ATAGTTCAC	TGTATTATAC	GTTAATGACA	3480
TACCTTTATT	AGTAATGACG	GTAATTAATT	GATCTTTTTC	AAAGCGCATA	ACACTAATCA	3540
AATCATCAT	TTCTTTAACT	TTAGTAGCAA	TTAAAGGTTT	ATTAAAACGC	GTTGTTTTAA	3600
ATAGAGGCAC	TGTACTTTTC	TTAATCATGC	CATTTTGAGT	CGCAAAAACA	TAAAATGCAT	3660
CTGTATTAAA	GTCCTTTTCA	TTAAAGACAT	TAATAACCAC	TTCATCTTCT	TCGATAGGAA	3720
CTATTTGTGA	TACATGTTGT	CCCAATTCTT	TCCACGAAT	ATCTGCTAAT	TTATGAACCG	3780
GTATAAATAG	ATAACGACCT	TTATTTGTAA	ATACTAGTAC	GGTATCTTGC	GTATTTACTT	3840
CTTGATGTTT	AAGTAAACTG	TCACCATCTT	TTAAACCAAT	ATCTTCAACA	CCGCTAGCAT	3900
TAAAGCTACG	AATAGAAGTA	CGTTTAATAT	ATCCATGACG	TGTCATACTT	AAAATAACTy	3960
CTTCACTAGG	CACCATAACT	TCTTTGTCAA	TTTTAATTTT	TTCAATTCTT	GCTTCAATTA	4020
AAGACAGTCG	TTCAGATTTG	AATTTCTTTT	TAATTTTCATT	CAATTCTTCT	TTTATGACAT	4080
TCAATAATGC	ATCATGGTTA	TCAAGAATAT	GACGTAATTG	TTTGATTAAT	GCTTCAAGTT	4140
CTTTATGTTC	ACCTTCAAGC	GCAACTATGT	CAGTATTTGT	TAAACGATAT	AACTGTAACA	4200
TTACAATTGC	TTCAGCCTGT	TCTTCTGTGA	ACTCGTATAC	TTCGATAAGG	TTTTCTTTAG	4260
CGTCACGCTT	GTTTTTAGAG	CwACGAATCA	ATTCGATTAC	TTTATCTAAA	ATTGACAACG	4320
CTTTAATCAA	ACCTTCAACG	ATATGCATAC	GTTTTTCTGC	ATATCTAAT	TCAAACCTCG	4380
TTCTATTTGC	AACAACCTCA	ATTTGGTGAT	TCAAATAACT	ATCTATAATT	TGACGAATAC	4440
CCATCAATTT	TGGACGACCA	TCACTAATAG	CGACCATGTT	GAAATTATAT	GAAATCTGTA	4500
AATCAGAGTT	TTTATAAAGA	TAATTTTTGA	TTGATTCACT	GTTACATCT	TTTTTCAATT	4560
CAATTGCTAT	TCGTAAACCA	GTTCTATCAG	TTTCATCACG	TACTTCAACG	ATACCATCGA	4620
CTTTTTTGTG	AGCACGTAAT	TCATCGATAC	GTTTTACTAA	GCTACTTTTG	TTCACTTCAT	4680
ATGGAATTTT	AGTAATAATT	AACTGTTTAC	GTCCATTGCG	TAAAGTTTCT	TCTTCAACTT	4740
TAGAACGAAC	TATAATTCTA	CCTTACCTG	ATTCATAAGC	TTTTTTAATA	CCATCAATAC	4800
CTTGAATAAT	ACCACCAGTT	GGAAAATCAG	GACCTTTAAT	ATATTTTCATT	AATTGATTGA	4860
CTGTAATATC	CGGATTATCA	ATATATTTAA	GTGTTGCTTG	AATCACTTCA	GCTAAATTAT	4920
GTGGTGGTAT	ATCTGTCGCG	TAACCTGCAG	ATATACCTGT	AGAACCATT	ACTAGTAAGT	4980
TAGGAAATCT	TGATGGCAAT	ACCATTGGTT	CGAGTGTCGT	ATCATCATAG	TTTGGAAATGA	5040
AAGAACTGT	CTCTTTATTA	ATATCACGTA	ATAACTCTTC	AGCTAGTAAG	CTTAACTTAG	5100
CTTCAGTGTA	ACGCATTGCC	GCTGGCGGAT	CATTATCGAT	ACTACCATTA	TTACCATGCA	5160
TTTCTATTAA	GACATGTCGT	AACTTCCAGT	CTTGACTTAA	ACGGACCATT	GCTTCGTACA	5220

CTGAGGAGTC TCCATGTGGA TGATATTGAC CAATAACATC ACCGACTGTT TTCGCACTTT	5280
TACGGAAATT TTTATCGTGT GTATTACCAC TTGAATACAT TGCATATAAA ATACGACGTT	5340
GTA CTGGTTT TAAACCATCA CGAACATCTG GCAATGCACG CTCTTGAATA ATATATTTAC	5400
TATATCTTCC AAAGCGATCA CCTAAAACAT CTTCAAGTGA TAAATCTTGA ATTATTTTAC	5460
TCACTAGATT TCCTCCTCAT CAAATTGATC ATTTTCAAGC ACTTGTA CTT CAGAATTATC	5520
TAAAATACTT TGGTCCTCTT GCATACCAAA CTCAACATGC TTTTCAATCC ATTCAGTCT	5580
AGGTTGTACT TTGTCACCCA TTAATGTTGT TACACGTTTA GATGAACGCA CTTCATCTTC	5640
AACTTG TACA CGAATTAAAG TTCGTGTTTC TGGGTTCATC GTCGTTTCCC ATAATTGTTC	5700
AGGGTTCATT TCACCCAAAC CTTTGTAACG TTGTAACGTG AaGCCTTTAC CAAGTTCTTT	5760
TTGCAATTTA TTAAGCTCTT CGTCTGTCCA AGCGTATTCA ACTCGCTTTG TTTTGCCTTT	5820
ACCTTTTTTCC AATTTATAAA GTGGAGGTAA AGCAATAAAT ACACGACCTG CTTGAACAAG	5880
CGGTTTCATA TATTTGAAGA AGAATGT TAA CAATAGCACT TGAATATGCG CACCATCAGT	5940
ATCAGCATCA GTCATAATAA TTACACGATT ATAATTAGA TCTTCAATTT TAAAGTCAGT	6000
ACCAACGCCT GCCCCGATTG TGTGGATAAT TGTATTAATT TCTTCATTTT TAAAAATATC	6060
TTCTAGACGT GCTTTCTCTG TATTAATTAC CTTACCACGT AATGGTAATA TCGCTTGGA	6120
TTTGCGGTCT CGTcCAAGTT TTGCTGAACC TCCCGCAGAA TCACCTTCGA CTAAATACAA	6180
TTCATTTTTT TCAGTGTTTT TACTTTGTGC AGGTGTTAAT TTACCAGATA GCAAAGTGTC	6240
TTTACGCTTG TTTTCTTAC CTGAACGAGC ATCTTCACGA GCTTTACGTG CAGCTTCCCT	6300
TGCTTGTTGT GCTTTAATCG CTTTTTTCAC AAGTGATTTA GACAATTGTC CTTTTCTTC	6360
TAAATAGAAT GGCAATTTGT CTGCAACAAC TGAATCAACA GCACCTCTAG CTTCAGAAGT	6420
ACCCAATTTA GATTTCTGTTT GTCCTTCAAA TTGCAATAAT TCTTCTGGAA TACGAACAGA	6480
CACAACAGCT GTTAAACCTT CACGAATATC ATTACCATCT AAGTTTTTAT CTTTTGTTTT	6540
AAGTTCATTA ATACGACGTG CATAATCATT AAATACACGT GTCATGCTG TTTTAAACC	6600
AACTTCATGT GTACCACCAT CTTTAGTACG TACATTATTT ACAAACTTA AAATACTTTC	6660
TGAATATTGA TCATTATATT GGAAAGCTAC GTCTACCTCT ATACCATTG CTTACCTGA	6720
AAATGTAGCC ACGTCATGCA AACTTCTTT TCCTTCATTG ACATAACTAA CAACTCTTT	6780
GATTCCTTCT TATAATGGTA TGTCTT	6806

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

GGGGCAnAAA TTCCAATACA CTCATTACCA AATATATACA CCACTTCCTG CTACAAGTnn	60
TTTTACTTGA TCTTGGTCTT TTCCGCAGAA AGAGCATTTT CAAATTTTCT TCATCTTCCA	120
TTGAATTTAA ACATTCTTTT TACACCCCTA TTCGTAAAG ACTATACTAG ATTGGATGTT	180
ACAATGCAAC ATATTAACAT ACAAACTTTT TGCTTAAAGA ATAGTAGCAG ATACATAAGC	240
TAkGCaTCKG CTACTCaTTT TkGTAATTTA ATATTTAAAtG aAGATTAATC TTCTTTAGTT	300
CCtTCAACGA ACTTTGCGTT ATCTCTTAAT AAATCGATAA CTTTTTGET ACGAACATCA	360
TTTTTAATGA TATCAGTATT ACCTAAAGTA TTTTGTATAT CTTCAACTGA GATATTAAAT	420
TGTTTACTCA TTTTTTCTAA TTCTTTATCG ATATCTTCAT CAGTAGCTTC GATTTTTTCA	480
GCTTCAGCGA TCGCAGTTAA AGTTAAGTTA GTTTTAACAC GTTGTCTGC ATCGTCTTTC	540
ATTTGCTCTC TTAATTGAGT TTCATCTTGA CCTGAGATTT GGAAGTACGT TTGTAAATCT	600
AAACCTTGTT GTTGAATTCT TTGTGCAAAT TCAGACACCA TACGATCTAA TTCAGTATTA	660
ACCATTGCTT CAGGAATATC GATTGTTGTA TTATCAGTAG CTTTTGTAAT CGCTTCTTCT	720
TTTTCAACAT TTTCAGCATC TGTAGCTTTT TGTTTACGTA AACGTTTACG TAAGTTTTCT	780
TTGTACTCGT CTACTGTATT TGCTTCTGCA TCTAATTCAT TAGCAATTTT ATCTGTTAAT	840
TCTGGGACTT CTTTAAATTT AATTTTCGTTA ACTTTTGTTT TGAAAGTTGC TTCTTTACCG	900
GCTAATTCTT CAGCATGGTA TTCTTCTGGG AATGTTACGA CAACATCTTT TTCTTGTCA	960
ACTTTCATAC CTTCTAATTG CTCTTCGAAA CCAGGTATGA ATGAACCTGA ACCGATTTCT	1020
AAATCGTAAC CTTCAGCTTG TCCACCTTCG AATTCTTctC CGTCAACTGA ACCACTAAAG	1080
TCGATGTTAA CTGTGTCGCC ATTTTCAACA ACACCATCTT CTTTAACGAC CATTTTCACT	1140
AAATGTCCTA AGCTGTGGTC AATCGCTTCT TGTAACATCAT CATCAGATAA TTCAGTTTCT	1200
TGTTTTTCAA TTTCAAGACC TTTATAGTCT CCTAATTTAA CTTCTGGCTC AACTGTAAC	1260
GTTGCTTCAA AAATGAAATC TTTACCTTTT TCAATTTGAG TAACACTTAC TTCTGGTTGT	1320
GCAACTGGTT TAATATCAGT TTCGTCAATT GCTTCACAT AAGCATCTGG TAATAAAATG	1380
TCGATAGCAT CTTGATATAA TGCTTCTACA CCAAAGCGTT GTTCAAAAAT TGGACGTGGC	1440
ACTTTACCTT TACGGAATCC AGGTACGTTA ATTTGTTTAA CCACTTTTTT GAATGCTTGA	1500
TCTAACGCTT TGTTTACTTT TTCTGCAGGA ACAGTAACAG TTAATAAACC TTCGTTACCT	1560
TCCTTTTTTT CCCAAGTTGC TGTCATGTAT ATATACCTCC ATGATTAAC	1620
TTCAACTTCC CTATTATATC ATACGTCTAT TCCCTATACA AACATTGAAA TCACAACGTT	1680

TATATATTTG TAAATCAACT TTTTTCGTCA AAATA

1716

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

TGACCAAGTA CGTTTCGAAG TTGCCATTAA AGCATTAAC CCATCATTGA AAGCATTCGC	60
ACCTGTACGT GAGTGGGCAT GGAGTCGTGA AGAAGAAATC GATTATGCAA TTAAACATAA	120
TATCCCTGTA TCAATCAACC ATGATTCACC TTATTCTATC GATCAAAATC TATGGGGCAG	180
AGCGAATGAA TGTGGTATTT TAGAAGATCC TTATGCTGCGCCACCAGAGG ATGCGTTCGA	240
TCTAACAAAT GCTTTAGAAG AAACACCAGA TACTGCTGAT GrAATCATTT TAACGTTTGA	300
TAAAGGCATC CCAGTTCAA TTGATGGCAA AACATATGAA TTAGACGATT TAATTTTAAC	360
GTTGAATGCA TTAGCTGGTA AGCATGGTAT CGGAAGAATT GACCATGTAG AAAATAGACT	420
TGTAGGTATC AAATCAAGAG AAATTTATGA GGCACCTGCT GCAGAAGTTA TTTTAAAAGC	480
GCATAAAGCA TTAGAAACGA TTACGTTAAC GAAAGATGTC GCACACTTTA AACCAATCAT	540
TGAGAAGCAA TTTGCTGAAC AACTATACAA TGGACTTTGG TTCTCACCTT TAACTGATAG	600
CTTGAAATTA TTTATTGATA GTACTCAGCA ATACGTAAGT GGTGATGTCA GAATTAAATT	660
ATTCAAAGGT AATGCCATCG TGAATGGTAG AAAATCACCT TACACATTAT ATGATGAAAA	720
ATTAGCAACT TATACAAAAG AAGATGCATT ThATCAAGAC GCTGCTGTTG GCTTTATCGA	780
TATCTATGGT TTACC	795

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

CGATTGAAAG AAGACGGTTC AGTTGAAAAG TTTCAAAGC CAGTAATTAG CCAACAACCA	60
GAAGGATATA CGAGTCATTT TAGAGATCCT AAAGTTTTTA AATATGATGr GaAATATTAT	120
GCAATCaTTG GTGCMCaAAA TAATGATCaG CaAGGTCGAT TATTACTTTA TAATACTGAA	180
GATATAATTA ATTGGCATT TTTAGGTGAA ATAAATACAG AGTTGGATGA TTTTGGATAT	240

ATGTGGGAAT GCCCAGATTA CTTTAATGTA GATAATCAAG ATGTCATACT TATTTGTCCA	300
CAAGGTATTG AACCAAAGG CGATCAGTTC AAAAATATTT ATCAAAGTGG TTATATACTT	360
GGAAAGTTTG ATATTGAAAA GTTAAATAT GAACATGAAA ATTTTGTCGA GCTTGATAAT	420
GGTTTTGATT TCTATGCACC TCAAACATTT TTAGATGAAA AAGGCCGACG AGTACTAATT	480
GGATGGATGG GGTTACCGGA AATCGAATAT CCTACTGATA ATGAAGGATG GGCCCATTGC	540
TTAACAATTC CTCGTGTATT AAATGTAGAA AATGGTCAAC TTAAGCAACG TCATATCCA	600
GCGTTGGAAA AATTACGTCA CAATAAAGAG ACAGCATTTA GGctACGCAA ATAAATTTAC	660
TCGAAAATTA CATCCGTATG AAGGTAAACA GTATGAATTA ATCATAGATA TTTTGGATAA	720
TGATGCTACC GAAGTGTACT TTGAATTACG TACATCTAAG ACTTCTTCAA CATTAATTGC	780
TTATAACAAG CGTGAAAATA AAATAACATT AGATCGCAGC GACAGTGGTT TATTGCCGAC	840
AAATGTTGAA gGTACGACGC GTAGTACGAT ATTAGACACG CCATTAA	887

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

TTGGAA _n CAA AAAACCATTG GTAAACCGTG TTA _n AACCGGA TTTCCGATGG ACCTTTTAA	60
AC _n ACCAAAT AGAAAGCTTT GATAAAAG _t AATTATGGTA CTGATAACAA ACAAGTTCAA	120
AAACATCATG ATTTAGTACG TATGCTTTTG ATGGATCAAG ATGGTTTTTTT AACTGAAAAT	180
AATAAAGTTG ATCATTTTCAT TGATGGAAAT GATTTATATG ATCAAGTTTT AAAAGATATT	240
AAAAATGCAA AAGAtATATC CATTTAGAGT ACwATACTTT CGCTTwAGAT GGTWAGGTA	300
AAAGAATTTT ACATGCTTTA GAAGAAAAAT TGAAACAAGG TCTAGAAGTA AAAATATTAT	360
ATGATGATGT TGGATCTAAA AATGTTAAGA TGGCAAATTT TGATCATTTT AAATCGTTAG	420
GTGGAGAAGT TGAAGCATTT TTTGCTTCAA AATTACCGTT ATTGAATTC AGAATGAATA	480
ATAGAAATCA TAGAAAAATC ATCGTAATCG ATGGTCAACT AGGTTATGTC GGAGGATTTA	540
ACATTGGTGA TGAATATCT _m GGATTAGGAA AATTAGGATA TTGGAGAGAT ACGCATTTAC	600
GTATACAAGG GGATGCGGTT GATGCACTGC AGTTGCGATT TATTTTAGAC TGGAATTCGC	660
AAGCGACCG TCCACAATTT GAATATGATG TTAAGATTT CCCTAAAAAG AACGGACCAT	720
TGGGCAATTC ACCAATTCAA ATAGCTGCAA GTGGCCCGGC TAGTGACTGG CATCAAATTG	780

AATACGGTTA TACAAAAATG ATTATGAGTG CAAAGAAATC TGTATATTTA CAATCACCAT	840
ATTTTCATTCC GGATAATTCA TATATaAATG CCATTAAAAT TGCTGCTAAA TCAGGTGTAG	900
ATGTACATTT AATGATTCCA TGTAAGCCAG ATCATCCATT AGTATATTGG GCGACATTTT	960
CAAATGCCTC TGACTTATTA TCAAGTGGTG TTAAAATTTA TACGTATGAA AATGGATTTA	1020
TACATTCTAA AATGTGCTTA ATTGATGATG AAATCGTATC AGTGGGCACA GCAAATATGG	1080
ACTTTAGAAG TTTTGAATTA AATTTTGAAG TAAATGCCTT TGTATATGAT GAAAATCTTG	1140
CTAAAGATTT AAGGGTGGCT TATGAACATG ATATTACAAA ATC	1183

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

GGTTATATGT TTGGTATTAC TCATTATATT GATTGGAGGT TGTGTCATTA TGACAAAAAC	60
AAATGGTCGA AACGCTCAAA TTAAAGAAAA TTTCAACA ACATTAAGTG TATATCTAAC	120
CAAGAATCTC GATGATTTTT ACGATAAGGA AGGTTTTCGA GATCAAGAAT TTGATAAAAG	180
AGATAAAGGG ACTTGGAATTA TTTATTCTGA AATGGTTATC GAACCAAAAG GGAAnAATAT	240
GGAATCGAGA GGAATGGTGC TCTATATCAa TCGCAATACT AGAACmACGA AGGGTAATTT	300
TATTGTCACC GAAATAACTG AAGATAGTAA AGGATATTCA CGTAGTAAAG AAAAAAATA	360
TCCTGTCAAG ATGGAAAATA ATCGAATTAT TCCAACAAAG CCTATACCGG ATGACAAGTT	420
AAAAAAGAG ATTGAAAAC TTAAGTTCTT TGTACAATAT GGAAATTTTA AAGATTTTAA	480
AGATTATAAA AATGGTGATA TTTCATATAA TCCTAATGTG CCAAGTTATT CTGCAAAGTA	540
TCAATTGAAT AATGATGACT ATAATGTTCA ACAGTTAAGA AAACGATATC ATATTCCAAC	600
CAAACAAGCG CCCGAATTAA AATTGAAAGG ATCCGGCAAT TTAAAAGGCT CATCCGTAGG	660
ATCTAAGGAT CTAGAATTTA CGTTTGTAGA AAATCAAGAA GAGAA AT TCT ATTTTTCAGA	720
TTCGGTCGAA TTTACACCTA GCGAGGATGA TAAATCATGA GTCAAACGGA ATATCAAATA	780
AAATCTGGCA ATATAAAAGG TAACTCTGAA GAAACAAGTA CAGTATCTAA TATAAGTTAT	840
GAAATAGAAA ACGCAAATAA CAGTGGTTTA AAACAAAATA AAATTGATAA ACAAATTAAA	900
AAGTTACAAG AAAAAAATAA ATTCCCTAAA AATCTTTCAT ATCTTAAAAG TTATACGGAC	960
CCCAAAACAG GCACGACTAC AAGCGCCTTT TTAAATAAAG ACACTGGCAA AGTTACTTTA	1020
GGTATGACAG GTACTAATGT ACACAAAGAC GCAATATTAA AACAAACATT TGGTGTTCCT	1080

TCTTATCAAG GATATATAGA CGTGAGTAA ACgCTaAAAAG ATATTGGGGC CGATGTCAAT	1140
ATTGGCCTTC ATTCCGTCAC AGATAAAGAT CCACATTATA AAAATACCCA AGACTTTATC	1200
AAAAATATCA AAAAAGACTA TGATATTGAT ATTATTACCG GACATTTCGCT GGGCGGTAGA	1260
GATGCGATGA TTTTAGGTAT GAGTAATGAT ATTAAACATA TCGTTGTGTA TAACCAGCT	1320
CCATTAGCGA TCAAAGATGT GAGCGGCCTT TATGCCGATC AAGAAGAACT TAAAAAATTG	1380
ATTGAAAAGT ACGATGGTCA CATTGTAAGA TTTGTGTCTG ATGAAGACGA ATTAGATGCA	1440
GGTGTCCGCA ATCATTATA TGAAACTGCT GGAGAAAAA TAGTACTTAA AAATGGAGAA	1500
GGCCATGCAA TGAGTGGTAT TTTAATGAGC AGAACACAGG CTATAATCTT AGCTGAATTA	1560
AACAAAGTTA AAGGCTACCA AGACGAAAAT AATAAAGCAT TAAAATCCGT TCGTAAACAA	1620
ACGAGGCATA GATTACATAA AGTAGAGACG TTAAGAGCGA ATTGGATTCA AACACGGGT	1680
GGATCACTCT CTTCCTCCCw ACAACAATTA TTAGAGCTT TAACAGCACT AACCATTGCC	1740
GAAGGCTTAA ATCAATTAGT GAATGAAGAA AGCCAACATT TGAAAAAATG TATCACGCGA	1800
TGGCACATAA ATTTGGAGAC AACTGGAAAA AAGCGCAAGA AGTTGGAAAT GAAATTGGTG	1860
AAAAATTAAC CTCTGAAGAG GTTATAGATG rATTAAGAAA AGGTGGCGCG TATGAAAGTa	1920
AACTTGAAAC AGATCCCAA AGAAAAATTG ATGATAAGAT AAAGAAATTA AATGATGTTT	1980
ATAAAAAATTG TAATGGCTAT ATCGCAAAAA TTAAACAGAG TATCGAAGCA ATTGTTTCTA	2040
ATGACCAAAT GTTAGCGAGC CAGATTGATG GGATGATGTA ATGTTTACTA CGTATAAnAA	2100
TATTAATGAA CTTGAAATG CCTATGATGA AGAAAGAAAA CAATTGAATG ATGCATTCAA	2160
TCAAATTGAT GAATTAAGAC ATCAAACACG CAAGAmATGT GAACAAATGT ATGATCATTT	2220
CTTATATCTC AAACATAAAA TGAATTmymS TGAAGACGCT ATGATCAGGA TGACACGTAT	2280
TATAGAATCT TTCGATAGAG AAACGAATCA ACGTATCCGA CACACGAAA TG	2332

(2) INFORMATION FOR SEQ ID NO: 478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 865 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

TTTACTACCC AGTATCTCTT TTTATAAATT ATATAGCCAC CACATATGGT GGAAAGTCTT	60
TTTAATTAGA ATTTTGTTTT TTCAGTTAAG AAAGCTTCTA ACTCTGAGAT TGGCATACGA	120
ACTTGTTCCA TTGAATCTCT GTCACGTACT GTAACCTGAT TATCTTCTAA TGAATCAAAG	180

TCGAATGTtA CACAATAAGG TGTaCCGATT TCATCTTGAC GACGGTATCT TTTACCGATA	240
GATTGTGATT CATCGAAATC GATTGAGAAT TTAGAACTTA ATTGCTCAAA AATCTTAATC	300
GtTCGCCAGA TAATTTCTTA CTTAAAGGTA AAATCGCTGC TTTATATGGT GCTAATGCAG	360
GATGGAAGTG TAAAACTGtA CGTGCATCTT TACTACCTTC AACGCCTTCT TCATCATATG	420
CATCACATAA GAAAGCTAAT GTTACACGAT CTGCACCAAG TGATGGCTCG ATACAATATG	480
GAATATATTT TTCGTTTCGTT TCTGGATCAT GGTATCTGAA ATCTTCACCA GAGTGTTCAG	540
CATGTTTACG TAAGTCGAAG TCTGTACGAC TTGCGATACC CCATAETCA CCCCACCAA	600
ATGGGAATTT ATATTCAATA TCAGTTGTTG CATTTGAGTA ATGAGATAAT TCATCTTCAT	660
CATGATCACG TAAACGCATA TTTTCACTGC TCATATTTAA GCTTGTTAAC CAGTCACTTG	720
CAAAAGTTTT CCAATAATTT TGCCATTCTGA TTTCTTCTCC AGGTTTACAG AAGAATTCAA	780
GTTCCATTTG TTcAAATTCT CTTGTTCTGa AAATGaAGTT ACCTGGAGTG aTTTCaTTAC	840
GGaATGaTTT ACCAATTTGG ACCGG	865

(2) INFORMATION FOR SEQ ID NO: 479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

TAATGAGTAA ATAAGTACCA GATAAAATCA TGAATATCAT CCAACATGCG GTTAACTCTA	60
CTAAATAATT AATAATAGTA TTTTCAGTAA ACAAAGAACT ATGTATACTT CGCATCACAT	120
TAGAATACGT ATGTTTCGCA TTTTGATCTG CAACAAATTG ATTGTTATGA TCTAGAAAGA	180
CGTAACGTTG ATTTCCCTGCC ATATCACTCA GTGTAATTCG TTTGTTATAT GGTTCATCAA	240
GTATGCTAAC TTTACTTACA AAGAATCCTT CATATTGTTG TTCAACTTt TGTACTGCAT	300
CATTTAATGT TTGATGCGTT TTTACATCAC TGTCACCAA AAACTCATTC TTATAAATAT	360
TATTTTCAAC TTCTGGAAAG AACAAGTAAC CAATGCCCGA AATGGTTAAA GTGATTAACA	420
GTGGAGCAAT AAATATTGCT GCATAGAAAT GTAATCTTTG TAATGGATTA AATGTATTTT	480
TCATATTTCC CTCCAATTG GCTATTATAC GGTGTCAATT CTGTGATGTG TGTGAACAAA	540
CTGTGACAAT ATTTATTTTC TAGAAAAATT TAACGATGAT TTGTGATTTT TAGAAAAATG	600
AACTTTTAAG TTGGAATGTT TGAAGAAAAT TGATTATTCG TATGTTTTAT CAAGCAGCTA	660
TGATAAAATT TAAACATAAT ACAATGCGAG CCATTTAACG ATCTATGTTT AAATGGACAT	720
CGATATTGTA TGAATTCGTT GTAACAAGCA AGCATTTCTA TGTGAACGAA CCAAAGGGGA	780

AAGTAACATG ATTAATAAAG AACAAATTAGA TCTTTTATAT AAATTAAAAA AAGAAGTTGA	840
AAAGTCGCGA AATGAAGCAC TTTTACATAC AATTAACCAA GTAATTAAGA AAGTAATTT	900
GCAGCAATAT ACATGTTTCGT TCGTTGGACA TTTTCTGCA GGTAAATCGA CACTGATAAA	960
TTTATTAATT GAACAAGATA TCTTACCAAG TTCACCTGTA CCAACGACAA GTAATACTGC	1020
TATTGTGTCA GTTTCAGACA ATCACGATAT TATTGCTAAT TTGCCGAATC AAACGTATGC	1080
CAAATTATCT AATTATGATG AAGTAAGGGA AATGAATCGC CAAAATGTCG ACGTTGAATC	1140
TGTAGAAATT AATTTTCAAT CAGCTAAATT TGAAATGGG TTTACGTTGC AAGATACACC	1200
AGGTGTTGAT TCAAATGTTG CATCACATCA GTCAATAACA GAACAATATA TGTATACAAG	1260
TAATATGATA TTTTATACGG TTGACTATAA CCACGTTAA TCTGAACTTA ACTTTAAGTT	1320
TATGAAGCAT ATAAATGATG TTGGaATACC TGTGTGTTT ATCATTAATC AAATTGACAG	1380
CATCCAAGAC GATGGAATTG TCATTCTCTA CGTnTTAAAT CTCGAGTTGG AAAAATCAAT	1440
TGGC .	1444

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ D NO: 480:

GCAGCAGCTT ATCGTGAGTT ATCATTATTA TTACGTAGAC CTCCAGGTCG TGAakCATAC	60
CCAGGTGACG TATTCTACTT ACATAGTAGA tTATTAGAAA GAGCAGCAAA ATTAAACGAT	120
GACTTAGGTG GCGGTTCAAT TACTGCATTA CCAATTATCG AAACACAAGC TGGTGATATT	180
TCAGCTTATG TACCAACAAA CGTTATTTCA ATTACAGATG GACAAATCTT CTTACAATCT	240
GATTTATTCT TCTCAGGTGT AAGACCAGCG ATTAATGCCG GACAATCTGT ATCTCGTGTT	300
GGTGGATCTG CACAAATTAA AGCAATGAAG AAAGTTGCTG GTACGTTACG TCTTGACTTA	360
GCGTCATACA GAGAACTTGA ATCATTTGCA CAATTCGGTTCAGACCTTGA TGAATTTACT	420
GCAAGTAAAT TAGAACGTGG TAAACGTACT GTTGAAGTCT TAAAACAAGA TCAAAACAAA	480
CCATTACCAG TCGAACACCA AGTGTTGATT ATTTATGCAT TAACAAAAGG ATATTTAGAT	540
GATATTCCAG TTGTAGATAT CACACGTTTT GAAGACGAGT TAAACCACTG GGCAGAATCA	600
AATGCTACTG AACTGTTAAA TGAAATCAGA GAACTGGTG GCTTACCAGA TGCTGAGAAG	660
TTTGACACAG CAATTAACGA ATTCAAAAAA AGCTTTAGCA AATCTGAATA ATAAACAAGT	720

TTAGTATAAG GTGGTGAGAT AGTGGCTTCT CTAAAGAAA TAGATACTCG AATAAAATCA	780
ACCAAAAAAA TGAAGCAGAT TACGAAAGCG ATGAACATGG TATCAAGTTC AAAACTTCGT	840
AGAGCTGAAA AAAATACAAA ACAATTCACA CCATATATGG ATAAAAATGCA AGATGCAATT	900
ACTGCAGTTG CAGGGGCAAG TAGCAATACA AACCATCCAA TGCTAAGACC TCGTAAAATT	960
ACTAGAAGTG GATATTTAGT TATCACGAGT GATAAAGGTT TAGCAGGEC ATATAGTGCA	1020
AACGTGCTTA AAAAATTGAT TACTGATATT GAAGCGAAAC ATCAAGATAG TAGCGAATAC	1080
AGTATTGTAG TTTTAGGGCA ACAAGGTGTT GATTTCTTAA AAAATAGAGG TTATGACATT	1140
GAGTATTCTC AAGTAGACGT ACCTGATCAA CCTTCTTTCA AATCTGTTCA AGCACTAGCT	1200
AACCATGCTA TAGACTTATA CAGTGAAGAA GAAATTGATG AATTAAATAT ATACTATAGT	1260
CATTATGTCA GCGTTCCTGA AAACAAGCCT ACATCTAGAC AAGTATTACC ATTATCTCAA	1320
GAGGATTCTA GTAAGGGGCA TGGTCATTTG TCTTCTTATG AATTTGAGCC AGATAAAGAA	1380
TCTATCTTAA GTGTAATCTT GCCTCAATAT GTTGAGAGTT TGATTTACGG AACAATATTA	1440
GACGCAAAAG CAAGTGAGCA TGCAACACGT ATGACTGCGA TGAAAAATGC CACTGATAAT	1500
GCAACTGAAC TTATTGATGA CTTATCATTA GAATATAACA GAGCGAGACA AGCAGAAATT	1560
ACGCAACAAA TTAGTGAAT TGTTGGTGGT TCCGCAGCGC TTGAATAATA TTTAAGGAG	1620
GAAAAATAGCA TGGGAATTGG CCGTGTAACCT CAAGTTATGG GTCCTGTAAT TGATGTTCGA	1680
TTTGAACATA ACGAAgTTCC TAAAATTAAT AACGCCTTGG TTATTGATGT GCCTAAAGAA	1740
GAAGGTACAA TACAATAAC ATTAGAAGTT GCGCTGCAAT TAGGTGACGA CGTTGTTTCGT	1800
ACAATTGCGA TGGATTCAAC TGATGGTGTC CAAAGAGGCA TGGATGTAAA AGATACAGGC	1860
AAAGAAATTA GTGTACCTGT TGGTGACGAA ACATTAGGTC GTGTATTTAA TGTACTAGGT	1920
GAAACAATTG ACCTTAAAGA AGAAATTAGT GATTCTGTTC GCCGCGATCC TATCCATCGT	1980
CAAGCACCAG CATTCGATGA ACTTTCAACA GAAGTTAAA TTTTAGAAAC AGGTATTAAA	2040
GTAGTAGATT TACTAGCACC TTATATTAAA GGTGGTAAAA TCGGATTGTT CGGTGGTGCC	2100
GGTGTAGGTA AAACAGTATT AATCCAAGAA TTAATTAACA ACATCGCTCA AGAGCACGGT	2160
GGTATTTCTG TATTCGCCGG TGTAGGTGAA CGTACTCGTG AAGGTAACGA TTTATACTTC	2220
GAAATGAGTG ACAGTGGTGT AATTAAGAAA ACAGCCATGG TATTCGGGCA AATGAATGAG	2280
CCACCTGGTG CACGTATGCG TGTTGCATTA TCTGGTTTAA CAATGGCTGA ATATTTCCGT	2340
GACGAACAAG GTCAAGACGT ATTATTATTC ATCGATAACA TTTTCAGATT TACACAAGCT	2400
GGTTCTGAGG TATCTGCATT ATTAGGTCGT ATGCCCTTCTG CAGTAGGTTA CCAACCAACA	2460
CTTGCTACTG AAATGGGACA ATTACAAGAA CGTATTACGT CTACAACAAA AGGATCAGTT	2520
ACTTCTATTC AAGCGGTATT CGTACCTGCC GATGACTATA CTGACCCAGC GCCTGCGACA	2580

GCGTTTGCCC	ATTTAGATGC	AACTACAAAC	TTAGAACGTA	AAT A ACTGA	AATGGGTATT	2640
TATCCAGCCG	TGGATCCATT	AGCGTCTACA	TCAAGAGCAT	TGGAACCATC	AATTGTAGGT	2700
CAAGAACATT	ATGAAGTAGC	TCGTGATGTA	CAATCAACAC	TTCAAAAATA	CCGTGAATTA	2760
CAAGATATCA	TTGCTATCTT	AGGTATGGAC	GAATTATCTG	ATGAAGATAA	ACAAACAGTT	2820
GAACGCGCAC	GTAGAATTCA	ATTCTTCTTA	TCTCAAAACT	TCCACGTAGC	GGAACAATTT	2880
ACTGGTCAAA	AAGGTTCTTA	TGTACCTGTT	AAGACAACAG	TTGCAAACTT	TAAAGATATC	2940
TTAGATGGTA	AATATGACCA	TATTCCAGAA	GATGCATTCC	GTTTAGTTGG	TAGCATGGAT	3000
GATGTTATTG	CAAAAGCTAA	AGATA E GGT	GTTGAAGTAT	AACAATTAGG	AGGAATGGAT	3060
AATGAATACA	TTAAACCTAG	ATATTGTCAC	TCCTAATGGT	TCTGTTTACA	ATCGTGATAA	3120
TGTTGAACTC	GTTGTTATGC	AAACAACAGC	TGGTGAGATA	GGTGTCATGA	GTGGACATAT	3180
TCCAACGTGA	GCTGCTTTAA	AAACAGGCTT	TGTAAAAGTG	AAATTTTCACG	A GGAACCTGA	3240
ATATATTGCT	GTAAGCGATG	GCTTTGTTGA	AGTTAGAAAA	GATAAAGTTT	CAATCATTGT	3300
TCAGACTGCA	GAAACTGCAA	GAGAAATTGA	TGTTGAAAGA	GCTAAATTAG	CCAAAGCAAG	3360
AGCAGAGTCT	CACTTGGAAA	ATGATGACGA	CAATACTGAT	ATTCATAGAG	CCGAAAGAGC	3420
TTTAGAGAGA	GCAAATAACC	GTTTGCGTGT	GGCTGAATTA	AAATAGTAAA	TAAAGGGTCG	3480
AAGATGTGAT	TTCATATCTT	CGACCCTTTT	TTGAATTATA	TTGATTTAAA	GATACAAAAC	3540
ATGAGAGGGG	GGAAGGAATT	GATAAAGAAC	CATTAAAGAT	TTATGATGTA	GTGGTTCTTT	3600
ATCATTA AAC	ACAGCTAATG	TGTATTTAAA	AA A GGaayA	CATgAGTAAA	ACTCATGTAT	3660
AAGAAATACT	AATTTCTAAA	GAAAAAGTAT	TTCTTTATGT	TGGGGCCCCG	TCAACTACTG	3720
CCAAATACAA	CACTATAGAG	TCTAGACATT	GATTTATGTC	CGACTCCCAA	GAATAGTTTT	3780
ACTTTTTTAC	AATCACTAAT	AGATTGCTAA	AATCAAAATT	TCCTTCACCA	CTATCTA CA	3840
TCGACATTTT	ATTTTTTGAA	ATTATCTACA	TTTTTTCATA	CCAAGATATT	TTATAGTTAT	3900
GATATTTATG	TAAAAAGAAT	TATATAGTAA	GTTAGCTTAA	ACTTTACTAA	AAACGGGTAT	3960
TAAACTTTGT	ATCATTATTT	AAATTTTTCA	TGTACAATGT	AATACAGTAA	TCTTATGAGG	4020
TGATAAAATG	GATTATATCG	GACAATATGC	AGTTATCCAT	TTAGTGTTAC	ATGTTGTATG	4080
TATTTGTATT	GCCTATTGGG	CTTTACAATC	AATTAGATTA	GATCAATTTT	TTAAAAAAGG	4140
ATACGCCACT	CAATTACAAG	TGTGTATGAT	ATTTGTTGCT	ATTTTATTAG	GCACTGCAGT	4200
AAGCAATTTT	ATTGTAGATT	TGTTACAATA	CTCGACGCAGG	TAAAATATT	TAATAAAATA	4260
AGTCTAACTC	TATGATTTGT	AATCAAAACT	AGATATAATT	AAATAATGAC	TTAAAATAAT	4320
TTTAAAATAG	GGAAATGTAA	AGTAATAGGA	GTTCTAAGTG	GAGGATTTAC	GATGGATAAA	4380

ATAGTAATCA	AAGGTGGAAA	TAAATTAACG	GGTGAAGTTA	AAGTAGAAGG	TGCTAAAAAT	440
GCAGTATTAC	CAATATTGAC	AGCATCTTTA	TTAGCTTCTG	ATAAACCGAG	CAAATTAGTT	4500
AATGTTCCAG	CTTTAAGTGA	TGTAGAAACA	ATAAATAATG	TATTAACAAC	TTTAAATGCT	4560
GACGTTACAT	ACAAAAAGGA	CGAAAAATGCT	GTTGTCGTTG	ATGCAACAAA	GACTCTAAAT	4620
GAAGAGGCAC	CATATGAATA	TGTTAGTAAA	ATGCGTGCAA	GTATTTTAGT	TATGGGmCCT	4680
CTTTTAGCAA	GACTAGGACA	TGCTATTGTT	GCATTGCCTG	GTGGTTGTGC	AATTGGAAGT	4740
AGACCGATTG	AGCAACACAT	TAAAGGTTTT	GAAGCTTTAG	GCGCAGAAAT	TCATCTTGAA	4800
AATGGTAATA	TTTATGCTAA	TGCTAAAGAT	GGATTAAAAG	GTACATCAT	TCATTTAGAT	4860
TTTCCAAGTG	TAGGAGCAAC	ACAAAATATT	ATTATGGCAG	CATCATTAGC	TAAGGGTAAG	4920
ACTTTAATTG	AAAATGCAGC	TAAAGAACCT	GAAATTGTCG	ATTTAGCAAA	CTACATTAAT	4980
GAAATGGGTG	GTAGAATTAC	TGGTGCTGGT	ACAGACACAA	TTACAATCAA	TGGTGTAGAA	5040
TCATTACATG	GTGTAGAACA	TGCTATCATT	CCAGATAGAA	TTGAAGCAGG	CACATTACTA	5100
ATCGCTGGTG	CTATAACGCG	TGGTGATATT	TTTGTACGTG	GTGCAATCAA	AGAACATATG	5160
GCGAGTTTAG	TCTATAAACT	AGAAGAAAATG	GGCGTTGAAT	TGGACTATCA	AGAAGATGGT	5220
ATTCGTGTAC	GTGCTGAAGG	GGAATTACAA	CCTGTAGACA	TCAAACTCT	ACCACATCCT	5280
GGATTCCCGA	CTGATATGCA	ATCACAAATG	ATGGCATTGT	TATTAACGGC	AAATGGTCAT	5340
AAAGTCGTAA	CCGAAACTGT	TTTTGAAAAC	CGTTTTATGC	ATGTTGCAGA	GTTCAAACGT	5400
ATGAATGCTA	ATATCAATGT	AGAAGGTCGT	aGTGCTAAAC	TTGAAGGTAA	AAGT A ATTG	5460
CAAGGTGCAC	AAGTTAAAGC	GACTGATTTA	AGaGCAGCAG	CCGCCTTAAT	TTTAGCTGGA	5520
TTAGTTGCTG	ATGGTAAnAC	AAGCGTTACT	GAATTAACGC	ACCTAGATAG	AGGCTATGTT	5580
GACTTACACG	GTAAATTGAA	GCAATTAGGT	GCAGACATTG	AACGTATTAA	CGATTAATTC	5640
AGTAAATTAA	TATAATGGAG	GATTTCAACC	ATGGAAACAA	TTTTTGATTA	TAACCAAATT	5700
AAACAAATTA	TACCTCACAG	ACAGCCATTT	TTATTAATTG	ATAAAGTAGT	TGAATATGAA	5760
GAAGGTCAAC	GTTGTGTGGC	TATTAAACAA	GTATCAGGAA	ACGAACCATT	CTTTCAAGGG	5820
CATTTTCCTG	AGTATGcGGT	AATGCCAGGC	GTATTAATTA	CTGAAGCGTT	AcTCAAACAG	5880
GTGCGGTAGC	TATTTTAAAT	AGTGAAGAAA	ATAAAGGTAA	AATCGCTTTA	TTTGCTGGTA	5940
TTGATAAATG	TCGTTTTTAA	CGTCAAGTAG	TACCTGGTGA	TACTTTAACG	TTGGAAGTAG	6000
AAATCACTAA	AATTAAAGGA	CCAATAGGTA	AAGGTAATGC	TAAAGCTACT	GTCGATGGTC	6060
AACTTGCTTG	TAGTTGTGAA	CTTACATTTG	CAATTCAAGA	TGTAAAATAA	AACAAAAAAA	6120
ACATTCAAAG	ATTTAATGTG	TTGGCATAAT	CTTTGAATGT	TTTTTATTTT	ACTCTTCTAA	6180
TTTTTCATCC	TTTAACTTTG	GTTTAGACTG	CaTCATTCTGA	TTAAATGATT	TTTTTAATTC	6240

TTCACCAGAT AATCCATC AT CAATAAGTTG GTTCTAATAA ACTTTCAGCA TACTGTTGGA	6300
CGTAAAGnG	6309

(2) INFORMATION FOR SEQ ID NO: 481:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1717 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

AGTTGCTACA CCAGACATGA TGGGTGAAGT TGGTAAATTA GGTCGTGTAT TAGGACCAAA	60
AGGTTTAATG CCAAACCCTA AAACCTGGAAC TGTAACAATGGATGTTAAAA AAGCTGTTGA	120
AGAAATCAAA GCTGGTAAAG TAGAATATCG TGCTGAAAAA GCTGGTATCG TACATGCATC	180
AATTGGTAAA GTTTCATTTA CTGATGAACA ATTAATtGAA AACyTCaATA CyTTACAAGA	240
TGTATTAGCT AAAGCTAAAC CATCATCTGC TAAAGGTACA TACTTCAAAT CTGTTGCTGT	300
AACTACAACA ATGGGTCCTG GAGTTAAAAT TGATACTGCA AGTTTCAAAT AATAAATGAT	360
ATAACAATT ACAGGCTGAA AGAAATATCT TTCAGTCTGT AAAAATATAT TGACAATAAG	420
TAATTTCCAA GTTATATTAC TTATTGTGAT TATTTTACCT AAGACAGTAG GAGTTATTTA	480
TAACTTAAAA TTTATCCTGC GAGGCTAAA ATTGACTTGA ACGTGATGAT CTATGATCTT	540
TCAAGCACTT TTTGCCGTGG GTAGAAAGTG CTTTTTTTAT TAATTTTAAA AAAAGCACCA	600
AAAATTTAAA TGGAGGTGTC TGAATGTCTG CTATCATTGA AGCTAAAAAA CAACTAGTTG	660
ATGAAATTGC TGAGGTACTA TCAAATTCAG TTTCAACAGT AATCGT AC TACCGTGGAT	720
TAACAGTAGC TGAAGTTACT GACTTACGTT CACAATTACG TGAAGCTGGT GTTGAGTATA	780
AAGTATACAA AAACACTATG GTACGTCGTG CAGCTGAAAA AGCTGGTATC GAAGGCTTAG	840
ATGAATTCTT AACAGGTCCT ACTGCTATTG CAACTTCAAG TGAAGATGCT GTAGCTGCAG	900
CGAAAGTAAT TTCTGGATTT GCTAAAGATC ATGAAGCATT AGAAATTAAA TCAGGCGTTA	960
TGGAAGGCAA TGTTATTACA GCAGAAGAAG TTA AA ACTGT TGGTTCATTA CCTTCACACG	1020
ATGGTCTTGT ATCTATGCTT TTATCAGTAT TACAAGCTCC TGTACGCAAC TTCGCTTATG	1080
CGGTAAAGC TATTGGAGAA CAAAAGAG AG AAAACGCTGA ATAATTTT TA GCGTAAAAAA	1140
ATTAAAAATA ATGGAGGAAT TATAAAATGG CTAATCATGA ACAAATCATT GAAGCGATTA	1200
AAGAAATGTC AGTATTAGAA TTAAACGACT TAGTAAAGC AATTGAAGAA GAATTTGGTG	1260
TAcTGcAGCT GCTCCAGTAG CAGTAGCAGG TGCAGCTGGT GGCGCTGACG CTG AG CAGA	1320

AAAAACTGAA TTTGACGTTG AGTTAACTTC AGCTGGTTCA TCTAAAATCA AAGTTGTTAA	1380
AGCTGTTAAA GAAGCAACTG GTTTAGGATT AAAAGATGCT AAAGAATTAG TAGACGGAGC	1440
TCCTAAAGTA ATCAAAGAAG CTTTACCTAA AGAAGAAGCT GAAAAACTTA AAGAACAATT	1500
AGAAGAAGTT GGAGCTACTG TAGAATTAAA ATAATTCAAG TATCTTAAAC TTAATAATCA	1560
AAGTTTTATA GCAAGTATTG CTATAATATA ATGATTCTTT GAGAAGTTAA AACCCCGTTA	1620
TTTTGATAAC GGGgTtTTAT TCaTTTAAAG ACTGAGTGAA ATGTTATAAT TATAATGACG	1680
AGTTACAAAG TGAAGATGAG GTGGGAATAA TGAGT@	1717

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

GTAAATCTGT TACTCGAAAT GTAACGATTA AAGAAAAGGG CTCATCTCAA ACATATATTT	60
TGTTAGGCTA TCCAACAAAA GCACAGAAGA ATAGTCATAG CAAATATAGT GGAGTCTTTA	120
TATATAAAGA CTTGAAATCA ATCGAAGATA CAAATAATGC TATTACGATT ATCACCAA	180
TTACGGCTGT TATTTTCTTA ACAATTACAA CAGTCTTTGC GTTTTCTTA TCGTCAAGAA	240
TTACAAAACC TTTAAGACGT TTAAGAGACC AAGCTACACG TGTATCTGAA GGGGATTACT	300
CTTATAAACC TTCTGTCACA ACGAAAGATG AAATTGGTCA ATTATCGCAG GCATTTAATC	360
AGATGAGTAC AGAAATCGAA GAGCATGTCTG ACGCATTATC CACATCTAAA AATATTAGAG	420
ACAGCTTAAT TAACTCTATG GTAGAAGGTG TCCTAGGTAT TAATGAGAGT CGACaAATTA	480
TCTTATCTAA TAAGATGGCG AATGATATTA TGGACAATAT TGATGAAGAT GCTAAAGCTT	540
TCTTATTAAG ACAAATAGAA GATACTTTTA AATCAAAA@ AACTGAAATG CGCGATTTAG	600
AAaTGAATGC ACGATTCTTT GTTGTGACCA CAAGCTATAT CGACAAGATT GAACAGGGAG	660
GTAAaAGTGG TGTTGTTGTG ACAGTTCGTG ATATGACTAA TGAGCACAAT CTAGATCAAA	720
TGAAGAAAGA TTTCATTGCT AATGTATCAC ATGAATTACG TACACCGATA TCATTACTTC	780
AAGGTTATAC TGAATCAATT GTAGATGGTA TTGTTACAGA ACCGGATGAA ATAAAAGAAT	840
CGCTTGCCAT TGCCTTGAT GAATCGAAAC GTTTAAATCG TTTAGTTAAT GAATTGTTAA	900
ATGTCGCACG CATGGATGCT GAAGGGTTAT CCGTAAATAA AGAAGTTCAG CCTATTGCAG	960
CGTTACTAGA TAAGATGAAA ATTAAGTATC GCCAACAAGC TGATGATTTA GGTCTAAATA	1020
TGACTTTTAA TTaYtGTAAG AAGCGTGTTT GGAGTTATGA TAwGGATCGC ATGGACCAAG	1080

TACTAACGAA CTTAATTGAT AATGCATCAC GTTATACGAA ACCTGGAGAT GAAATTGCAA	1140
TTACTTGTGA TGAAAATGAA AGCGAAGATA TTTTATACAT TAAAGACACA GGTACAGGCA	1200
TTGCACCAGA ACATTTACmA CAAGTATTTg ATCGTTTTTA TAAAGTTGAT GCAGCGnAnA	1260
ACCCCGnGGT AACCAnGTA	1279

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

GAGCTGTTGT TACTTTGATG CCTGCAGCTT TATTACGGCT GACTTGGTAA TGATAAGTTT	06
CAGCATATTG CTCAATATAT GCTATATCAT ATTGAATGGT ACGAGGTGAT ACACCAAGTT	120
GATTAGCAAT GGTATTGATT GGAATAAACG TTTGCTCATG AATTAAAAGA TACAAAATTT	180
CGATTTGTCT ATAACCTAAC AACGTAATAT CCTCCTATTT GTAATTGTAA GCGATTTCTT	240
AAAAACGTAG ATATGCAATC TCTTCATAT TTTAATCCGA AAAATTGCAT ATCAAAATGT	300
TTATGGCGCA AGATTTTATA GGAACCTTTTA AAATAAATTA rATATTCATG TTGACAATTT	360
AAAAATGTCG CAGTATATTT AGTTAGACAT CTAACGAAAT GGTGGTGCAA TAAATGGAAT	420
TCACTTATTC GTATTTATTT AGAATGATTA GTCATGAGAT GAAACAAAa GCTGATCAAA	480
AGTTAGAGCA ATTTGATATT ACAAATGAGC AAGGTCATAC GTTAGGTTAT CTTTATGCAC	540
ATCAACAAGA TGGACTGACA CAAAATGATa TTGcTAAAGC ATTACAACGA ACAGGTCCAA	600
CTGTCAGTAA TTTATTAAGG AACCTTGAAC GTAAAAAGCT GATCTATCGC TATGTCGATG	660
CACAAGATAC GAGAAGAAAG AATATAGGGC TGA CTACCTC TGGGATTAAA CTCGTAGAAG	720
CATTCACTTC GATATTTGAT GAAATGGAAC AAACACTCGT ATCGCAGTTA TCTGAAGAAG	780
AAAATGAACA AATGAAAGCA AACTTAACTA AAATGTTATC TAGTTTACAA TAAATGATAA	840
GTGTGACTGG TAGAAATCAG TCACTTTGTC TTTAATATTA TAGTTAGATA TCTAATTGTT	900
AGTAAGCTAA TTATTGGAAG AGACAAGGAG TATTGAACAA TGAAAGACGA ACAATTATAT	960
TATTTTGAGA AATCGCCAGT ATTTAAAGCG ATGATGCATT TCTCATTGCC AATGATGATA	1020
GGGACTTTAT TAAGCGTTAT TTATGGCATA TTAAATATTT ACTTTATAGG ATttTAAGAm	1080
GAyAGCCACA TGATTTCTGC tAatCTCTCT AACACTGCCA GTATTTGCTA TCTTAATGGG	1140
GTTA	1144

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

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ACAACCAATT TTACTAAACA TGGTrrTCAT gCATTtTCAA TATTtTAGATG TCGACCGCAT      60
AATCGAAGAA TCGCCGACAA TAGTACTTAT CGATGAGTTA GCACATACGA ATATtTCTAG      120
AGATCGTCAT GAGAAACGAT ATATGGATAT TGAAGAAATT TTAAATCATG GTATCGATGT      180
TCATACCACT TTGaACATTC aaCATATTGA AAGTTtAAGT AGTCAAATTG AACTGATGAC      240
CGGTGTACAT GTTAAAGAAC GTGTACCCGA CTATTTCATA ATGAGCGCCG ATGTATTAGA      300
AGTCGTAGAT ATCTCACCTG AACAATTAAT TAAACGCTTA AAAGCTGGCA AGGTATATaA      360
AAAGGATAGG CTAGATGTAG CATTTAGTAA TTTCTTTACG TATGCCACC TAAGCGAAtG      420
CGTACATTGA CGTTAAGAAC AGTTGCCGAC TTGATGAGTG ATAAAGAAAA AGTCCGAOA      480
AACCATAAAA CGTCACTCAA ACCTCATATT GCTGTGGCAA TTAGTGGGAG CATTTATAAT      540
GAAGCAGTAA TTAAAGAGGC ATTCCATATT GCTCAAAAAG AACATGCGAa GTTCACTGCT      600
ATTTATATAG ATGTATTtCGA AAAAAACAGG CAATATAAAG ATAGTCAAAA GCAAGTGCAT      660
CAACATCTCA TGCTTGCAA ATCATTAGGA GCAAAGTAA AAGTAGTTTA TAGCCAAACC      720
GTTGCATTAG GATTAGACGA ATGGTGTAaA AATCAAGATG TAACCAAATT AATTATCGGA      780
CAACATATTA GAAATAAGTG GCGAGACTTT TTCAATACAC CTTTAATTGA CCATTtAATG      840
TCCTTTGAAC ATAGCTATAA AATCGAAATC GTTCCAATCAAACAAATACC TGTTGAATTG      900
AAAATGAACA AATCACCCTA TCGTCCTAAA GGCAAACGTT TCGCCATAGA TATGTtAAAA      960
ATGATTTTGA TTCAAATAAT TTGTGTAATG ATGGGACTGT GGATTTATCA ACTTGATAAG     1020
CATGAGTCTA GTACGATTAT TTTAATGATT TTTCTCATCG GCATCATTTT ATTATCCATT     1080
TGGACGCGGT CCTTCATCAT TGGCTTTTaG CAGCAATTAt TAACGTATTT GTgTkTAATT     1140
ATktTTTTtAC GGAACCTA                                     1158
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(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

ATCATATGGT CGATTTAACA GATCCAACGT ACTGcTAAAT AATTACATGA CGTTTAAACA	60
TAGCATTGAT TATAACTMT TCTAAGTCTT CGCATTATTT GCGATGATGT GGGAAATAGTT	120
ATTTTTATTT AAAAATATAA AAAAATAGAT GCAGCAAAAT TTTAAAGCAT TTTATTTTGA	180
ACATATTAAA AGGGAGCGTA TCATAATGGA ATGTAATGTT TATATCGTAT GCATTACGGA	240
TAAATAATAT ATAAATCATT CTTGAGGAGT GAAAGAATAA TGbAGACTA CACAAAGCAA	300
TACATTAATG GCGAATGGGT AGAAAGTAAT AGTAATGAAA CGATAGAAGT TATAAATCCA	360
GCAACCGAAG AAGTAATCGG GAAAGTTGCT AAAGGTAATA AAGCTGATGT TGATAAAGCC	420
GTCGAGGCGG CAGACGATGT TTATTTAGAG TTCCGTCATA CATCTGTGAA AGAAAGACAA	480
GCGTTATTAG ATAAAATTGT AAAAGAmTAT GAAAACAGAA AAGACGATAT TGTACAAGCT	540
ATTACGGATG AATTAGGTGC TCCTTTATCA TTATCTGAGC GTGTCCATTA TCAAATGGGA	600
CTAAACCATT TTGTTGCAGC GAGAGACGCA TTAGATAACT ACGAATTTGA AGAACGCCGC	660
GGAGATGATT TAGTTGTTAA AGAAcAATC GGTGTATCTG GATTAATTAC ACCGTGGAAC	720
TTCCCTACAA ACCAAACATC ATTAAAATTA GCAGCAGCAT TTGCGGCTGG TAGTCCAGTT	780
GTA CTTAAAC CATCTGAAGA AACACCATTT GCAGCTGTTA TTTTAGCTGA GATTTTTGAT	840
AAAGTCGGTG TTCCTAAAGG TGTATTTAAC CTTGTTAATG GTGATGGTGCTGGTGTGGG	900
AATCCTTTAT CTGAACATCC TAAAGTACGC ATGATGTCAT TTACAGGATC AGGCCCTACT	960
GGTTCTAAAA TTATGGAAAA AGCCGCTAAA GATTTTAAAA AGGTATCATT AGAGCTTGGT	1020
GGCAAATCAC CATATATCGT CCTAGATGAC GTAGATATTA AAGAAGCGGc TAAAGCAACa	1080
aCAGGCAAAG TTGTTAATAA TACTGGTCAA GTATGTACAG CTGGTACACG TGTTTTAGTG	1140
CCTAACAAAA TTAAAGATGC ATTCTTAGCT GAATTAAAAG AACAATTTAG CCAAGTGCCT	1200
GTCGGTAATC CAAGAGAAGA TGGTACACAA GTAGGCCCTA TCATTAGTAA AAAACAATTT	1260
GATCAAGTAC AAAATTATAT TAATAAAGGT ATGAAGAAG GTGCTGAATT ATTTTATGGT	1320
GGTCCTGGTA AACCAGAAGG ACTTGAAAAA GGATACTTTG CACGTCCGAC AATTTTTATT	1380
AATGTAGATA ATCAAATGAC GATAGCACAA GAwGAAATTT TTGGGCCAGT AATGTCAGTT	1440
ATCACTTATA ACGATTTAGA TGAAGCGATT CAAATTGCAA ATGATACAAA ATATGGTTG	1500
GCAGGATATG TTATTGGTAA GGACAAAGAA ACATTGCATA AAGTAGCTCG TTCTATTGAA	1560
GCAGGTACAG TAGAAATAAA CGAAGCAGGT AGAAAGCCAG ATTTACCATT TGGTGGCTAT	1620
AAACAATCTG GTTTAGGTCG TGAATGGGGC GATTATGGTA TTGAAGAGTT CTTAGAAGTG	1680
AAATCTATAG CTGATATTT TAAATAAATT TGATTTTTGA ATTAAAAATC GCAATAAAAC	1740

AGTGCACATG ACTAATTAAG TTTTGTGTAC TGTTTTAATT TTGCAATTTT TATAAATAGA	1800
TTTTGTAAAT AAAATAAAAA TTTGCTATAG TTATTCATGT ATTTAAAAGG TTGGGGATTA	1860
GCATAATGGG ATTGTGCTAG CACAGTTATT TATGCATTGTCATGCCTATC TATTACTTAC	1920
TAACTAAAAA ATAATGAAAT GGGTGTAAAC TATATGCCTG AAAGAGAACG TACATCTCCT	1980
CAGTATGAAT CATTCCACGA ATTGTACAAG AACTATACTA CCAAGGAACT CACTCAnAAA	2040
GCTAAAACTC TTAAGTTGAC GAACTATAGT AAATTAAATn AAAAAGAACT TGTTCTAGCT	2100
ATTATGGAAG CACAAATGGA nAAAGATGGT AACTATTATA TGGAAGGTAT CTTAGATGAT	2160
ATACAACCAG ATGGTTATGG TTTTTTAAGA ACAGTGAACCT ATTCTAAAGG GGAAAAAGAT	2220
ATTT	2224

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

ACATTACnTT GAATCGMAAG TTTCATAAAC GACTTGAATG CCAGTTTCTT TTTCAAATTT	60
CTTAATTAAC TCTGGATCAA TATATTCGCC CCAATTGTAT ACGTAAATTT TTTGATTTGT	120
ATGCACTTGT TCTTTAGATT TAAACCAATG ACTTAAAGTA AGACAAAGCA TACCCACAAC	180
TAATGCACCT ATAATGAGTT GTAAAAATCG TTTCAATTATT TACACCTCG CTTGATTAGT	240
TTTTTCTTAT TTATCACGTA TTGAATCAAA TAATATCCTA GTATTCCTAA TACAATAACA	300
GCAACAATA ATGTTGAAAT CGCATTAATT TCCATACTAA TTCCTTTTCT CGCCATAGCA	360
TAAACTTCAA CTGATAACAC ACTAAAGCCA TTACCAGTAA CGAAGAACT TACTGTGAAA	420
TCGTCTAGTG AATAAGTTAA AGCCATAAAG AATCCTCCTA TAATAGAAGG TAAATATTA	480
GGAATAATAA TGTTGCTTAA TAATTGTGGT TCAGTCGCTC CTAAATCTCT TGCAGCATTT	540
AACATATTAT TATTCATyTC ATACAGTTGT GGTAAGACGA TAATCACAAAC TATAGGTATG	600
CAAAATGCAA TATGAGATAT TAGACTGTC CaAAAkCCTA AACCAAGACC AGTAAAATGG	660
CCAATCGTTG TAAACATAAT TAAGAATGAT GCACCTATGA CAACGTCGGA TGATACCATC	720
AAGACATTAT TCAATGTTAG TAAAGTTACT TTAACTTTT TATTTCTTAA ATAATAAATA	780
GCAATGGCAC CAAATGTACC AATAACTGTA GAAATTGAGG CTGCTAAAAGTGCTACAGCT	840
ATCGTATTAA AAATGACCGA CATTAAATGA TCATTTTGAA ATAATGATTG ATAATGCTCT	900
AATGTAAAAT GTTCAAAGTG AATCATATTA CCAGCCGAAT TGAATGAATA GAACATTAAA	960

AAGAATATTG GGATGTATAA AATCGCTAAA AGTATCCCGA TATACAGCTT TCCATACCAT	1020
TTCATATGAT TCACCCTCTC CCATTAGATG ATTTTGTAAT GATTAAAATG AATGCCATAA	1080
ATACAATTAA GAATATAGCT ATAGTTGATC CCATACCATA ATTTTGAATT GTTAAAAATT	1140
GTTCTCTAT TGCCGTACCT ATATTTATGA CTTTATTACC TGCAATTAAT CTTGTAATCA	1200
TAAATAATGA AAGTGATGGA ATAAAGGTTA CTGAATCCC AGTCATAACA CCTTCTTTTG	1260
TTAACGGCAT GATTACTTTT CTAAAAGTAT AGAAAGGACT GGCACCTAAA TCACTTGAGG	1320
CCTGCAATAA ATTATTAGGA ATTGCTTTCA TGCTATTAAA TATAGGTAAA ATCATAAATG	1380
GTATATAAAT GTAACCTGCC ACTACTAAAA ACGCACCAGT TGTAATAAAC AAATTGATG	1440
ATGGTAAATT AAATAAGTGG AAAATTGATT AATCACGCCA TCATGACTTA ATAAACCTAT	1500
AAAAGCATAT GTCTTTAACA ATAAATTTAT CCATGTTGGA ATAATCATT TCAATTAATA	1560
GATATTTTGA AATTTGGAAC GAGTAATATA ATAGGCAGnT GGATAACTGA TAGTCAAGGT	1620
AATAATTGTT ATTGAAGCGG CATATAAAAT TGAATATGCA AACATTTTCA AATATTTTGT	1680
AGTAAAAATT	1690

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

ACGAAAAGAA ATATTATGAT GAACAAAAAG AAAGAATAAC GATTTATATG AAGTACAATG	60
TGAAAGGTTA TAAAAATATA AGCTTCGCTA ATTTAAAGA AAACCCAATG GATGGTTATT	120
CTATTAGTGG TTATATAAAT AAtGaTAAAA AGTTATCATT TACAGCTGGT ATAAGATCTG	180
TTGATGATTT TCAATTTGAT ACCGATATTT CTTATACAGA TGAATTGGGT AGAAAATTTA	240
ATAAAAATCC TAAGTCAGTT TCTGAAATAA AAAAAGAGCA AAATACGTCC AATAAATAAT	300
TGTTTCATATT GTGATGAAAC AAAAATATAA GTCATTAGAT GAGTTTAACT ATGTTATAAA	360
TATTTGTAGT ATCTATAAAA ATCTCGACAC TATTAAAATG ATAAAGTGCC GAGGTTTTCT	420
TACTTATTTA GTTAATTCAA AGTTTATGCC AGATTCATAA GAATTTGTGA CACTTTTAAT	480
AGTGTAcCAT TGATTATTAC AATTTATCAA ATGGTCCTTT AGAAGGTATA AATAACAAAA	540
TAAAAATTAAT TAAACGTACA TCTTTTGGTT ATGGAAGTTA CAATCATTTG CGCAATCGAA	600
TATTATTATG TTCAAAACTT TACGCTCCAA AAAGTAAAAA GGAAGTTAAG CAATGTTTAG	660

TTGCTTAaCT TCGGaTATTG AACGCATCAG TCCAATTTGA aTAGAGCCT TTTTtagTTC	720
TTGATGTTTC TCTTTAAAC CTTGCATATT TTACAAAAG AAAAATTAGC AGTATAATTA	780
AGACAACGAA AATAAGTATT TACTTATACA CCAATCCCCT CACTATTTGC GGTAGTGAGG	840
GGATTTTTAT TGGTGCGGCT ATATGTCACC TATTTTGTAT TGCGTCTACT TAGCCAATAA	900
GAAAAAAACG CAATGGCACA GCCACTGATG ACTGGTGCTA TGATGTGAAC GaAAATAAGC	960
ATCACCTTAT ACACCTCCTC TCTGCGTCTA AATTGACGsC TGAGaGrTAG GcGACTCTAC	1020
TATTATATCA TCGGCAAATA TACAAGCACA GTCACTTGCT TCTGATAAGT TATATGATTC	1080
TAGCTGATAG ATTGAATCGT CTACACTTAA TTGGACAAAT TCTATGAGAA TAGATATTGT	1140
TAATTTAAGA AAGTAGGCGA TTTTATTATG ACAAGAGAAA GAAGATCATT TAGTTCAGAG	1200
TTTAAGTTAC AAATGGTTAG ATTATATAAA AATGGTAAGC CTAGGAATGA AATTATACGC	1260
GAGTATGATT TCACACCTTC GACGTTTGTA AATGGCGGTT ATAAAATG GAAATGGA	1320
TAAAGCAACA TCAAAACACG GGTACATTCA ATCACCAGA TAACTTATCG GATGAAGAAA	1380
AAGAGCTGAT TAAATTACGC AAAGAAGTTC AACATTTAAA AATGGAGAAC GATATTTTAA	1440
AGCAAGTAGC GCTGATTATG GGGCAAAAAT AGAAGTCATT CAAAAGAATG CACATCAATA	1500
TTCAGTATCA GCAATGTGTA AAGTCCTGAT AATACTAAGA AGTACCTATT ATGATTCTAT	1560
AAAAAGAAAA GATAATAAAA TCACTAAAGA TGATTCAAAC ATAGAACATG CCGTCATAAA	1620
TATTTTAAAT TCTAATAGAA AAGTCTTTGG TACAAGACGA ATTAAAAATC ATTTAAATGA	1680
CAAGGGTCTC ACTGTATCTG GACAAAAGATAGGTCGATCA TGAAAAAATC TAGTTTCTGT	1740
TTATACGAAA TCTAAATACA AAAATCATCT AAAAGAACT AATGAAAAAC GAATTAAAAA	1800
TCTTTATTAT TAGCTGCTGG TGTATTATTT GTTAGTCCA TTTCAATTATC TTATAATTCA	1860
GATGTAGCTC ATGCTGAAGA TAAGTTAGAC CATTCTCAAG CAAAGGTAAT ATATTGAGT	1920
AACCAAAATT TATTTGATGA ACTTGAGAAA AAAGGTTATA AACTGGAAGA TATATTTACA	1980
AAAGAAGAAA TAAAAAATA TAAAGCTGAA GACCAATTGA GAGCGGGTAA AACTCAATAT	2040
GTAGAAACAG GTAAAGATAC TGCAACATTA TATCTTTCTT CTGCATATAC AAAACAATA	2100
GCTGCTTTAG GT	2112

(2) INFORMATION FOR SEQ ID NO: 488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

GTAGGCACAC ATCTGCCATA TAAACATTCT TTTATACTAG TGTTCTCATA TAGTGTAGAG	60
TTATAGTCTC CTTCTTGAAT CTCGAATAAT TCAATCAACC TATCAACCTT AGTCTCTTCC	120
GTTACTTCTT TTTCAATATC AACTATGAAG GGGATCAAA TTGGAATAAA ACTTGACGTC	180
GAACACTTAT TTGTATTTGG ATGAAAACGA ACGAATCCAT CACTAAATCC TGTTGAAAAA	240
AATATTTTTTC CTTGTGATAG ATCCGGATTT TCTCGCGCCC ATTTAATTAA TTCATCTAAT	300
CTCATTTCTT TTTTAACTTT GATTTTCATT GTTATATCTC CTCTTGAACA GTAAATTTAT	360
CGTTAAATGA TACGTATCCA GTCACATTAC ATAAGATGCT ATCAACATCA AAAGTCACAC	420
AACAGTTGCG TTCAACATCA TTTGAATAGA ATCT	454

(2) INFORMATION FOR SEQ ID NO: 489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

TTGTCAGAAAT TAGAATGCTT TTGAGTTACT TCATAATACT CATCAGTTTT TTGTGTATCC	60
TTTTGACTTT TATTTATTC TTTCCACTTA CCAGTATGAC TTTCTTTTTT TACAGTTATT	120
TTCGGTTTGT TTAAAAAATG ATAACCGATG TTCTTTTTGG TATCTGTGGA CTCTAAAAG	180
ACTGAATTGT TTCCTGATT ATCAGAATTG GTTGTGTTGTT TATCGTCTGT ATATAACGTA	240
TACCCATTCG CTTTGCGATT TTCAATCGTT GTAACGAT TCTTTGATGA ATCAGTACTT	300
TTAATGCCAG TTCCTAAGAA GACAATTTTA TCGTTTAATA TGAAATATGA TTTTTGGCA	360
GTTAAAGTTT TGTCTGATT TTCAAAATCC ATTCCGATAC TAGCATGTTG GTCATCAACT	420
TTTGTTCGCG CAACAAAAGT TTTACTCGAC TTTTATCAT CCGTATCTTT TAATATTTCA	480
TTGTCTAAAG TTGTTGTACC TGATAAACGT TTCATATCGG CTGTCACCCA GAAGTTATCA	540
TGATAGTGTT TGACATCGCT GTTATATAAA TAAGACATTC CAGCACCAGT GTGCCAACCT	600
TTTAAATTCT CTCCGTTGAT ACTTTCATAG CGTGCTACGT TTTTCGACGT CATACTTAA	660
CCAAATGCAA AGTCTAAGTC TTTGTTATGA TAGGTGACAC GATCCATGTC ATTATATATT	720
TTAAGTTGTT GTGTTAATCC GTTTTTAGAA AACTGTTAT CTGTCATTAA AGACTTCATT	780
TTATCTATGT CCGAATATGA ATTTAAATAA TCATTTTGTT TATAACTTGA ATCTGACTCT	840
ACTGAAGATT TGACAATCTT TTTATACTTA GCTTTTGTTG AATATCCAT GGCATCACTT	900
AATCTCAACA ATGATTTTCAT TACTGTTGCA GATGCTGAGT GACTGGTTTC ATTTTCACGA	960

CTGATAGCTC TACCTCGTGA TAAATCCATC ATTTACACCTT TATAAATGAG TGGCATAAAT	1020
CCGTCGTCAA TCCATGACTT TAAGGTTGTA TCATTTTGGG TTTTATCATT AAAAGGTGTT	1080
TCTTTTATCA TCGGCATCAT TTGAGAAATC CCCTCTAAGA GTACAACGCC ATAAGCACCA	1140
GTGTATGGAA CGTCTTGATG ATCAATGTAA GAGCCATCTT TATAAAATCC ATTACGTTCT	1200
TTACCAGTGG CAGAATCTTG AACGTAAGTG AAGACTTTAT TAAATGAATC TATAGACTTT	1260
TTCATCATAT CTTTATCTTC TTCGATAATA CATTCTAAAA GTTTCACCTT AGAAATGTCT	1320
ACTAnATTTT CGCCTTTAGC AAGTTCAGnT TTTCTACAC AAGATAATAT TT	1372

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

ACAACAATAT AGTAAAGCGT CGTTAATTAA ACAATGGGAC CAATTTGTTT GTCTTATATA	60
AATGTACTTT aCCTTTATTT TTACAAAAAT AGCATTTTCC TATGTCATT AACTAAACAT	120
GTAAGTTCGT ATGAACGAGG TTTGTTAAAT AGATGATTCT AGGAAAATGC TTTTTCTTT	180
TGACTTAGTT TAAAATATTT TGCCACTTTG TACTGATAGT AGTTGCATTG TACTGTTGTG	240
CAGATTCTAT GCTATTAATT GAAAAGTGT GCAATTTTTG AGTATTATTT AGTAATTGGT	300
CGACCTTTTC AACCATTGTA TTGATGTCAC CTTGAGGTAC TAAATAGCCA TTAAATCCAT	360
CTTGaATCAG TTCTGaTGGA CCATAATCTA CATCATAACT GATCACTGGT GTACCTACTG	420
AAAgCGACTC TAAAATTGCT AAGCCAAAAC CTTCCATTTT ACTTGTCGAT AACATCAGTT	480
CTGCTTTAGC AATCTCTTCA TTAATATGCG TCTTAAACC ATGAAATTTA ACATGTTCCA	540
GATATnATGA TAATCTTCTA CAAG	564

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TATCCACCCC ACGAnAGCCC CGGAAACTTA TTGTGTTACA AGATATATAA GCAGAAACGA	60
ACAACAGTTA ACAAATAAAA TGAAATTAAA CGTTTTAAAA ATGAAACAAATGAAATCATC	120

TATTAGGTTA TGAAACTGTT TATAGCTTGA ATAGAAGCAT TTATTTTTTA GGAGGACAAT	180
TATTATGCGT CAAACATTTA TGGCAAATGA ATCAAACATT GAGCGCAAAT GGTATGTTAT	240
CGATGCTGAA GGCCAAACAT TAGGTCGTTT ATCATCAGAA GTAGCATCTA TCTTACGCGG	300
TAAAAATAAA GTAACCTACA CACCACACGT TGATACTGGT GATTATGTAA TCGTTATTAA	360
TGCATCAAAA ATCGAATTTA CTGGTAACAA AGAAACTGAC AAAGTTTACT ACCGTCCTC	420
AAATCACCCA GGTGGTATCA AATCAATCAC TGCTGGTGAA TTAAGAAGAA CTAACCCAGA	480
ACGTTTAATT GAAAACTCAA TTAAAGGTAT GTACCAAGC ACTCGTTTAG GCGAAAAACA	540
AGGTAAAAAA TTATTTGTAT ATGGTGGCGC TGAACATCCA CACGCTGCAC AACAACCAGA	600
AAACTACGAA TTACGTGGTT AATTAGAAGG AGGAAATGAC TTTGGCACAA GTTGAATATA	660
GAGGCACAGG CCGTCGTAAA AACTCwGtAG CACGTGTACG TTTaGTACCa GGTGAAGTA	720
ACATCACAGT TAATAACCGT GACGTACGCG AATACTTACC ATTCGAATCA TTAATTTTAG	780
ACTTAAACCA ACCATTTGAT GTAACGTAAa CTAAAGGTaa CTATGATGTT TTAGTTAACG	840
TTCATGGTGG TGnTTCACTG GACAAGCTCA AGCTATCCGT CACGGAATCG CTCGTGCATT	900
ATTAGAAGCA GATCTGAAT ACAGAGGTTC TTTAAAACGC GCTGGATTAC TTAATCTGTA	960
CCCACGTATG AAAGAACATA AAAAACCCAGG TCTTAAAGCA GCTCGTCGTT CACCTCAATT	1020
CTCAAAACGT TAATTGTCGG ACGATATATA CAAAACACCT CGATATTATG TCGAGGTGTT	1080
TTTTTGGCGT TTTTGCGGCG AATATGGAAT GTGTAGAATATAAATGAATT TTTACCTTCC	1140
CACCATAAAA GATGAAGAAC CATGAATGTG GAGAACAATA AATAGTTGGA TATTCTGTTA	1200
TTTTTTTGGGA AGTGGAAGTG GATTTGGAAT ACTTTACTCn AAACGATTAA AAGGTTTAAA	1260
AAAACAACAA AnAGAAA	277

(2) INFORMATION FOR SEQ ID NO: 492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 673 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

nTCAACACCT TTTATnCCAC CAAGTTATTC CACTCTTGT TGATAAGTAC GCATGTTCTC	60
TTATTGACAT TGTTTTTATC CAAAATTCAT TGTTAAGACA TTTTCTTTAT GAAATAATAA	120
TnATATTGAA GTATATTTTT ATTATTATTA AAAATAAATA AGGGGATACT TATGAGCACA	180
AATCAAACAT TTTTAATnTT TGTTATAGCA ATTATTCTAC TTACATCTGT AATAGGAATT	240

GTTGGACGAT ACATGAGTCG TCAACGTCTA TTAAATCTA TGGAAACATT ATGGCAAACG	300
ATTTCTCCAT TAGAAGCTTT TATCAGACCG AACTCACATT TCGACTATGA GTATAAGCTC	360
TACAAGGAAA AATTTGAATC ACATTCATTA GTTGATGATA AAETTGGTC CGACTTAAAT	420
ATGAATGCAA TCTTTCATAA GATGAATTAT AATTTAACAG CTATTGGTGA AATGAAGCTA	480
TATGCCTGTT TACGTGGAAT GCTTTC AATT ACGAACAAAT CATTACTTAG TTTATTTAAT	540
GATAATGCTG AATTTAGAAA AAACGTAACA TATCATTTAG CTTTGATTGG tAAAACTGTT	600
aTCCAACATT TCCAGACCAA ATCACACCGG kAAACGTCCA AATATATTGn TCTATGCCCG	660
GTTTACCAGT ATC	673

(2) INFORMATION FOR SEQ ID NO: 493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1240 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

AAAAAAGTT AATGCTGACG GTGTATTAAC TTTTGATATT CTAGAAAATA AATATACTTA	60
TGAAGTTATT AACGCTATAG GGAAAAGATG GATTGTTAGT CATGTCGAAG GTGAAAACGA	120
CAAGAAAGAA TATGTAATAA CTGTCATTGA TAGGAAATCA GAAGGCGACA GACAACTGGT	180
TGAATGTACT GCTAGAGAGA TTCCCATAGA CAAGTTAATG ATTGATAGAA TTTATGTTAA	240
TGTAACAGGA TCTTTTACAG TAGAAAGATA TTTTAACATT GTGTTCAAG GTACTGGAAT	300
GCTTTTTTGAA GTCGAGGGCA AAGTTAAATC TTCAAAGTTT GAAAATGGTG GTGAAGGCGA	360
TACAAGGTTA GAAATGTTTA AAAAGGGATT AGAACATTTT GGTTTAGAAT ATAAAATAAC	420
GTATGACAAA AAGAAAGACA GATATAAGTT TGTATTGACG CCTTTTGCAA ATCAAAAAGC	480
GTCTTATTTT ATTTCTGACG AAtCAACGCC AACGCTATAA AACTCGAGGA AGATGCAAGT	540
GATTTGCGCA CCTTCATTAG AGGATATGGT AATTATTCAG GAGAAaGAAAC ATTCGAACAC	600
GCTGGGCTCG TAATGGAAGC TAGAAGTGCA TTAGCTGAAA TATACGGCGA CATCCACGCA	660
GAACCATTTA AAGATGGTAA AGTGACTAC CAAGAAACTA TGGATAAAGA ATTACAATCG	720
AGATTgAAAA AGTCGTTAAA ACAATCTTTG TCTTTGGACT TTTTGGTGTT AAGAGAATCA	780
TATCCAGAAG CAGACCCACA ACCCGGAGAC ATAGTACAAA TAAAATCTAC CAACTAGGT	840
TTGAATGATT TAGTCCGTAT AGTACAAGTT AAAACGATTA GGGGTATAAA CAAGTAATT	900
GTTAAGCAAG ATGTAACGCT TGGTGAGTTT AATCGAGAAC AACGATATAT GAAAAAGTT	960
AATACTGCAG CTAACATATG TTCTGGATTA AATGATGTTA ACCTTTCTAA TCCTAGTAAA	1020

GCGGCAGAAA ACTTGAAGTC TAAAGTAGCG TCAATAGCTA AATCAACACT CGATTTGATG	1080
AGTAGAACTG ATTTGATTGA AGATAAACAA CAGAAGGTAA GCTCTAAAAC TGTGACTACA	1140
TCTGACGGCA CTATCGTTCA TGATTTTATa GATaAATCmA ACATTAAaGA TGTA AAAaMCG	1200
aTTGGAACGa TTGGCGATtC TGTAGCTAGA GGATCACATG	1240

(2) INFORMATION FOR SEQ ID NO: 494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

ACGGTGGATT TAGCCTAGAA GATTTAACGC ATCAAGGTAA ATTaTCAGCA TTTAGCTTTA	60
ATGATCAAaC AGGTCAAGCA ACATTGATTA CTAATGAAGA TGAAAACCTC GTAAAAGATG	120
AGCAACGTGC TGGCGTAGAT GCAAATTATT ACGCTAAACA AACATATGAT TATTACAAAG	180
ACACATTTGG TCGTGAATCA TATGaCAACC AAGGTAGTCC AATTGTTTCA TTAACGATG	240
TTAATAACTA CGGTGGTCAA GATAACAGAA ATAATGCCGC ATGGATCGGT GACAAAATGA	300
TCTATGGTGA TGGTGATGGT CGCACATTCA CAAGTTTATC GGGTGCAAAT GACGTAGTAG	360
CACACGAATT aACACACGGT GTGACACAAG AGACAGCGAA CTTAGAATAT AAGGACCAGT	420
CAGGCGCTCT AAATGAAAGC TTTTCAGATG TTTTGGATA CTTTGTAGAT GACGAGGATT	480
TCTTAATGGG TGAAGATGTC TACACACCTG GAAAAGAGGG AGACGCTTTA CGCAGCATGT	540
CAAACCCAGA ACAATTTGGT CAACCAGCTC ATATGAAAGA CTATGTATTC ACTGAAAAAG	600
ATAATGGTGG CGTACATACG AATTCTGGAA TTCCAAAAA AGCAGCTTAT AACGTGATTC	660
AAGCAATAGG GAAATCTAAA TCAGAACAAA TTTACTACCG AGCATTAACG GAATACTTAA	720
CAAGTAATTC AAACCTCAAA GATTGTAAAG ATGCATTATA CCAAGCGGCT AAAGATTTAT	780
ATGACgAGCA AACAGCTGAA CAGGTGTATG AAGCATGGAA TGAAGTAGGC GTGGAGTAAA	840
AATATATAAA CaAGAAGAAG TAATGTTAAA CACTTATAAA TAATTAAATT TTAAATACAG	900
CTTATATATG GGGTATACCT ACATTGATAA TTGACTTTGT AGGTATACCC TCTCTTTGTA	960
ATTAGATGAG AGGAGTGTGA GGGTTGTCTG CCGAAAGACT ACTCGGCAGT CTAAAATCAT	1020
TACAAGTAGT AGATATGTGA TAATTAAATG CTGACTTAGA ATACAAAATT CATTTTAAAA	1080
GTTGTCACAA AAAATTTTACA TGTATTTTTTA TTATCTTTTG CAAAACAAAG TGTAAATTA	1140
TAAATGAaAC ATGCATGAAT TTATTTTTTA ATACAAGAAA CGTAACTACC AAAGGAGTTT	1200

ACAATATGAA GAAAAGTAAA CGATTAGAAA TTGTTTCTAC AATACTAAA AAGCATAAGA 1260
 TTTATAAAAA AGAACAAATc ATTTTCATATA TTGAAGAATA TTTTGGTGTA A 1311

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1761 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

TGCACTTTCT AAAAATACTT GCTTTACTTG TTCCAATTCC TTGTCAGACA TTGATTCGGC 60
 TAATTTATTC ATTATTGCCT CAAATACGTT AATTATGTCA TCCATTTTCAG TACTATAAAA 20
 ATCAAACCAT TTTGCCGTAT CTTTTTCTCT ATTAAGCTTA TGATCACTTT GAGAGCGCTT 180
 AGCTAATTCT GCATAAATAT ATGGACAAGG TGCCATTGCA GCAATTGTAT AAATAGCATT 240
 TTCACGACTA TGCGCTTGGA AATACATATG TTTTATGTAA TGGTCGCCAC TTGGAGGCCA 300
 AACTTTTGTT TTAATGATTT CTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG 360
 CGCAAGTACT TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT 420
 CATGCTATTC ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT TAAATACGC 480
 AGCATCAGCT TTTAAGTAAT GCGGTAATGC GTCAGcTCCT ATATCTCGG ATAACATCTT 540
 CTGAATAAAG TCATCCTCAT AAATATCATT AATGATTGGC TTTGCAGCTT GGTACAATTT 600
 TTGTGAAAAT TCCATTGTAA AAAATCCTCC CTAAATAAAA AACTACTTC CAACATGAAA 660
 GTAGTTTGAT GGCAATGTTG CTATACTAGC CCCATCACTT CAATAACTAC TTTCTACGT 720
 TGGTACTAAC CAAATCAGGT CATAAGGGTC TGAACAATTC ATCTCAGCCA TATCATTAGG 780
 CTCCCCTAGT AGTTCCTTAG TATTCAATTG CAAATTAATC TTAGCAAACG GTTTCAACAT 840
 TTTCAATTAT TGTGCTCAG TTGTATTATT ATCTTTAAAT AATAATTCTA TAATGACATA 900
 TATTTGCGAA ATAAAAAAC CGGAACATATCGAGAATTCC CCGATATATT CCAATCTAAA 960
 AGTTACTTAT ATAACTATTA ATTAGCTATG CATAAATGGC TTATGCAGTA ACCCAATGTC 1020
 CAGCGCCACC AGTGTTATAT AATTTTACTG CTGCGGCATC TTGAACACTT TCAGGAGCAT 1080
 TTGCTGGTGA TACACCTTTA TATTTAGCAG GTGCTACTGA ATCCCAAGTT GATTGAAGA 1140
 ATTGATACTT ACCAGCTGCA CCTGgATGTT GG rTTTACAG CATGAATATT GCCACCTGaT 1200
 TCACGTTGrG CAATTTGTTT TAGATGAGCa TTCACATTTA CTGATGAACC TTCTGATGAT 1260
 TTTGATyCAG TTGGTGTTGC AGTAACTTGT GAATTGTTTG ATGTTGATGC TTGTGGTTGT 1320
 TGAGTTTGAG CATTTTGTGG TGCTTCAACT TCTTGTGATT GTACTTGATT AGCTTGAACA 1380

GCTGATGGTG CAACATTATT AGTTGCAGGT GCTTGTGCAC TCATGTCTGC TCCATTAGTA	1440
CCTGTTGCAT GGTAATTCCA AGCAAAGTGT GTACCATCTG ATTCAAAGTG ATAAGTAAAC	1500
CCTTCATAGT CAAATGTATA ATTATAAGCC CCAGCTTAA TTGGTTTTTG ATTTAATGTT	1560
TGATCATTTG ATTGCGCCAT TTGCCTGAAA GATGCTTTAT TTAAGTCCGC TTCACnTGCA	1620
TGGGCTTCGT GGACCTGCAT TTCCTGGCTA CGATTCTTAA ACCTACTGGC nAAnGATGAT	1680
GCGAGTAATG TTTTCTTCAT AATCTTAAAA TCCTCTACA AGTGAATTTG TGTCTCTAAA	1740
AGTTTTACAG TGGACGACTG T	1761

(2) INFORMATION FOR SEQ ID NO: 496:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 794 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TCATTTATGA AAAATGTCGG AnAGAnCCaa GaAAmaCAAT TGAgCGTGAA GAAAAAGCAA	60
GACTTAAAGA AGAACAAAAG GCACGTCAAA ATGAACAGCC ACAAATAAAA GATGTGAGTG	120
ATTTTACGGA AGTGCTCAA GAAAGAGATA TTCCAATTTA TGGGCATACT GAAAATGAAA	180
GTAAAAGCCA GAGTCAACCA AGTCGAAAAA AACGAGTGTT TGATGCAGAG AATAGTTCGA	240
ATAACATCGT AAATCATCAT CAAGCAGATC AGCAAGAACA ATTAACAGAA CAAACTCATA	300
ACAGTGTTGA AAGTGAAAAC ACTATTGAAG AAGCTGGTGAAGTTACGAAT GTATCGTATG	360
TTGTTCCACC GTTAACTTTA CTTAATCAAC CTGCAAAACA AAAAGCAACA TCTAAAGCTG	420
AAGTGCAACG TAAAGGACAA GTACTAGAGA ATACATTTAA AGATTTTGGG GTAAATGCAA	480
AAGTGACACA AATTAAAATT GGTCTGCAG TAACTCAATA TGAAATTCAA CCAGCTCAAG	540
GGGTTAAAGT GAGTAAAATT GTAAACTTGC ATAATGATAT TGCATTAGCT TTAGCAGCAA	600
AAGATGTTAG AATCGAAGCG CCAATACCTG GTCGTTCTGC AGTAGGTATT GAAGTGCCAA	660
ATGAGAAAAT TTCATTAGTT TCACTAAAAG AAGTTTTAGA TGAAAAATTC CCGTCTAATA	720
ATAAACTAGA AGTTGGATTA GAGAGAGATA TATCAGGTGA TCCAATTACT GTTCCACTAA	780
ATGAAATGCC ACAC	794

(2) INFORMATION FOR SEQ ID NO: 497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
AGCCAGTTTT GcATTTTCGTC AAATCGCAAT GAATATATTG ATTGCTTGTC AAAATTTGGA      60
AGAAAATTTAT TCTTCTTTTT CTTTTCAGCA GTTATCATTC CTATTGTCC TTTCTTTTTTA      120
TCTTAGTGAT AAAGAATCCA TCTGAATTAA AGTCTTGCGG CATGATTTGT AACGTTTTGA      180
CCAACTCTCC AGTTATCGGA TGTGAAACG GTTCAAATTC GAAGTTTTTA TTATTTTTCA      240
AAAACGTATA AATCACGTTT TCATTTTCTA GTTGCTCAAT TGTACATGTT GAATAGATGA      300
TTTCTCCACC TATTTTTACA TTGTTTTTTA CATTTTCCAA TATTTCAAGC TGTAATTCAA      360
CTAGTGACTC AATATGTTGT TTGCTTTGAG TATACTTAAT CTCCGGCTTA TGTCTCATTA      420
CACCTAATCC GCTACATGGT GCATCAACAA GTATCTTATC GTATGTTTTA TCATAAGGTT      480
TTGTGCGCATC ATGTTGAAAA GCTTTAATAT TTGTTAATCG TAATTnTTTT ATATTAAAAT      540
TAATTAAGTC TATTTTGTGA TCATGTATAT CTGAAGCGTC AACTTGCCCT TCTGGCATT      600
AAACTTCAGC AATGTGACAA GCTTTACCGC CAGGTGCACT ACATGCATCT AATACGTGAT      660
CATGTCGGTC TACATTCATA ATGTGTGCAa CAAACATTGA GCTTTTATCTTGAATTGAAA      720
CGAATCCATC TTAAATGAA CGAGAATGAA TAATTGGTTG TCCTCCTATA TGGAGACAAT      780
AAGGTAAGTC ATGATCTTTT TCAACGTCAT AACCTTCGTC TTGCAACTTT TCAATAATAT      840
CATCTAATGA TGCTCGCGTC AGGTTGGCAC GCACAGTTGT TGATGTCGTT TCTAAAAATG      900
ACTGTAAAAAT TTTTTCAGTT TCTTCGAGAC CATAATGTGT TGCCCAATGA TCTATAATCC      960
ACTTCGGCAT ACTATACTCG ATTGCCATTC TTTTTTTAGG ATCTGCAATT TCATTAAAAT      1020
CAGGTAAGTC ACTACGCATC ATTGTACGTA AAATACCATT TACGACATTA CCATTATGAT      1080
AGCCACCGCG TTCTTTTGCT ATTTCAACTG CTCATTAAT AATGGCATGA TTTGGAACCT      1140
TATCTAnATA nACATATTGA T      1161
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(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

```
AGCTCACGTC ATCTTCGGCG GCGCTAAATT AAAATAATCA ATTTCTGAGT TAACTTTTA      60
TTTACAACAT ACTATTACTA TACATTACAA ATTTTAAAA TATACATTAC ACTATTACT      120
```

CAATGGmAAG CGTATGATTT CmCAGCCCCC CTAGCTTGTA GAAATCATAC TTTCTTTTTT	180
TCAATATATA TACAACTATT AAATCCCATA AGATTGCAGA GCACATAAGT AAATTTTTTT	240
AGAGCTTGAG GTTTGTTTAG CTTAAGCAAC CCATGAGCTC AAACACTTCC TGTTACATA	300
ACACTACAAA TCGCATTATG TTGCTTAATC TTATGTTTAT ATAAATTACA CACAATAAAT	360
AGAAAGAATG TGAACATCAT GAATAAATTA TTGCTACTCG TTACATTTAT CATTCTGTGTG	420
GGTTCAGGTA TTGTTATGTT AATGCAAGGC TACGAAAAT TAACGGGCGG ATTTACGCTG	480
AAAGGTTTAG TACCAGTCAT CGCTAACAAT ACTGATCAC CAGAGTGGTA TAAGTGGTTT	540
TTCGCAAATA TAGTTGCACA TACGACGTCA TTATTTGATA TTGTTGTCCC ACTCGGAGAG	600
ATTGCAATTG GATTAGGTTT AATTTTTGGA GTTTTGCAT ATGCTGCTAG TTTCTTTGGA	660
GCCTTTGTTA TGATAAATTA TATCTTAGCA GATATGATAT TTACGTATCC TCTTCAATTA	720
ACTTTCTTTA TCCTTTTACT AATGAGTCAC TCATTGTAA AACAGATTTC ACTTAAAGAA	780
ATCATTAATT ACTTTAGAGG TCGTAAGAAC AGAGGTGAAA AAATAGATGA CCCACTTACT	840
GATCGTGGAT GATGAACAAG ACATTGTAGA CATTGTCAA ACCTATTTTG AATATGAAGG	900
TTACAAAGTA ACAACGCAA CTAGCGGTAA AGAAGCAATT TCTTTACTAT CAAATGATAT	960
TGATATCATG GTACTTGATA TCATGATGCC AGAAGTTAAT GGTTACGACA TTGTCAAAGA	1020
AATGAAAAGG CAAAAATTAG ATATCCCCTT TATCTATTTA ACTGCCAAAA CACAAGAACA	1080
TGATACCATT TACGCCTTAA CTTTAGGTGC AGATGACTAT GAAAAAAC CATTTAGTCC	1140
AAGGGAAGTC GTTTTACGTA TTAATAATTT ACTTACAAGA ATGAAGAAAT ACCATCATCA	1200
ACCAGTTGAA CAACTGTCGT TTGATGAATT AACACTTATT AACTTAAGTA AAGTtGTGaC	1260
tGTAAaTGGT CACGAaGTCC CTATGCGTAT TAAGGAATTT GAGTTATTGT GGTATTTAGC	1320
TTCTAGAGAA AATGAAGTTA TTTCTAAATC AGAATTACTT GAAAAAGTTT GGGGATATGA	1380
CTATTACGAA GATGCTAATA CCGTGAATGT CCATATACAC CGTATTAGAG AnAAATTAGA	1440
AAAAGAGAGC TTTACAACAT ATACCATCAC AACTGTATGG GGATTAGGAT ATAAATnTGA	1500
nAGG	1504

(2) INFORMATION FOR SEQ ID NO: 499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

ATTGAAAGCG ATAATTCGTA nTAATTGAGT TTGTTGAAAA ATTTAGGGTA ATGTAAAGAT	60
ATAAAAGATA CATAGAyTGG AGAGATATAA AGATGTTGAA TGAGATACAA ATATTaATA	120
aTGGATACCC GATGCCTTCA GTTGGGTTAG GTGTTTATAA AATCCTGAC GAAGATATGA	180
CTAAAGTTGT AAATGCTGCA ATTGACGCAG GCTATAGAGC GTTTGATACA GCATACTTTT	240
ATGATAATGA GGCTTCACTA GGACGAGCAT TAAAGGATAA TGGCGTCGAT AGAGAAGATT	300
TGTTTATAAC AACGAAGTTA TGAATGACT ATCAAGGTTA TGAGAAAACA TTCGAATATT	360
TCAACAAATC GATTGAAAAT TTACAAACTG ATTATCTTGA TTTATTTCTA ATACATTGGC	420
CTTGTGAAGC AGATGGTCTA TTTTtagAAA CATATAAAGC TATGGAAGAA CTTTACGAGC	480
AAGGTAAGGT AAAAGCAATA GGTGTATGTA ATTTTAATGT TCATCATCTA GAAAAATTAA	540
TGGCTCAATC AAGTATCAAA CCAATGtGA ATCAAATTGA GGTACATCCA TATTTTAACC	600
AACAAGAATT ACAAGAATTT TGTGATCGTC ACGATATTAA AGTGA CTGCA TGGATGCCTT	660
TGATGAGAAA TAGAGGACTA CTAGACGACC CTGTCATTGT TAAAATTGCT GAAAAATATC	720
ATAAACACC AGCACAAGTT GTATTACGTT GGCATTTAGC ACACAATAGA ATATTATTC	780
CAAAATCTCA GACACCTAAA CGCATTCAAG AAAATATAGA TATTTTAGAT TTTAATTTAG	840
AATTAACAGA AGTAGCTGAA ATTGATGCTT TAAATAGAAA TGCAAGACAA GGTA AAAATC	900
CAGATGATGT GAAAATTGGG GATTTAAAAAT AACTGGATGT TAAATTTTAC GTTTATGAAT	960
GCCTTTTAAT GTGTACATTA AAATAAATGA GTTGGTTTTT ACTATTTGAT AAAACAATAC	1020
TCAGGTACAT TCAAAATCTT TTAAATAAAA AGGATGGACA TAGATGAAAA TTAGAGTCGT	1080
CATTCCTTGT TTTAATGAAG GGAAGTCAT TACACAAACA CATCAACAAT TAACTGAAAT	1140
ACTTTCACAA GATAGTAGTG TGAAAGGCTA TGATATAAT ATGCTTTTCA TAGATGATGG	1200
TAGTACGGAT ACCACTATAG ATGAAATGCA ACATCTTGCC ACAATAGATA GGCATGTCAG	1260
CTTTATTTCT TTTAGTAGAA ATTTTGGAAG AGAAGCAGCT ATGATTGCAG GTTACCAGCA	1320
TAGTACTGAA TTTGATGCAG TCATCATGAT AGATTGTGAT TTGCAACATC CACCTGAATA	1380
TATTCCGAAA ATGGTTGAAG GTTTTATGGA AGGCTATGAT CAAGTGATTG CAAAGCGTGA	1440
TAGAAGTGGT GAAAATTTTA GTCGCAAAAC ATTAAGCCAT TTGTATTATA AGTTAGTTAA	1500
TTGCTTTGTA GAAGAAGTAC AATTTGATGA TGGTGTGGT GATTTTAGAC TTTTAAGCCA	1560
AAGAGCTGTT AAATCCATTG CATCACTTGA AGAATATAAT CGnTTTTCAA AAnGnTATT	1620
TGA	1623

(2) INFORMATION FOR SEQ ID NO: 500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 605 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

AAAGTnGGTG AAnCTATATA CTTAATCTAT ATTTATATAT TAACCATTAG GGTTAAAAAT	60
TACTCTAGCA TTTATGAATA GATGGGAGTT TATTTTATA TTATATAGGA GAGATGTTGA	120
ATGACACATC GCGCACTATT AGTTGTTGAC TATTCATATG ACTTTATCGC AGACGACGGC	180
TTACTAACAT GCGGTAAACC TGGACAAAAT ATTGAAGATT TTATTGTTTC TCGTATCAAT	240
GACTTTAATT ATTATCAAGA CCATATATTC TTTTTrtTGG ATTTACATTA TTTACATGAC	300
ATTCATCATC CTGAAAGTAA ATTATTCCCA CCACACAATA TCGTAGATAC AAGTGGTAGA	360
GAATTATACG GTAAAGTAGG TAAATTATAC GAAACAATTA AAGCGCAACC TAATGTACAT	420
TTCATTGATA AAACGCGCTA TGATTTCGTT TTTGGTACCC CGCTTGATAG TTTATTGAGa	480
GAAAGAAGTA TTAATCAAGT CGAAATCGTT GGTGTATGTA CCGATATTTG CGTGTTACAT	540
ACAGCAATTT CTGCATACAA CTTAGGtTAT AAAATTTTCTAG TACCTGCTGA GGGAGTGGCT	600
CATTT	605

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1739 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

TAGGTTnAAA GCATAGnTTT nTCAAAAAGA CAAATCATTCATATATTGGA GGATATTTTG	60
GTGTAAGATA TAGTGCAACC ACAATTGCTA AAGACTTGAA GGAACATAAT ATATATCGTG	120
TCCCTATCGA TTGTGAGACA TGGATTTATA AAGCTATTAA TAATCAAACA GAACAAGAGA	180
TGAGAGAAAA GTTTAGACAC TATTGTGAAC ATGAAGTTCT AAGTTCAATC ATCAATGGTT	240
CATACATTAT CGTCAAACCC TCACCTGGTT TCGCCCCAAGG CATAAACTAT TTTATCGATC	300
AGCTAAATAT AGAAGAGATA TTAGGTACGG TGAGTGGAAT TGACACTACA TTAATCTTAA	360
CTGCCTCAAA TGATATGGCA GAATACGTAT ATGCAAAATT ATTTAAATAG ACATGTATCA	420
AATGAATAAT AAAAATTTGT TCGTATCAC GTGTACTCAA GTTAGTTACC AAATATTAAC	480
TTGTGTACGC GTTTTTTTAT GGAAAGAAAAG AATTCATAGT CATTCAATTG ACTGTATAAA	540
AAACTTTATA CAACATGTTT TTATGGGTAT TTTTGAATAA AAAATGTATA TTTTGACCCA	600

AAATACCTTT ATTTATGTAT AAAAATCCAT TATTATGTAT TGTATAAA AA AAAGATATGA	660
AATTTTCGAC TTTCTTTATG TGAATATAAT CACATGTAAG CGTTTGAAGA TTGTCTATAC	720
TCTAAATGAA TTCAAAGATA AAAGGAGGAA ATAGACATGA CAGATGGTCC AATTAAAGTA	780
AATAGCGAAA TTGGAGCTTT AAAA ACT GTG TTACTTAAGC GTCCTGGaAA AGAATTAGAA	840
AATTTAGTAC CTGATTATTT AGATGGATTA CTATTTGATG ATATTCCATA TTTAGAAGTA	900
GCTCAAAAAG AGCATGACCA TTTTGCGCAG GTGCTAAGAG AAGAGGGTGT TGAAGTACTT	960
TACCTTGAGA AGTTAGCAGC TGAAAGTATT GAAAATCCTC AAGTAAGAAG TGAATTTATT	1020
GATGATGTAT TAGCAGAGTC TAAAAAACA ATATTAGGTC ATGAAGAAGA AATTAAGGCA	1080
TTATTTGCGA CACTTTCTAA TCAAGAACTT GTAGATAAAA TAATGTCAGG GGTACGTAAG	1140
GAAGAAATTA ATCCGAAATG TACACATCTA GTAGAGTATA TGGATGATAA GTATCCATTC	1200
TATTTAGATC CAATGCCAAA CCTTTATTTT ACTAGAGATC CACAAGCCTC AATAGACAC	1260
GGTATAACAA TCAATCGGAT GTTCTGGAGA GCACGACGAC GAGAATCAAT ATTTATTCAA	1320
TATATTGTAA AGCATCATCC TAGATTTAAA GATGCGAATA TTCCAATCTG GTTAGATCGA	1380
GATTGCCCAT TCAATATTGA AGGCGGCGAT GAACTTGTTT TATCTAAAGA TGTCTTGGCT	1440
ATAGGCGTTT CAGAACGTAC ATCTGCACAA GCTATTGAAA AGTTAGCGCG ACGTATTTTT	1500
GAAATCCGC AGGCGACGTT TAAAAAAGTA GTAGCAATTG AAATTCCAAC TAGTCGAACT	1560
TTTATGCACT TAGATACAGT ATTTACAATG ATAGATTATG ACAAATTTAC AATGCATTCA	1620
GCCATTTTAA 'AGGCAGAAGG CaATATGAAT ATATTTATA TTGAATATGA TGACGTAAAT	1680
AAAGATATTG CCATCAAACA ATCTAGTCnT TAAAAGATA CTTTAGAAGA CGTACTAGG	1739

(2) INFORMATION FOR SEQ ID NO: 502:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

CTGTACATAC AGCAATATCG TTAACAAATG AAAACAGTAT TTTAGGATTG TAAACCATGA	60
TAAACCTAAA ATACTGTTAT TTTTATTACT TAAATTTCTT CTTCAATGCC TTTTCA ACT	120
AAGGTGGAAC GAATTCAGAA ATATCTGCTC GATAAGCTGC AACTTCTTTA ACAATACTTG	180
AACTTATAAA TGAATAATTA GTACTAGACA TCATATATAA CGTTTCAATT TCATTGTTCA	240
ACTTTTTTATT CATTGAAGTT AAGCGTAATT CATATTCAAA ATCACTGACT GCTCTTAAAC	300
CACGTATGAT TGTTTTAGCT CCTACTTGTT CACAATAATC GACTAGTAAA CCACTAAATT	360

GATGAACCTT GACATTAGGT AAATGTTTAA CAGATTGTTC AATTAAATCC ATACGCTCTT	420
CTAAACTAAA CGTACCTTCT TTTTACTAT TTTTAAGAAC ACAGACATGA ATTTTCATCAA	480
ATCTATCTGT ACTTCTCTCA ATAATGTCTA AATGACCATAAGTAATGGGG TCAAAACTAC	540
CCGGAATGAC CGCTATTGTA TGTTCATGC TATTCTCCCT TTTCTAATAA CAATGTGTCT	600
GTCAACCCAT AATGGTAACG TTTAATCATA TTAAACGGTT GATAATCtAT TTCTTCATGA	660
TTGCTAAATT CACAAACGAT GATACCATTT TCTTTCAATA AATTAAACTC TGAAATTAGT	720
TTTAAAGCTT TATCAATGAG ACCTTTATTA TAAGGTGGAT CTAAaGAAAAT GACATCAAAT	780
TGAATATCAC GTTTTGACAA TGCTTTTAAA GCTCTATCTG CATTATTTTT ATAAACTTCA	840
GATTGTGCCT CTAAATCCAA ATTCGCAAGA TTTGaTTTAA TAACTTTTAC AGCTTTAAAA	900
TTTTGaTCAA CAAAGATTAC CtTATCCATA CCTCGAGAGA GTGcTTCTAT TCCAAGCGCC	960
CCGCTTCCTG CAAATAAATC TAAACCTATA CCTGACACAT CATATAAACT ATTAAAGATA	1020
CCTTCTTTAA CTTTATCCAT AGTTGGTCTC GTATTACGGC CTTCCATACT TTCTAAAGCT	1080
TTACTTTTAT GTTTACCTGC AATGACGCGC ATGTTGTTCA CACTTCAAT TCATTTAGTT	1140
ATTTAATATA ATTTATTGAG AAAAAGGAGA ATGATAAACC AATGAAACAA ACATTTATTA	1200
CACTTGGTGA AGGTCTAACA GATTTGTTCG AATTCATGAC GATGATTGAA TATAACCATC	1260
AACGTATTGA TAAAATTATC TATTTTCATT CACCACAAGC TGAAAATAAA AAGTCATCTG	1320
TAGCAATCAT TATGAACCCT ACAACTGGCA ATCATTTCCA AGCATTTTAT ATCATGATAA	1380
ACGCTATTAA ATATCCATAT CCAGATTCAA ATAAAAAGTT TCAAATGATA AATGATTGTG	1440
CTGAAAAATT CGACATACCA ATTTTAGGTA TCGATGTACA GCCCCCTCAA GCATTTTCATG	1500
ATTTATCGTT ATATTATAAT TATTTAATA GTGTGTTAAG GCTCCAAAAA TGGATACCAG	1560
aACTTCAATA ATATTAATTA TATATTTCTG GTTTCTCTTT TTCGTAAGTT TTCTTTAAGT	1620
ATTTATATGG TGAGCCATCA ATGTGTCTAA CGTATTTAAG TTGCATTAGT TTATGTACAA	1680
TTTGATCAAC ATCTTGCTCA TTCACATACA TAATTACAAA TTTACGATCT CTATTGAAT	1740
GAACG	1745

(2) INFORMATION FOR SEQ ID NO: 503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1035 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

TCGTCTTTAA TCTTGCTGAC TTTAGAAGGC TTACGAGTGC GGTTACCATT TTTTGCATCT	60
TTAACTGATT GAACTAAAGC TtGACGTGTA GATTTATCAG CTAAACTAAT TGCACCACCA	120
ATTACGGCAC CAATTAAAT ACCAGGAACA AATTTATTTT CCATAAAAAA CTACCCCTCT	180
TTCAAATTTG CATCTTTTAC GATGTAGTCT ATTAAATTAT CACAAGATGA TAATACCATG	240
TCGTATACAC CTTCAAATTT ATTTCGTGTAG TATGGATCTG GTACATCACT CTCTTCCATA	300
TTACTAAATT CTAACAGTTT GAACAATTGT CCTTAAGAT TAGGATTGAT AGATTTAATA	360
TTATCAACGT TACTTTGATC CATAGCCACA ATGTAATCAA AATCATCTGT CGCTTCGAAT	420
AATTCACTAA TCATGCCATC AAATGGAATA TTGTGTTTGT TGAGAATTTT TTGTGTACCT	480
TCATGAGGTG GCTCTCCTAA ATTCCAGCTA CCAGTACCTC TTGAATGTAC TTTAATACA	540
TGAATATTTT TGTCTTTAAG TCTTTGTCGC ATGATTGCTT CTGCCATTGG AGAACGACAT	600
ATATTGCCAA GACAGACAAA TGCTACATCT ACCATTTTGA TTCCTCCAAA CTATGTAGTT	660
ATATCCCCAT TTTATAGCGA CTTTAAACAA TAAGAAAGCA GATTATATAA AATTCTATTA	720
AAGTTTATTA AATTGTGATA CTTTGATAAC ATAACTATTA TTAGAGGTGA ACATTGTGGC	780
TATGACAAAT GAAGAGAAAG TnTTAGCTAT TAGAGAGAAG TTAAATATtG TTAATCAAGG	840
ATTATTAGAT CCTGAAAAAT ATAAAAATGC AAATGaAGAA GAATTAACAG ATATATATGA	900
TTTTGkTCaA yCAAGAGaAA GATTGTCGCC AAGTGaAGT mCAGCTATTG CTGaCGCTTT	960
AGGACAATTG CGACACGAAT AGGAGTGGA ATTTTACTA ATTACAAAGA AAAGTTACAA	1020
CAATACGCTG AACTA	1035

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

AnCCTGACAA GATTCTTATA TTCATAGATA TGAGAGCTAA AAATGAAATC AACAAACAnA	60
CAATAAAGTA AACGATAATA GCCCATATAC CATTTTGTA CCATATTACA AATTGTGTTG	120
TATTATAGCC ATTTCCAGCT AATAATTGCT GGATAAATGC ATTATTGTTT AATGTATTTT	180
CAAGATTAGC AAtCGATGTG TTATTACTGA ATGAAACAAG TGCTATAAAC ATCGTAATGA	240
CAGTAAGCAC TAATAACATC ACCCAACATA ACCAACCTAG AACTTTTTCA GTTAATCTAC	300
TTACTGGACG TTTAATTTGA GTAAATTGTT CTCCAGTCAT TCGTTACAAC TCCTTATAGT	360
ACTTATCCCG TTATTATAAC TAAATATACA GTAAATAACT ACTATTTATG ATTTTATTTT	420

AATGACATTT TGAAATTCAA AAAGTTTTCA TTGTATTAC TAAAACTTC AGGTCCTAAA	480
TCTTTATAAA CTTCAAGGCG TTCTTGCTCT TTCTTAGTCG GATAAAAACG ATGGTCGTCT	540
TTAATCTCTT TAGGCAACAA TTGTCGAGCA GCCTTGTTTG GCGTTGCATA GCCTACGAAT	600
TCTGTATTTT GCTTGTTATT TTTAGCATCT AATAAAAAAT TCATAAATTT ATATGCACCC	660
TCTTTATTTT GTGCCGTTTT TGGAATTACC ATATTGTCGA ACCATAAATT CGATCCTTCT	720
TTAGGAATAA CATAATTATA TTTATCCCCT TCTTGCACTA GAGGTGCTGC AACACCACTC	780
CAAACAACCG CTATGTTACC TTCATTTTGT TGAAGCATCA TGGTAATTTT ATCACCTACG	840
ACACCTCTTA CTTGTGGTGC TAGTTTGGTT AAATCTCGCT CTGCTTCTTT TAAATGGTGC	900
GAATTACGGT CATTAAGATT ATACCCAAGT TTATTCAAAC TCATGCCTAT AATCTCTCTA	960
GCACCGTCAA CTAGTAAAAT TTGGTTTTTA AATTTAGGAT TATACAATGA CTTCCAATA	1020
TCAAATGATT CATTGGATA CTTTTCTTTA TTATATAAAA TACCTACA TCCAAAGAAA	1080
TAAGGTAAAG AATATTTATT GCCTCTATCA AATGACATAT TCATATAATC TGAATCTAAA	1140
TTTTTAATAT TAGGTACCTT ATTATGATCT ATTGGTAACA ATAAATGATC TCTTTTCAAT	1200
TTTTGAACTG nATATTCAT AGGAnAAGCA ACATCATAAT GTGTACCGCC AGTGCGAATT	1260
TTGGnGTCCA nCGCTTCATT TGAA	1284

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

ATAATTAACA TCTTTTGCTA TATACCACCA GTTGATACA TAAATATCG CAGCAATAAT	60
ATCATGTTTA ACCCTAATGA TATTATCTGA TTTAATAAT AAGGTTGCTG TCCCTACAAC	120
CATTAATAAA ACTATGACTG CTGGTATTA ACGTTTTAAA CGACGTATCC AAAAGCTTTT	180
CAATTTAATG ATACCTGTGT CATCATACTC TTTGAGTAAT AAGCTTGTA TTAATAACC	240
AGAGATCACA AAAAATGTAT CCACACCTAA AAAGCCACCT GtCAACCATT GCTTATTTAA	300
GTGGTAAATA ATAATTCCTA GAACAGCGaT TGCCCTCAAA CCATCGAGCC TGGAAATATA	360
TCTCATTTTC TTATACTTTG TAAAACCCTT TGTTTTGTTC ATTTTTGCAT TCTTCCCTTT	420
TAAAACTGTT CTTCTTAGAT GCTTAATTAA ATTTAGTTAT GCTGTTTAAA AGAATATTGA	480
AATGCATATG TATATTATTG AATTACGACA TCATCAAAT CATATTGACT AAAATACTGT	540

TAAATTAAAA AAATTACCAA TGATGATTCT TACTTCGAAA TCCAATTTGT AATGCAACTC	600
GGCAACTTAA AAACATGAA GTATTATGTA TTGTAATATA ACTGTAATAT AAATTCAATT	660
TATTATAAAA ATTTTCAAGA AAATATTCAA CTAGAAAATG AATTGTGCAC TCTTGAAGT	720
GCAAGTCACT GTCTTAATTC ATATTTTTTG AA CA AAGTTA GATATAAATT TTCAAAATAA	780
AATCAGAAAC TAGAACATAA ATAAGGCTCC CTTCAAAATT TTCATTTTTC AATGTCTACT	840
TTGAAGGGAG CTTATTACACA ATGAATTATA CTCTACAATG TTATATTGAC TGC GG CCCCA	900
AACACAGAGA ATTTGAAAA GAAATTCTAC AGGCAATGCA AGTTTATGTT AGCTCACAC	960
AAGTGCAATC TTAGCGTAAC GTGACATCAT ATCTTTTGTC CAAGGTGGAC TCCATACGAT	1020
ATTCACCTCA GTATCCTGAA TTTCAGGAAT CTCTGCTAAT ACTGTTTTAA CTTGaTCAAT	1080
AATTTGAGGT CCCATTGGAC ATCCCATTGA TGTAAAGTC ATATCAACTG TACATACGCC	1140
TTCATCATCA ACATTCACCT TGTATACTAA ACCCAAATTA ACGATATCAA TTCCTAATTC	1200
AGGGTCAATT ACCATTTCTA ATGCACCTAA GATACTATCT TTCAATGCCT CTTCCATCCA	1260
TATCACCTCT TTAATGTCAT ATTATTCATA ATATATCAAA TATCCGACAA AACGCCAATA	1320
AAATGCTATG ATGTATCTAT ATGAACTAAG CAACTTATGAGGAGAGAT ATGCAACCAC	1380
ATTTAATATG TCTAGACTTA GACGGAACAT TATTAAACGA TAACAAAGAA ATTTTCATCAT	1440
ATACTAAACA AGTATTAAAT GAATTACAAC AACGTGGaCA CCAAATTATG ATTGCGACTG	1500
GCAGACCTTA TCGTGCAAGT CAAATGTATT ATCATGAATT AAATTTAACG ACACCAATTG	1600
TTAATTTTAA TGGCGCTTAC GTACATCACC CTAAAGATAA AAACCTTCAA ACTTGCCATG	1620
AAATTTTAGA TTTAGGCATC GCACAAAACA TTATTCAAGG ATTACAACAA TATCAAGTAT	1680
CGAATATTAT AGCAGAAGTG AAAGATTATG TTTTCATTAA CAATCATGAT CCAAGATTAT	1740
TTGAAGGTTT TTCAATGGGT AATCCAAGAA TTCAAACCTG TAATTTACTT GTCCACTTGA	1800
AAGAATCCCC TACCTCAATT TTAATTGAAG CCGAAGAAAG TAAATACCT GAAATCAAAA	1860
ATATGCTTAC TCATTTTTAT GCCGATCATA TTGAGCATCG ACGCTGGGGC GCACCATTCC	1920
CTGTCATTGA AATTGTAAAA CTTGGTATTA ATAAAGCAAG AGGCATT EG CAAGTTAGAC	1980
AATTTTTTAA TATTGACCGA AATAATATTA TTGCATTGCG TGATGAAGAT AATGATATTG	2040
AAATGATTGA GTACGCGCGT CACGGTGTTG CTATGGAAAA TGGTTTGCAA GAACCTAAAG	2100
ATGTAGCGAA CAATATTACA TTCAACAATA ATGAAGATGG CATTGGTCGA TATTTGAATG	2160
ATTTCTTTAA TTAAATATT AGATATTACT GTTAATTTAT AACTAATCAT TTTATAATAT	2220
TTTAAACAA TAGGAGGTAA GTTACGATGC CAAAATAGT CGTAGTCGGA GCAGTCGCTG	2280
GCGGTGCAAC ATGTGCCAGC CAAATTCGAC GTTTAGATAA AGAAAGTGAC ATTATTATTT	2340
TTGAAAAAGA TCGTGATATG AGCTTTGCTAATTGTGCATT GCCTTATGTC ATTGGCGAaG	2400

TTGTTGAAGA TAGAAGATAT GCTTTAGCGT ATACACCTGA AAAATTTTAT GATAGAAAGC	2460
AAATTACAGT AAAAAGTTAT CATGAAGTTA TTGCAATCAA TGATGAAAGA CAACTGTAT	2520
CTGTATTAAA TAGAAAGACA AACGAACAAT TTGAAGAATC TTACGATAAA CTCATTTAA	2580
GCCCTGGTGC AAGTGCAAAT AGCCTTGGCT TTGAAAGTGA TATTACATTT AACTTAGAA	2640
ATTTAGAAGA CACTGATGCT ATCGATCAAT TCATCAAAGC AAATCAAGTT GATAAAGTAT	2700
TGGTTGTAGG TGCAGGTTAT GTTTCATTAG AAGTTCTTGA AAATCTTTAT GAACGTGGTT	2760
TACACCTAC TTTAATTCAT CGATCTGATA AGATAAATAA ATTAATGGAT GCCGACATGA	2820
ATCAACCTAT ACTTGATGAA TTAGATAAGC GGGAGATTCC ATACCGTTTA AATGAGGAAA	2880
TTAATGCTAT CAATGGAAAT GAAATTACAT TTAAATCAGG AAAAGTTGAA CATTACGATA	2940
TGATTATTGA AGGTGTCGGT ACTCACCCCA ATTCAAATT TATCGAAAGT TCAAATATCA	3000
AACTTGATCG AAAAGGTTTC ATACCGGTAA ACGATAAATT TGAAACAAAT GTTCCAAACA	3060
TTTATGCAAT AGGCGATATT GCAACATCAC ATTATCGACA TGTCGATCTA CCGGCTAGTG	3120
TTCCTTTAGC TTGGGGCGCT CACCGTGCAG CAAGTATTGT TGCCGAACAA ATTGCTGGAA	3180
ATGACACTAT TGAATTCAAA GGCTTCTTAG GCAACAATAT TGTGAAGTTC TTTGATTATA	3240
CATTTGCGAG TGTCGGCGTT AAACCAAACG AACTAAAGCA ATTTGACTAT AAAATGGTAG	3300
AAGTCACTCA AGGTGCACAC GCGAATTATT ACCCAGGAAA TTCCCCTTTA CACTTAAGAG	3360
TATATTATGA CACTTCAAC CGTCAGATTT TAAGAGCAGC TGCAGTAGGA AAAGAAGGTG	3420
CAGATAAACG TATTGATGTA CTATCGATGG CAATGATGAA CCAGCTAACT GTAGATGAGT	3480
TAACTGAGTT TGAAGTGGCT TATGCACCAC CATATAGCCA CCCTAAAGAT TTAATCAATA	3540
TGATTGGTTA CAAAGCTAAA TAAATGAATC ATGCGATTCA ATCATCTT AATTGTCTAG	3600
GTTAGAATTA TGTTGGACTG GTACTACTAT CCAGTCCATT TTTTATGTTT AACATTTTTA	3660
GAATCAAAAA AGACATAAGG TCTTGGACTA ATAATTGTCC ATGCCTTATG TCATATACTA	3720
TATGTCTTAT CAATTAGCCA ATACCGAATA ATTTTGATAT AGGSCCTAAC GGTAGAATGA	3780
CACCTAATAC CATTGTGATG ATAATTAATG CAATTGTTAT CCAAAACATT GTGTGACTTT	3840
GTTCATGTCT CTTTCTTTTA GCAATCGACA CTTCCATCAA TCCAACTACT GCAACACCAC	3900
ACAGCATTTT CAATGTAAGC AACATATGAT TTGCCCCGCC ATTCATAAAT GACTGAATTA	3960
ATATCCAAAA TCCTGAAATT AACGTACA GCATAAATAA GCGTAAAATC ATGTGCAACG	4020
GTTTGAAAAA TGGTGATCTG CCTTGATTTT TTGAAATGTT TAAGTATGTA GCGATAAATA	4080
AAATAATCGC TAATACCCAA CTTAATATAT GTAAATGTAA CATACTGATT CCCCCACTT	4140
TAATTATTTA TATTATTAAA TTAAAGCTTC TTGGGATTAA TACCCACTTG TTGTAATTT	4200

AATCATGATT	TGATTATACA	CGAATATATA	TTCTACCACA	CTTCTATATT	TGAGAGGAAG	4260
AACATGACAT	TTTATTCCTT	ATTAGAATAT	TGTGAATCTG	CTGTAAAATA	ATCAACTACT	4320
TCTTAATATC	AATATTTTAC	TTTCATCTCA	AAATGGTAAC	ATTATAAATA	ATTTATCTTT	4380
AACACCTTTT	TAGAAAAGCA	AGAAAAAACT	AACCAATCTA	TATAAAGACT	GGTTAGCTTT	4440
TTAAATGATA	ATTATTTAGC	GATATAAGTT	GTCAGCGTTC	CAATATTATC	AATAGTCACT	4500
TTAACTTCAT	CACCTGGTTG	TAAAAATTTA	GGTGGTTGCA	TACCTGCACC	AACGCCTGCT	4560
GGTGTACCAG	TTGCAATAAT	ATCTCCCGGA	TGAGTGCAA	CATATTTTGA	AATTTCTTCT	4620
ATTAATTCAT	CAATTTTAAAG	AATCATTTTCG	CCAGTGTTAC	CATCTTGTCT	AATTTTCATTG	4680
TTAACTTTTG	TAACAATATT	TACATTTTCA	GGTAATGGTA	GTTCTGCTTT	AGTAACGATA	4740
TAAGGACCCA	TTGGGCAACC	GCCAGTTAAA	CTTTTGTATA	AAAATGCTTG	ATCTTGTG	4800
CTTTGTGCTT	TGCGATCAGT	GATATCGTTA	ATAATTGTAT	AGCCGTAAAC	ATAATCTAAA	4860
GCTAATGCTT	TTGGAATCTT	TTCACCAGAC	TTACCAATAA	CAATACCTAA	TTCACCTTCA	4920
TAATCTAATT	GATCAGTAAT	ATCTTTATGA	TTTGGGAATTG	TTGCATTATC	TCCTGTTAAA	4980
GATGACGCTG	CTTTGTAAA	TACATATAAT	TTTCCACTT	CATGATTTAA	TTCGTTGCA	5040
TGATCTTTGT	AATTTCTACC	AAAAGCAATC	ACATTATTCG	GAGGTGTTAC	TGGTGGTAAA	5100
AATTCAATGT	CATTAAATGA	AATTTTATAG	TCTTCAGCTT	TGCCGCTATC	TTCTGCTGCT	5160
ACAACCTGCTT	TACGTACTTG	TTCTTGAAAA	TCTAAAGTATG	ATTTTGTG	TAAACCAGCT	5220
AACAATGTTT	TAGGATGGAA	ATCTCCTTCT	GCAAAGTCAG	CAAATACTTG	TGTTAAATCC	5280
CATACAGCAT	CTTCGCGTTT	TACTTTAACG	CCATATGAAG	TTTTGTCATT	ATACTTGAAT	5340
GATAAGAATT	TCATTCATTC	TCAACTCCTC	ATCTTTATCT	TAATTCACAT	TATAACTTTT	5400
TTGTTATCA	AATAACAAAT	AAATAAGTAA	GACAATTTTG	AAAATGAGTT	GTGTTCATTC	5460
TGCTACAAGG	ACTTTGCACT	TAATCGAAAT	TATTTTTTAT	TCTTTTGAAA	ATCAAATAC	5520
TATAGTTGCA	ATGTACCAA	TTTGAAGAAG	TATAAATAAC	CTTTAACTTC	TTTATTAAGA	5580
ATCGTTTGAA	GCGTATTTTG	ATAATATTTT	ATCTGTATCT	TATATTTATT	TTTTAATTGT	5640
GTACCAATTT	CTTCATCTGT	CATCCCACGG	CGACGATTAA	ATGCATCGGT	TTTATAGTCT	5700
ACAAAATAAT	GCACACCATC	TTTAACAAAG	ATTAAGTCAA	TCATACCTTG	AATAATTGAG	5760
ACG						5763

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

CCATATGATT TTGTGCAATA ACTCTTTTTC TTTCTTCTTT TCGTAAAAAG TTGTACATCG	60
CTTTTGTGTT TAAGAGACTA TTGTTTTCTT TAGGTTTTTG AACTTCACTC AGTGTATTTC	120
TAGTTGTTAA CACTAAAATT CCAACTGTTG TATCTTTGTA TCTAGCCATA ACTTTATTCA	180
GATGTTTGTC ATTTGTAATA ACTACGACAT AATTAAACAC TTCATAATAA TCATTAATTT	240
GATTATCTAA TCTATCCAGC TTATCTAATT CTGTTTTAAT CTCATAGACA ACGCCTTTGC	300
CGTTTAACAA TATAAAATCA GCaATACTTT TCCCTATGGG CATCTCAGAA AGTGCAGTAG	360
TTGTATTAAT AGAATGTCGT CCTAGAGGA GTkTATTAAG TATnGTGTTT TTGTAAAAAT	420
AT	422

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

GCTTATGTAT TCTCAAATA TTTATGTGAT ACGCAAAGGA GACATGGTTA TTCGACCAGC	60
ATTTGATGAT GACGATCAAA GAAACGGTAG TGAAATAATT CGGTTT E CA AAACGCGTAT	120
TCAAATCCT TTAAAGTCC AGAAAATCAT TGAACGCTCT TGCAAATTTT ATGGTAATAC	180
TTATCTTGGC AAGAAAGCAG AGACAAACCG CATTACTGGC ATTTCTAGTA AACCACCTAT	240
TTTACTAACA CCATTATTTT CAACTTATTT TTTCCCAACA CATTCTGACA GACAAAATGA	300
AAATATTTGG TTAAATATGC ATTATATCGA AAGTATTA A A GAATTAAAAA ATCGTAAATG	360
TAAAGTGACA TTTATTAATA ATGAATCAAT CATTCTTCAT GTTTCATACC ACAGTTTATG	420
GCATCAATAT AACAATTCCA TTTTTTACTA TTACATGGTA GATAAACAAT CTCGCATGAT	480
ATCAAAAAAT CCCGACCAAC CAATAGAT A TAATAAAGCC ACATTGAATG TGTTTGAAGC	540
ATTGACACGC TATTCTTTAT TTGAAGATAA ATAAATTGTT TATTTTTTAA ATATGCGGAA	600
TGTTTTATAA ATATAGTGTA AATGTTCTGC ATATTTTTTT AAGGTATCTA TTGCAAATTA	660
ACTTAATCTT GTTATAATAA TATTTGTGCT TGaTATTCAA ACACATACAA ATTATCCAC	720
AGTAGCTCAG TGGTAGAGCT ATCGGCTGTT AACCGATCGG TCGTAGGTTT GAGTCCTACC	780
TGTGGAGCCA TTGGAAACGT ACTCAAGTTG GCTGAAGAGG CGCCCCTGCT AAGGtGTAGG	840

TCGCGAAA	gG	CGCGAGGGTT	CGAATCCCTC	CGTTTCCGTT	ACTTGCTAAA	ATGGTATATA	900			
CCATTTT	AnC	TTTTTTGTTT	ACTTATATAT	AATGAATGAG	AATTTCACTG	TTCTTTTATA	960			
TCAATTTT	TAA	AATTCTAAAA	ACCTTTCCTA	GATAATCTTC	TCTAAGAAAG	GTTTTTATAC	1020			
TTGTTGAACT		TATAATTAAT	TTATTACATA	GCAATATTTA	CCTGTTTTTA	ACTATAAAAT	1080			
TATCACTACA		TGAAATACGA	TAATTCCG	aT	CTCTTACTT	CTCTGC	aATT	AATG	tACTCA	1140
TTG	gTTTT	CAT	CGTATGATTC	ATGTATAATA	GCATTTkTTA	AATAATTC	1188			

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

CCCAACTTCG	GTTATAAGAT	CCCTCAAAGA	TGATGAGGTT	AATAGGTTCG	AGGTGGAAGC	60			
ATGGTGACAT	GTGGAGCTGA	CGAATACTAA	TCGATCGAAG	ACTTAATCAA	AATAAAT	120			
TTGCGAACAA	AA	tCACTTTT	ACTTACTATC	TAGTTTTGAA	TGTATAAATT	ACATTCATAT	180		
GTCTGGTGAC	TATAGCAAGG	AGGTCACACC	TGTTCCCATG	CCGAACACAG	AAGTTAAGCT	240			
CCTTAGCGTC	GATGGTAGTC	GAACCTACGT	TCCGCTAGAG	TAGAACGTTG	CCAGGCATAA	300			
TATTAATCCA	CAGTAGCTCA	GTGGTAGAGC	TATCGGCTGT	TAACCGATCG	GTCGTAGGTT	360			
CGAGTCCTAC	CTGTGGAGCC	ATGGCTCCTT	GGTCAAGCGG	TTAAGACACC	GCCCTTTCAC	420			
GGCGGTAACA	CGGGTTCGAG	TCCCGTAG	gA	GTCATACAAG	CAGAAGTGAA	ATATCGCTTC	480		
TGTTTTTTT	TA	TTACATATTT	ATTGTTGAGG	AAGGTTGTCCGAGCTGGCCG	AAG	aGCACGC	540		
CTGG	aAAGTG	TGTAGGCGTC	ACAAGCGTCT	CAAGGGTTCG	AATCCCTTAC	CTTCCGTAAA	600		
GG	cGCTTAAA	TTGGTTTTAC	CCATTTTAAG	CGCTATTTTT	ATTTTGGACT	CAATCCCTTG	660		
ATATATCTGC	ATTTGAGCTA	TTATCCTCAT	TTTTACACTT	CTTATTTATT	TATATCCATT	720			
TAA	ATTTTTT	TAGCCACAAT	GTGACTAATT	TTTG	aTGAAT	AATCCTAATT	TTAG	tCACAA	780
GATTTTGAAG	TTTAGTCACA	AAACAAATCA	TTCAGATTTT	TTTCy	ATAAAA	TTTAGTTTCA	840		

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

TTCTATGAAA CTATCAGCTG TTTCTTTTTC CTTGGTAAAA ATCGTTTTTAA CGCCATGATA	60
CATGTATTCT CTTTCAaCAC CCGATTGGTC ATAAGCATCG AAAACACAAA TAATTTTCATC	120
TGAAATAACT GCATTATAAT TTGCAATTGC ATCTATTAAT TGCATTCTAG CTTCTTCTAA	180
ATTCTCTTTT GCAATGGCGC TTAGCGTTGG TGATTGTCCT ATCATATTGT ATCCATCAAT	240
GATTAAGTAA CGTTCTTTCA TTATATTTCT CCAACATCAT GTTTTTTTCG AAATACTTCG	300
TACATCATTA AACTTGCTGC AACCGAAGCA TTCAAAGTGT TTACATGTCC AACCATTGGA	360
ATCTTAATAT AAAAATCGCA TTTATCACTT ACTAGGCGAC TCATACCCTG TCCTTCGCTA	420
CCAATTACAA TAGCCAATGA CATGTCCGCT TCTAGATTTC TATAATCTGT TGCATTATTA	480
GCTTCAGTGC CAGCTACCCA AAAGCCATTA TCTTTTAGTT CATCGATAGT TTTAGCTAAA	540
TTTGTCACTC GAATAACTGG TACATGTTCA ATTGCACCTG TTGAGGCTTT TGCAACTGTT	600
TGCGTTAGTG TAACTGAACG ACGTTTAGGA ATAATAACAC CATCAACTCC CGTTGCATCG	660
GCTGTTCTTA AAATTGATCC CAAGTTATGT GGGTCTTCTA AGCCGTCTAA TATAAGTACT	720
GTCAATAAAC CTTCTTTTTTC TTTTGTCTGT TTTAAAAATT GATCGAAGTC AGCATATTCA	780
TATGGTGCAA TAAGCGCTGC AACACCCTGA TGTGGTGCAT TTGCTAAAAA ATCTAATTTA	840
GATTTTGGTA CAGTTTGAAC AATGATTTTT TGATCTTTTG CATTTTTTAAAATTTTCATTA	900
ATTTGTTGCT TTTTAATACC TTCTTGAATC AATATCTTAT TTAyCGGATG CCCAGTAATA	960
ATCGCTTCTC TAACAGCATG CCTACCAACA ATAACCGTAT CTTCCACATC GTCACTmCCT	1020
TTCGTTTACT ATTGTTATTA TTTTATTTAA TAATGCCTCT AATCGTTCTT CTCTTTTTTC	1080
TAAATAaAGA AAACCTATCA CTGCTTCTAT CkCTGAACTT TTACGATATG TTTGAACATC	1140
AGTGTTTTTA GCTTTAGTAT GACTTTTCGC GTTACGCCCT CGCTTCAAAA TATCCATTTT	1200
TTCGTCTGTA AACCATTCTT GCTCCATTAA ATATTCTAAC GTTTGCGCCT GACTTTTGGC	1260
AGATACATAT TTTTtagaca TTTGATGTAG TTATTAGGC TTACTTTTAA GCTTTAAAAC	1320
GATATAGGTA CGTACATATT GATCTAaGAC TGCGTChCCC ATATATGCTA AGG	1373

(2) INFORMATION FOR SEQ ID NO: 510:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 717 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

TCAAGTGCCA ACTACACAAC TGATTTACAT TCTTTAGGTC AATATGTACA AGAAGGCCGT	60
CGCTTCTTAT TCGAAACAGT TGTAAAAGTA AATCATCCTA AATATGATAT TAAATTGAA	120
AAAGATAGTG ATGATCTAGA CGGATTAAAT TATTTAGCTG GTAAAACAAT CGACGAAGTT	180
AACACAAAAG CATTCGAAGG TACATTATTA GCGCATACTG ATGGTGGTGT TCCTAACATG	240
GTAGTGAACA TTCCACAATT AGATGAAGAA ACTTTCGGTT ACGTCGTATA CTTCTTCGAA	300
CTTGCTTGTG CAATGAGTGG ATACCAATTA GCGGTAAATC CATTTAACCA ACCTGGTGTA	360
GAAGCATATA AACAAAACAT GTTCGCATTA tTAGGTAAAC CTGGTTTTGA AGaCTTGAAA	420
AAAGrATTAG rAGAACGTTT ATAAAATACA TTAATTCAAA GATTAGTGAA GTTTGAAAAG	480
ATAGAACTAG ACGTTAACTA TTAAAGCAT ATTTGAGG TTGTCATTAC AAATGTAAAA	540
ATGTAATGAC AACCTCGTTT TTATTTATAT GCAAGAACTA GGTTACTAGC TAaTGTGACA	600
AGATGTTAAG AGAAAATTAA aGATAAAATA ATATCTGCCT TACAATAATA TTGTTATACT	660
ACTAGnGACT GATTTATTAG CATGATTACA TGTTAATGTT TCTTTACTTA GTAATTA	717

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

AATCTAATTT TTCCTCCTAA TCTCGGATTG GATAGTGGTC AATTTTTCTG GCCCGCCATT	60
TTAGCGTTTG TTCTAACTGG GATTGGTTTA CCATTATTAG GTGTGATTGT AGGTGCACTT	120
GATAAAGAAG GATATATTGG CGCATTAAAT AAAATTTTAC CTAAATTTTC AATATTGTTC	180
TTAATCATCA TTTATTTGAC TATAGGACCA CTTTTTGCAA TACCTAGAAC TGCATCTACA	240
TCTTTTGAAA TGACAATTAC ACCAATTATA CATAGCAATA GTAGTATCGC TTTATTTATA	300
TTTACGATTA TCTACTTCAT AGTCGTTTTG TATATTTGTT TAAATCCATC TAAGTTAATC	360
GATCGTATTG GTTCATTATT AACACCATTA TTATTGATA CTATTTTAGC GATGATTATT	420
AAAGGATACT TAGACTTTAG CGGTAATAGT GCTGGAAAGG GCAATGAAGC ACTATATCAT	480
TCTAATTTTT CAAGTTTTGC TGAAGGCTTT ACACAAGGCT ATTTAACAAT GGATGCCATT	540
GCAGCAATTG CTTTTTCAAT GATTGTTGTT AATGCAGTAA AACTAACAGG CATTACTAAA	600
ACAAATCAAA TATTCAAACA AACTTTGACT GCTGGTTTAA TTGCAGCCGT AGCTTTAATT	660
TTCATATATA TTTCATTAGG TTATATTGGT AATCATATGC CAGTAAGTGA CATGACGTTA	720
GATCAATTGA AATCCAAAGA TCGAAACATT GGGACATATT TATTAACGAC AATGGCTTCA	780

ACAGGATTTG GTTCATTTCGG AAAATATTTA TTGGGCATCA TTGTGGCGCT GGCATGTCTA	840
ACTACAGCAT GCGGGCTTAT TGTTCAGTT TCTGAATATT TCCATAGAAT CGTACCTAAA	900
GATCATACA AAGCATTTGT ATTAGTTTTT ATTTTAATGA GTTTTATTAT TGCTAACCAA	960
GGTTTAAATG CTGTTATCTC AATGTCAATT CCGGTATTAA GCATGTATA CCCAGTAGCA	1020
ATAACTGTTG TATTATTAAT TTTAATTGCC AAATTCATAC CGACAAAACG CATTTACAA	1080
CAAATTCAG TTATTATCGT ATTTATATTG TCGATTTTCA GTGTTATTAG TAAGTTAGGT	1140
TGGcTGAAAA TTAACTTTAT AGAATCATTG CCTCTAAGAG CGTATTCTTT AGAGTGGkTC	1200
CCAGTAGCAA TTATTGCAAC GATATTAGGC TATCTAGTCG GCATATTTGT AAAACAAGAT	1260
CCAATTAAAT ATCAACAGGA ATAACGAATA ATATAAAGA GGTGGGACA TAAATCCCTA	1320
AAAAACAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT	1380
ACAATACTTC GTATTGAATG GCTTCGTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG	1440
ACTGGCACTG CTCCCTCAGG AGTCTCGCCA TTAATACTAC GTATTAACGT GTAATTTTAC	1500
TTTGAAATAC TTTAAAAAA TAAGACACTT TGCCCAACTT GCACATAAAT GTAAAATTCA	1560
ATAAAATAAA TTTTCTGTGT TGGATCCCTT CGTATAATTT AATAAATACT ACAAATAA	1620
ATTAACGAGG TGCCTTATGT ATAAAAATTA TAACATGACC CAACTTACAC TACCAATAGA	1680
AACTTCTGTT AGAATTCCTC AAAATGATAA TACGCGATAT GTTAATGAAA TTGTTGAAAC	1740
GATATCTGAT AGCGAATTCG ATGAATTTAT ATGTCCTAAT AACAAAAGAA TAGGTTTTAA	1800
AAGATATGCA TACCGTAATG ATAGATATAG TTTTAAACGT GACTTCAAGC TATATGAATG	1860
TGATGACTGT TCATCATGTT CTTTGAGACA TCAATGCATG AAGCCAAATT CGAAATCCAA	1920
TAAGAAAATT ATGAAGAATT ATAATTGGGA ATACTTTAAA GyCCAAATTA ATCAAAAGCT	1980
TTCTGAACCA GAAACGAAAA AAATCTATAG TCAAGAAAA ATTGATGTAG AGCCTGTTTT	2040
TGGATTTATG AAGGCTATTT TGGGTTTCAC TCGAATGTCA GTTCGAGGAA TAAATAAAGT	2100
TAAACGAGAG CTAGGTTTTG TATTAATGGC ACTTAATATA AGGAAAATAG CAGCTCAACG	2160
AGCTGTACAT TATAAAATAC ATATCAAAAA AGCTGATTTT TATCAAATAA TTAATAGAAA	2220
TCAGCTTTTTT TACATTGCCT AAGAATTTAA TGTCCCAAGC CCTTTTTATC GAATAACTTA	2280
TTGTAAACCT TGTCTTTCTT GGTTATTGTT TTCGTTATTT TTTTCGTGTT TTTGTTTCCA	2340
CTCTTTTTTGA GTCATTACAT CGTCAACTTG CATGTAACT TCAACTACAT CTAAACCAGT	2400
AATATATTTA ACTTGTTCTT TAACTAATTC AGTTACTTTA CGGAAGATTT TTGGTGCTGA	2460
TTCACCATAT TCTAAGATTA CTTTTAAGTC TACAGCAGCT TGTTTTTCAC CAACTTCAAC	2520
AGATACACCT TGAGTAACAT TGTTGCCACT TGAGAATGCA TTAGTGAATG TATCAGTTAA	2580

GCCACCTTTC ATATCTAAGA TACCTTTAAC TTCACGTGCA GGATACCAG CAATTTTTTTC 2640
 AACAACTTCA TCAGAGAATG TTAATTTGnT TTTGAATTGA GGCTCCTGAT TTnGTTcNtG 2700

(2) INFORMATION FOR SEQ ID NO: 512:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

ATCAAATACA ATAATTAAAA TAaTGGCTAA TACaCCTAaA ATaATAATcG AGTTaGAGTA 60
 GCCTAAGCGA yCACCcTAAC aGTArACATT CTAGGCATAT ATTTaTCTTT AGACATTGAA 120
 GCCGCTAACA TCGGAAAAGC TGTAATCCA GTGTTGGCTG CTAATACCAA AATCATCACG 180
 GTCGTTGCCT GTACAAAATA GAAGGCAGCA TTATCACCAA ATATTTGCAT AGCTAATTGT 240
 GATAAAACTG TCGTTTCCGT TTGTGGcAAA ATTCCATAAA CATATGCTAA ACCAACGATA 300
 CCAACTAATA AAAACGCTm AATTGAACCC ATAGCAATTA ACGTTTTTCAC AGCATTTTTTA 360
 GCACTTGGCT CTCTAAAATT GGTTACCGCA TTTGAAATAG CTTCAACACC CGTTAACGAT 420
 GAAGCCCCTG ATGAAAATGC TTTTAATAsC AAGAATAATG TTA CTCCAGG AACCGCAGTT 480
 CCTACTGATG CATGCATATG TGGTTGAATa TCTCCTGTcG CCAeCGGAA AGTACCTATA 540
 AATATTAATA TCACTAACCC TATAATGAAA AGATATACTG GATAGGATAA TACGGTGGCA 600
 GATTcAGTTA AACCACGTAA ATTTAATATT AAAATAAAAA GTACAAGTAw ACATGCAATC 660
 AGTrCkTTAT GCCCATATAA ACTTGGAAT GCAGCAACAA ATGCATCAGC ACCAGATGAT 720
 ATmCTAACAG CGACAGTCAG TATGTAATCG ACTAATAATG AGCCTCCTGC AAGCAATCCC 780
 CATTTTTCTC CTAAATTGGT CTTGGACACC ATATACGCGC CGCCACCTTT AGGATATGCA 840
 TAAATAATTT GCCTATAAGA CATAATTAAA GCAGCTAATA AGATCAGAAC AGCACCTGCA 900
 ATCGGTAAAG TATACCAAGT TGCAACTGCA CCCACTACTG ATAGTGTAAT CAGTATTTGT 960
 TCGGGACCGT AAGCCACTGA AGATAATGCA TCCGACGAAA GAATCGCTAA CCCTTTAAAC 1020
 TTCGATATCT TTTCGTCTTT TAGTTCTCTG TTTTTTTTAG GTTGCCCTAT AATAAGtCTT 1080
 TTAAATTGAT kGAcATAAtC TCCTATTCCT TTTTATAGTT TTnGATGGAA eCAC 1135

(2) INFORMATION FOR SEQ ID NO: 513:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

TTATGGTAAA ACTTTAACAC AAGCATTACA TAAATCGCAA TCATTATGT GGCAAAAACG	60
TTGAATTTAA GCCATTTCTA TTCATTTTAC GTAATTATTA GCCGTATATG TGTAATAATA	120
CACATTTTAT TCAGATTTTT TATCGCGCTC CATTAAATCT TTTACGCATT CTTTTACTGA	180
GATATTTTCA AATAATACTC TATATAATGC ATTTGTAATT GGCATATCCA CATTTTTTTC	240
TTTAGCTAAA TGATAAACTG ATTTAGTTGT ATAAATACCT TCAACAACCA TATTCATTTT	300
AGATAATGCT TGATCCATTG ATTCACCTTG TCCAAGTTTA TATCCTAATG TGAAATTCCG	360
AGAATGTGTT GATGTGCAAG TAACGATTAA GTCACCGATA CCACCTAAAC CTAGAAATGT	420
CATAGGATCG GCACCTAACT TTTCACCTAA TCTACTAATT TCCGCTAAGC CACGAGTCAT	480
TAATGCAGCT TTTGCATTAT CACCGTAGCC AATTCCAGCT ACGATACCAC TTGCTACTGC	540
GATGATATTT TTCAATGCAC CACCAAGTTC AACACCAATC AAGTCATCAT TCGTGACAC	600
ACGCAAATAA TCATTCATAA ATAAATCTTG CGTTAATTTA CTTACACTTT TATCTTTTGA	660
TGAAGCAGCA ACTGTAGTTG GTTGCTTGAC TACAACTTCT TCCGCATGAC TTGGCCCTGA	720
CAACACGCCA ATACCTGCAT TATATTCAGG TGAAATAGAA TCTTCAATCA TTTCTGACAC	780
ACGTTTAAAC GTCCCATTTT CAATACCTTT AGCAACATGT ATAAAAGtCT TTTTAGAGGT	840
CAGCTTATCA TTAATTTGAG AAGCAACTTC TCGCATTGCT TTAGTAGGTA AAGCCATTAA	900
GTAAATATCT GCAAATTG	918

(2) INFORMATION FOR SEQ ID NO: 514:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

CAATACTCGG TATTATAGAT AGTCCTACTA CATTATATG GGTTTGATC ATTACATTAA	60
TTGCACATCA ACTTGAAGGT AATATCATT A CACCAAATGT AATGGGTAAA TCTTTAAGTA	120
TCCATCCTTT AACAATTATC GTTGTTATTT TAGCAGCAGG AGATTTAGGT GGCTTTACAT	180
TAGTTCTGAT TGCAGTGCCA TTATATGCTG TACTTAAAAC GGTTGTTAGT AATATTTT	240
AATACCGCCA ACGCATTATT GATAAAGCAA ACAGTAATGT TAAGGACTAA TTCTGTGGAT	300
GTCTTTTAAG AATATAAGAT ACTATCGCAT CAAAAGTTGA AACTACAGCT TTTGAGGCGA	360

TTTTTTTGTG CATAAAAAAT CAGTCmAAATG AAATATCAAA TAATTTTCCA TCAGTCCGAT	420
TATTATAAAA GCAAAAAAGC TTTGCTCACA TATATAATAA CGTGAACAAA GCTGTTGAAT	480
GATATTATTT AATTGCGTGG AATCCGCTAT CTACATGAAT ATTTTCACCT GTAACGCCAC	540
TTGATAAATC ACTTAATAAG TAAGCCGCAG TTTTACCTAC TTCTACT	587

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

GGTTCATTCC AAAAAAGTAC GCGATAATTA GCGAAGAGA ATTTGAAAAT TTAAATGTTG	60
TTAAACCAAAA TAAAAATAAT GTTTTCTGGT CAGTTATAGG AAGTTCGGTT TTGTTTGAG	120
TTACTTTAAG GAAATACATA CATGTTTTTG ATGTTCAATT AGATAAGCTA GTTGTAATGA	180
TATTGTGTGC TCTCGCTTTA ATTTGTGTTA TAGTTTTTTA TTTTAACTTA AATAGAAAGC	240
TTAAGTTAAA AGTGTTTGAT ACAAATATTG AAAAAATAA GAGAGTTATA TAAAwAcCAA	300
CGTTTAAACT TGGCTGTTTT TTAGTTTTCG GATATATTTT CGCTGGAAGT TTTTCAATAT	360
TTTCATTAAT TGCCCTTATG ACAATCGAAC CTCAAAATAT AATAATATTT ATTTATTGGA	420
TTATGATGAC AATGCTTTTC TTTTGTGTTA ATATGACTTC GATAGGTAAT GAAAAAGTTC	480
GCGTTATAAT GAAAAATAAT TGATTACATT TAAAATATTC TAAATGTTGT CGACACAATC	540
CTTTTAAGAC GCTAGTAGAA TTTAAATGAC TTCTAATGTA TATGAAAGTG TATCAATATA	600
AAACCAATTG AAAAGAAGTG GAGACATTGC TTTGTGAAAC TGAAATATT AATAAGAATC	660
CCAAATATAG AATTATCAAA TACAAAGATG AATATTTGAT GATTGATTTA GTAAGTACAT	720
GGTTAGCACT CTTTTTCCCA ATGATTAATT GGCTGATTCC AAAAAAGTAC GTCAAAATCA	780
GCGAAAAAGA TTTTGAAACT TTAAACATTG TG	812

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

GTTCTATTAT TTCTTCCAAT GGTAATGGAT TTTCGTAAAA TGATTGATAT AAGTTGATAA	60
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TCTCAATAAC TTTTAATTGA TCTGGAAACA TCGTTTTTTG GAACATTATA CTGCGATTTT	120
CACTTTGTAA TAACCTGTCT TTATCAAATA TCTCACCAGA ATTAGCATTACATTACCAA	180
TTAATATATC AATTAACGTT GACTTTCAG CACCATTTTT TCCAATTAAA GCGATACATT	240
TACCTTGTTT AATATCGAAC GAAATATTTT TTAGAACACA TCTTTTATTA AATGACTTGT	300
TGATATTAGA TATTTGAATC AATTTAATCA CCTCTATTTT TTTCTTAATT TAATATTAGT	360
AAATTTATTA GATTTAAAT AGAACACTTT GTCATAGATT TGAAATGGA AATGTCATTA	420
TTAGATkTAC ATAATATATT TATCGTtATT TTAATTTTGG GCAAAATAAA AAGAGCCTCT	480
ATAATCGrGc TCCTTACAAA TAaATTATAA AAttGGCGAA cTAAAT	526

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

TGGGTTGATG AAGTTGATAA GTGGAACCAT TTAAATCATC TGAAAGTGTC TTTAGTCTTA	60
GGAACACCTA AAGAAAGAAA TGATGCATTA AACACAGAGG CTGATATCTA TGTAACCAAT	120
AAAGAAAATA CTAAATGGTT ATGCGATCAA TATAAAAAG AATGGCCATT TGATATGGTT	180
GTAATTGATG AACTGTCTAC ATTTAAAAGT CCTAAGAGTC AAAGGTTTAA ATCTATTAAA	240
AAGAAATTAC CACTCATTAA TAGATTTATA GGATTAACAG GAACACCTAG CCCAAATAGT	300
TTACAGGATT TATGGGCTCA AGTTTATTTG ATAGACAGAG GCGAAAGACT TGAGTCTTCA	360
TTCAGTCGTT ATCGAGAAAG GTACTTTAAA CCAACACATC AAGTTAGCGA ACATGTTTTT	420
AACTGGGAGC TAAGAGACGG ATCTGAAGAA AAGATATATG AACGAATAGAAGATATATGT	480
TTAAGCATGA AAGCGAAAGA TTATCTAGAT ATGCCTGACA GAGTTGATAC TAAACAAACA	540
GTAGTCTTAT CTGAAAAAGA AAGAAAAGTA TATGCAGAAT TAGAAAAAAA CTATATTTTA	600
GAATCGGAAG AAGAAGGAAC AGTTGTAGCT CAGAATGGGG CATCATTAAG TCAAAAACCTA	660
CTTCAACTAT CTAACGGTGC AGTTTATACA GATGATGAAG ATGTAAGACT TATACATGAT	720
AAGAAGTTAG ATAAGTTAGA GGAAATTATA GAGGAGTCTC AAGGCCAACC AATATTATTG	780
TTTTATAACT TCaAACATGA TAAAGAAAGA ATACTTCaAA GGTTTAAGGa AGCAACCACA	840
TTaGAGGATT CAAACTATAA AGAACGTTGG AATAGTGGAG ACATTAAGCT GCTTATAGCA	900
CATCCAGCAA GTGCAGGGCA TGGATTAAAC TTACAACAAG GTGGGCACAT TATTGTTTGG	960

TTTGGACTTA	CATGGTCATT	GGAATTATAC	CAACAAGCAA	ATGCAAGATT	ATATAGACAA	1020
GGACAAAATC	ATACGACTAT	TATTCATCAC	ATTATGACCG	ATAACACAAT	AGATCAAA	1080
GTATATAAAG	CTTTACAAAA	TAAAGAACTA	ACGCAAGAAG	AATTGATGAA	AGCTATTAAA	1140
GCAAGAATAG	CTAAGCATAA	GTAATGGAGG	TATAAGATGG	GAAAGGCATC	ATACGATATT	1200
AAGCCAGGTA	CATTTAAATA	TATTGAGTCA	GAGATATATA	ACCTACAAGA	GAACAAGAAA	1260
GAGATAAATA	GATTGAGAAT	GGAGATACTT	AACCCAACGA	AAGAGCTAGA	CACTAACATT	1320
GTGTATGGAC	CGTTGCAAAA	AGGTGAACCA	GTTAGAACAA	CTGAACTAAT	GGCAACAAGG	1380
TTATTGACTA	ATAAGATGTT	ACGAAACCTA	GAAGAAATGG	TCGAAGCAGT	TGAAAGTGAA	1440
TACTTAAAGT	TACCTGAAGA	TCATAAGAAA	GTAATTAGGC	TAAAGTATTG	GAATAGAGAT	1500
AAGAAGCTAA	AGATAGAGCA	AATAGGAGAT	GCATGTCACA	TGCATCGTAA	TACAGTTACT	1560
ACTATACGAA	AGAACTTTGT	TAAAGCGGTA	cGwtATCATG	CAGGTATCAA	ATAACATTGT	1620
GCAAAGATTG	TGCAAAAGGC	CTACAAATCT	GTAGTAATAT	GATAGTATCG	GAAAGATGTA	1680
TAAAGTTATC	TAAAAGTTAT	ACGACACAAG	TACACGAGGC	ACATCGCTAT	GCGtGTGTCT	1740
TTTGTTATGC	AATCAAAGAG	GTGTAAGAGA	TGACCAAGCA	TAATAACATT	TATAAGCATG	1800
GTCGTAAGTC	ATATCAATAC	GATTGGTTCT	ATCATTCAAA	AGCATGGAAG	AAGTTAAGAG	1860
AGATAGCATT	AGATAGGGAT	ATCATCTTT	GTCAAATGTG	TTTACGTGAA	GACATAGTAA	1920
CAGATGCAAA	CATAGTGCAT	CATATTATTT	ATGTTGATGA	AGATTTTAAT	AAAGCTTTAG	1980
ACTTAGATAA	TTTGATGTCA	GTTTGTATA	GCTGTCATAA	CAAAATTCAT	GCAAATGATA	2040
ATGACAAAAG	TAATCTTAAG	AAAATTAGAG	TATTA AAAAT	TTAAATAAA	AAATAATTTA	2100
TTTTTATAGC	CCCCTACCCA	TCGGCTTAAA	ATGTTTTTTC	GACGGGTACC	GGCGGGGGCC	2160
CTTCGCTTGC	AACGCGGATA	AAC TTTTATG	AAAGGGGGTC	TTTATATGAA	ATTAACAAAA	2220
AAACAGCTGA	AAGAATATAT	AGAGGATTAT	AAAAAATCTG	ATGACATATT	AATTAATTTG	2280
TATATAGAAA	CGTATGAATT	TTATTGTCGG	TTAAGAGATG	AACTTAAAAA	TAGTGATTTG	2340
ATGATAGAGC	ATACAAACAA	GGCTGGTGCG	AGCAATATTG	TTAAGAATCC	ATTAAGCATA	2400
GAACTGACAA	AAACAGTTCA	AACACTAAAT	AAC T TACTCA	AGTCTATGGG	TTTAACTGCA	2460
GCACAAAGAA	AAaAGATAGT	TCAAGAAGa	GGTGGATTCTG	GTGACTATTA	AAGTTTTTAA	2520
TGAACCTTCA	CCAAA ACTAT	TAACAACATG	GTATGCAGAG	CAAGTCACTC	AAGGGAAAAT	2580
AAAAACAAGC	AAATATGTTA	AAAAAGAATG	TGAGAGACAC	CTTAGATATC	TAGAAAATGG	2640
AGGTAAATGG	GTATTTGATG	AAGAATTAGC	GCACCGTCCT	ATTCGATTCA	TAGAAAGTT	2700
TTGTAAACCT	TCCAAAGGAT	CTAAACGTCA	ACTTGTATTA	CAACCATGGC	AACATTTTAT	2760
TATTGGCAGT	TTGTTTGGTT	GGGTT CATAA	AGAAACAAAA	CTGCGCAGGT	TTAmAGAAGC	2820

TTTGATATTT ATGGGGCGAA AAAATGGTAA AACAACTACT ATATCTGGTG TTGCTAACTA	2880
TGCTGTTTCT CAAGATGGAG AAAACGGCGC TGAAATCCAT CTTTtagCAA ACGTAATGAA	2940
ACAAGCTAGG ATTCTATTTG ATGAATCTAA GGCGATGATT AAAGCTAGCC CAAAGCTTAG	3000
AGAAAATTTT AGACCTTTGA GAGATGAAAT TCATTACGAT GCAACTATAT CTAAAATTAT	3060
GCCACAGGCT TCAGACAGTG ATAAGTTGGA TGGTTAAAT ACACATATGG GCATTTTTGA	3120
TGAAATTCAT GAATTTAAAG ATTATAAATT GATTTcAGTT ATAAAAAACT CAAGAGCGGC	3180
AAGGTTACAA CCCCTTCTTA TCTACATTAC GACAGCAGGG TACCAACTAG ATGGACCACT	3240
TGTTAATATG GTAGAAGCGG GAAGAGACAC CTTAGATCGA ATCATCGAAG ATGAAAGAAC	3300
TTTTTACTAT TTAGCTTCTC TCGATGATGA CGATGATATA AATGATTCGT CGAATTGGAT	3360
TAAAGCAAAT CCTAACCTAG GTGTTTCTAT CGATTTAGCT GAAATGAAAG AAGAGTGGGA	3420
AAAGGCTAAG AGAACACCAG ATGAACGTGG AGATTTTATA ACCAAAAGGT TTAACATCTT	3480
TGCTAATAAT GATGAGATGA GTTTTATTGA TTATCCAACA CTTCAAAAAA ATAATGACAT	3540
TATTTcCTTA GATGAGTTGG AAGGTAGACC ATGTACTATA GGTTATGATT TATCAGAAAC	3600
AGAGGACTTT ACAGCCGCAT GTGCCACTTT TGCATTAGAT AATGGCAAAG TTGCTGTCTT	3660
AACACATTCT TGGATTCCTA AGCATAAAGT TGAATATTCT AAGAAAAGA TACCCTATAT	3720
AGAATGGGAA GAAGACGGAT TACTAACAAT ACAAGATAAT CCTTATATAG ACTACCAAGA	3780
TGTTTTAAAT TGGATAATAA AGATGAATGA GCATTATGTT GTCGAAAAAA TCACTTATGA	3840
TAGGGCGAAT GCTTTTAAAT TAAATCAAGA GTTAAAGAAT TATGGCTTTG AAACAGAAGA	3900
AAcWAGACAA GGGGCTTTGA CCTTGAGCCC TGCaTTGAAG GATCTAAAAG AAATGTTTTT	3960
AGATGGGAAA ATAATATTTA ATAATAATCC TTTAATGAAA TGGTATATCA ATAATGTTCA	4020
GCTGAAACTA GACAGAAATG GGAActGGCT GCCATCTAAA CAAAGCAGAT ATCGTAAAAT	4080
AGATGGTTTT GCAGCATTTT TAAAACATA TACAGATATT ATGAATAAAG TTGTTTCTGA	4140
CAAGGGTGAA GGAAACATAG mATTTATTAG TATTArAGAT ATAATGCGTT AAGGAGGTGA	4200
ATGTTATCGC AAAAGAGAAT ATTGTCACAC GCATAAAGAA AAAATTGATA GACAATTGGA	4260
TTGaTCAGTC AGCTTCTAAG CTTTATGACT TTAGCCCATG GAAAAATAAATCTTTTTGGG	4320
GTGTAATCAA TAATACGCTT GAACTAATG AAACGATATT TTCAGCTATT ACnAAGTTAT	4380
CTAATTCGAT GGCTAGTTTG CCCTTGAAAA TGTATGAAGA TTATAAAGTA GTTAATACAG	4440
AAGTATCTGA TTnACTTACA GTGTCACCGA ATAATTCTCT GAGCAGTTTT GATTTTATTA	4500
ATCAAATTGA AACAATCAGA AATGAAAAAG GTAATGCATA TGTG	4544

(2) INFORMATION FOR SEQ ID NO: 518:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 881 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

CATGGCAGAA TATTGAAGCT GTAAAAAAG GACATGTAAT TTCATATAAA GCAGAAGATT	60
ATTGGTTCAC AGATCCTATT ACATTAGAAC ATTTGAGAAG TAAATTAAAA AAAGAAATTT	120
TAAATAAAAA ATAATAGAAA TAAGTTGTAA AAATTTTCTT ATGCATTGGT ACTAATGTTT	180
TTAAGGAGTG ATTAAATGAA GCAACTGGTT GGAATTCCTG AATCAATGTT AATTCCTTTG	240
ATAGCTCGAG CAAAAGAGTA CGAAAACGAA AAACCAATAA TAAAAGACGC ACTATCAAAA	300
AAAATATTTG ATGTTTTAGA TGATATGTAC AAAAATGTTA CATGTGATGA CATCTCAA	360
ATTGGAATTA GTATACGTAC TGTGATAATA GATTGTGTTA CTAAGAGGCT TATCAAGGAT	420
AATAAAGATT TAATCGTGGT CAATATAGGT TGTGGCTTAG ATACAAGGTT TCAAAGATTT	480
AATAAAGAAA AAATATCATG GATAGATTTA GATGTACCAG AATCAATAGA AATACGAAAA	540
ACATTTTTTA AAGAAAGTAA TAGTTATAAG ATGATATCTA AATCTATGCT AGATTACAGT	600
TGGATTGATG ATGTCAAAAA TTATAAATTT TTTAATAGTA AGTCAGATAT ATTGTTTATT	660
ATTGAAGGTG TATTGATGTA TTTTGATGAG AGTGTAATGA CTCAATTATT GGACACTATT	720
ATCAAAAAGA TGGGAGATCA TAATTTGACA TTTGCATTg AATTTTGCTC aAAAACAATT	780
GCGAATAATA CnAAGAGACA TCAATCGGTA TCCAAGTTAT CCTCACCACC TGTTTTTAAA	840
TATGGGTACC ATGATTTAnA AAAATTGGAT GAnATTTACC C	881

(2) INFORMATION FOR SEQ ID NO: 519:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

TGAATaaAAA TATATTAATA GATAAACACA AATGTGTCcA AATACCCCTA GAGGTATTG	60
ACnAGTTCCA TCCAAGTGT TAAAATACCC CTACAGGTAT TTTTAGGGAG GTTATTATGA	120
AACAATACGG AGAAAaGTTT ATCGATGAAT TTAGTAAAGC AGAATTGGAA AAAGTAGCCA	180
AGCAAGGGCA ATTAATTGAC GTTAGAACAG AAGAGGAGTA TGCATTAGGA CATATCAATG	240
GTTCCATACT TCATCCTGTT GATGAGATTG AGTCATTCAA TAAAGAAAAA AATAAACCT	300

ATTATGTAAT CTGTAGAAGT GGTAACAGAA GTGCTAATGC TAGTAAATAT TTAGCTAAAC	360
AAGGTTATAA CGTTATAAAT CTTGATGGTG GTTATAAAGC TTATGAAGAA GAAAACGATA	420
GTTATGATAC ACAAGAAGAA TATAAAAGTA TAGAAATTAGCAGATCGT AAACAATTTA	480
ACTATCGTGG TCTTCAATGT CCAGGGCCAA TTGTAAAAAT TAGTCAAGAA ATGAAGAATA	540
TTGAAGTAGG TGACCAAATT GAAGTCAAAG TCACAGACCC TGGATTCCCT AGTGACATTA	600
AAAGTTGGGT GAAACAAACA AGGCATACTT TAGTTAAGCT TGATGAAAAT AACAATGGAA	660
TTAATGCGAT TATTCAAAAA GAAAAAGCAA AAGATTTAGA TATAAATTAT TCTGCTAAAG	720
GTACTACAAT TGTATTATTT AGTGGAGAAT TAGACAAAGC TGTAGCAGCG TTGATTATTG	780
CAAATGGTGC TAGAGCTGCT GGAAAAGATG TAACTATCTT CTTTACTTTT TGGGGGCTTA	840
ATGCATTAAA AAAAGTGCAA ACAGTTAATG TTAAAAAGCA AGGTATTGCA AAAATGTTTG	900
ATTTAATGTT GCCCAAAAAG AATATACGAA TGCCTCTTTC CAAAATGAAT ATGTTTGGTT	960
TAGGAAATAT GATGATGCGC TACGTAATGA AAAAGAAAAA TGTTGATTCA TTACCAACAC	1020
TTATCAATCA AGCTATTGAG CAAAATATCA AATTAATCGC TTGTAGATG AGTATGGATG	1080
TCATGGGTAT TCAGAAAGAA GAACTTAGAG ATGAAGTTGA GTACGGTGGT GTAGGCACTT	1140
ATATTGGTGC TACTGAAAAT GCGAATCATA ATTTATTTAT CTAATTAAAT CTATTAATAA	1200
AAGGAGTTGT TATCATGTTT TTAAACAGT TTTACGATAA TCATTTATCT CAAGCATCAT	1260
ATTTAGTGGG TTGTCAACGT ACAGGAGAGG CAATAATAAT AGACCCTGTT CGTGATTTAT	1320
CGAAATATAT AGAAGTTGCA GATTCTGAAG GTTTAACAAT TACACAAGCT ACAGAAACAC	1380
ATATTCATGC TGATTTTGCT TCAGGAATTC GTGATGTGGC TAAACGCTTA AATGCAAATA	1440
TATATGTGTC TGGCGAAGGT GAAGATGAT TAGGGTATAA AAATATGCCA TCAAAAACAC	1500
AATTTGTTAA ACATGGAGAT ATCATTCAAG TAGGCAATGT TAAATTAGAA GTTCTGCATA	1560
CTCCAGGACA CACGCCTGAA AGTATTAGCT TTTTACTCAC TGATTTAGGT GGTGGTTCAA	1620
GTGTTCCGAT GGGATTATTT AGTGGTGAAT TATTTTTTGT TGGTGATATA GGAGACCTG	1680
ATTTATTAGA AAAATCTGTT CAATAAAAGG GTTCTACAGA AATTAGCGCG AAACAAATGT	1740
ATGAGTCCGT TCAAAATATT AAAAATTTAC CAGACTATGT TCAAATCTGG CCGGGTCATG	1800
GTGCTGGAAG CCCTTGTGGT AAAGCATTAG GTGCCATACC TATATCTACA ATAGGTTATG	1860
AGAAAATTAA TAACTGGGCA TTTAATGAAA TTGATGAGAC TAAATTTATT GAATCATTA	1920
CATCAAATCA ACCAGCACCA CCGCATCATT TTGCACAAAT GAAACAAGTT AATCAGTTTG	1980
GTATGAATTT ATATCAATCA TATGATGTTT ATCCTAGTTT AGATAATAAG AGAGTAGCAT	2040
TTGATCTTCG TAGCAAAGAG GCCTTTCACG GTGGCACAC AAAAGGAACA ATCAATATAC	2100

CATACAACAA	AACTTTATT	AATCAAATTG	GTTGGTACTT	AGATTTTGAA	AAAGATATAG	2160
ATGTAATTGG	AGATAAATCT	ACTGTTGAGA	AAGCGAAACA	CACTTTACAA	TTAATTGGGT	2220
TTGATAAGGT	AGCAGGCTAT	CGTTTGCCAA	AATCAGGCAT	TTCAACCCAG	TCCGTTTATA	2280
GCGCTGATAT	GACAGGTAAA	GAAGAACATG	TATTAGACGT	ACGTAATGAT	GAAGAGTGGA	2340
ATAATGGACA	CTTAGATCAA	GCAGTTAATA	TTCCGCATGG	TAAATTATTA	AATGAAAATA	2400
TTCCTTTTAA	TAAAGAGGAT	AAAATATATG	TACATTGTCA	GTCAGGTGTT	AGAAGTTCAA	2460
TTGCAGTGGG	TATATTGAA	AGCAAAGGTT	TTGAAAATGT	GGTGAATATT	AGAGAAGGCT	2520
ATCAAGATTT	TCCAGAATCA	TTAAAAATAAT	TTAAGGATGT	GGAAAAAATG	AATAAGCATT	2580
ATCAAATTGT	TATTATTGGT	GGCGGTACAG	CAGGTGTTAC	CGTAGCATCA	AGACTATTAA	2640
GAAAAAATCA	AACTTAAAA	GAGAAAATAG	CAATTATAGA	TCAGCAGAC	CATCATTACT	2700
ATCAACCATT	ATGGACGTTG	GTTGGTGCAG	GGGTATCTAG	TTTGAAAAGT	TCTCGTAAAG	2760
ATATGGAAAAG	TGTTATACCT	GAAGGTGCTA	ACTGGATAAA	ACAGGCTGTT	TCAAGTTTTTC	2820
AACCTGAAAA	TAATAGCGTT	ATTTTAGGAG	ATAATACAGT	CGTTTATTAT	GATTTTTTTAG	2880
TAGTAGCTCC	AGGATTACAG	ATTAATTGGT	CTTCAATTAA	AGGACTAAAA	GAAAATATAG	2940
GTAAAAATGG	TGTTTGCTCT	AACTATTCAC	CTGACTATGT	TAACgAAACT	TGGAACCAAA	3000
TTTCTAATTT	TAAACAAGGA	AATGCCATTT	TTACGCATCC	AAACACTCCT	ATAAAGTGTG	3060
GAGGTGCgCC	TATGAAAATT	ATGTATTTAG	CTGAAGATTA	TTTTAGGAAA	CATAAAATCC	3120
GT						3122

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ATAnAGATAT	AnATnAATAT	ATTGAGGTCA	AACGATGATA	ATTAAAAATTT	TAACAATTCT	60
ATTACTACTT	TGTATATTGA	GCTATTTGGT	TACAAATAGA	AAGAECCTT	TTCTGTTCTT	120
AAAGACACTC	TTTATGGGTG	TGGTATTTAT	CTTTATAGGA	TATATTTTAC	TGGCAATATC	180
TGCCGTAATT	ATTTATGGTA	TTATTCAATT	TATCACAATT	GATTTTGGTA	GTTTTTTTCTT	240
AATGGGTATT	ATATTGATCT	TGATTTCAAG	TATATTCCAA	TTATTTATAG	TTAGATTACT	300
TTTTAGAAAA	AAGAATGTCG	ATTTGACAGA	GGTTGTCGTT	TTAsAsCATT	TAATTCAATG	360
GTTCTTAGTT	TACTTTGCGA	TCTATCAAGC	AGTAAATGAA	AAAATGGACA	TTAATGATAT	420

TAATATCGAC AATTTCCAAT CTGTCTTTTT TGACGTGTCT AATTTGAATT TAGTAATTCT	480
ACCAACGTTA ATCATTAGCT GGGTCA CA AT ATTTAACTAT AGAATGAGAA GTTACAAATA	540
AAATCTATGA GATTATACCT TCAGACACCA ACATTCAAAT GGTGTCTTTT TTGTTGTGTG	600
GTTTTATTTT TGAAATTCGA AAAAGTAGAG GCATGAATTT TTTGACTAGT GTATAAGTGC	660
TGATGAGTCA CAAGATAGAT AGCTATATTT TGTCTATATT ATAAAGTGTT T AG TTAAT	720
TAATAATTAG TTAATTTCAA AAGTTGTATA AATAGGATAA CTTAATAAAT GTAAGATAAT	780
AATTTGGAGG ATAATTAACA TGAAAAATAA ATTGATAGCA AAATCTTTAT TAACATTAGC	840
GGCAATAGGT ATTACTACAA CTACAATTGC GTCAACAGCA GATGCGAGCG AAGGATACGG	900
TCCAAGAGAA AAGAAACCAG TGAGTATTAA TCACAATATC GTAGAGTACA ATGATGGTAC	960
TTTTAAATAT CAATCTAGAC CAAAATTTAA CTCAACACCT AAATATATTA AATTCAAACA	1020
TGACTATAAT ATTTTAGAAT TTAACGATGG TACATTCGAA TATGGTGCAC GTCCACAATT	1080
TAATAAACCA GCAGCGAAAA CTGATGCAAC TAT AAAAAA GAACAAAAAT TGATTCAAGC	1140
TCAAAATCTT GTGAGAGAAT TTGAAAAAAC ACATACTGTC AGTGCACACA GAAAAGCACA	1200
AAAGGCAGTC AACTTAGTTT CGTTTGAATA CAAAGTGAAG AAAATGGTCT TACAAGAGCG	1260
AATTGATAAT GTATTAAAC AAGGATTAGT TAAATAAAC TTCAATCGTT GCTGTTATCT	1320
GGAAATAATT AATTAAATGT TATGTTAATT TTTGTTAATG AAAAAAGTAA TCTATTTAAT	1380
GACAGGTTAA TGTAATTGTC CTGAAATTGA CTATATACTC AGTAAGTATC AATTTTAAGG	1440
AGAGCTTATA ATGAAATTTA AAAAATATAT ATTAACAGGa ACATTAGCAT TACTTTTATC	1500
ATCAACTGGG ATAGCA ACTA TAGAAGGGAA TAAAGCAGAT GCAAGTAGTC TGGACAAATA	1560
TTTAACTGAa aGTCAGTTTC ATGATAAACG CATAGCAGAA GAATTAAGAA CTTTACTTAA	1620
CAAATCGAAT GTATATGCAT TAGCTGCAGG AAGCTTAAAT CCATATTATA AACGTACGAT	1680
TATGATGAAT GAATATAGAG CTAAAGCGGC ACTTAAGAAA ATGATTTTCG TATCAATGGC	1740
TGATGCTAAA GTTGCATTAG AAAAAATATA CAAAGAAATT GATGAAATTA TAAATAGATA	1800
ATAAATAAAA CAGGTTGAGA CAAAAAATGG TCTTAACCTG TTTTCAATTT GCATATGTGA	1860
TAAATTCTAT ATCAAAATGC TTATGTATAA TGAATGACAT T T AAAAGTAG GGGAGACAAA	1920
TATAAATACA ATAGTTCCTA GGATTACTCT CAAAATAACT ATATCAATTA TTTACTTTGC	1980
TCTCCTATTT TTTAAATAT GTACATGTTT AAACAATCAA AAGTGTACAA TATTAAATTA	2040
TCATTTCCAG TTCTAGTGCT ATATTGGTAG TAGTTGACTA AATGAAAATA AGCTTATAAC	2100
AAGTTTTTTC AATACTCGTG GG C CACAAC AGAGAGAAAT AGGATCACCA ATTCCAACAG	2160
ACAATGCAAG TTGGCGGGGC CCCAACATAG AGAAATTGGA TCACCAATTT CAACAGACAA	2220

TGCAAGTTGG GGTGGGGCCC AACACAGAAG CTGGCGAAAA GTCAGCATAC AAAAATGTGC	2280
AAGTTGGCGG GGCCACAACA GAGAGAAATA GGATCACCAA TTCCAACAA CAATGCAAGT	2340
TGGCGGGGGC CCCAACATAG AAGCTGGCGA AAAGTCAGCT TACAAAAATG TGCAAGTTGG	2400
CGGGGCCCCA ACATAGAGAA ATTGGAACCC CAATTTCTAC AGACAATGCA AGTTGGGGTA	2460
GGACATCGAT AAAGAAATAC TTTTCTTTA GCAATTAGTA TTTCTTATGC ATGAGCTTTA	2520
CTCATGTATT CATTTTTTAA GTACaCATTa GCTACAGCTA ATGATAAAGA ACCACTACAT	2580
AATAAATCAT TAGTGGTTCT TTATCATTTT TATCTACTC TTTTACTGGA AGAAAAAGTT	2640
TACGTTTGTA GAACATGCCA CAATACCAAA AATAATTAAG AAAAAATAAGA CGATAAGCAT	2700
GATGACACTT TTCAAACAAC CTCTATCAGT TTCTTTTCGAT TTTCTTTGTT GAACCTTTTT	2760
ATAATCTTCA AGTAGTTTTG CGGCTTTTTT ATTTATATGT TTATTCATGA TGTTGACTCC	2820
TTATAATATA TGTTTAATTC ATTAAAATAG TTGAAAACAT GACTTGAAAT AAAGATATAA	2880
AGCTAAAGTA AGGATGTTCA ATTGTTTCAA ATTTTATGAA AGTATAACGT TAAATAGTT	2940
AATTTGATGA TGATATTTGC TTTTATTTT CCAAATGGAA TTTACTTAAA CTGATGCATT	3000
AAAATATTAA TGAAGCACTA GAATACATAA ATGAATAGTa ATGGTGcACA GTATAGAATA	3060
ATTAAGGCTA TATTAAGTAT AAATATCGTT AACTGTAAGC TATCTTTAGT TTTAATATAA	3120
ACTATTAGGA TAATCGACGT AAGAAGAATC ATATATATTA ATGATGAAGA AGTCCATACA	3180
AAATCCGCAT CATTTGTTGT TAATAATGGG ACTATAATTA ATCCGAAATT AATCATGCAT	3240
GCTATATATA CTATAATGTT ATACACAATG TTAATTTTTG TTCACCACCT TATACTTCTA	3300
TTTTAAAAAC TTCTTTATAA TGATATATTG TTTAATGTG AAATAATTAG ATTATCTAAT	3360
TTTCATTTGC TTTACATGTA AAAGGCTATA TATAGTATGC TCTTTATGAT TCTAAATGCT	3420
TTTTAATATT TAATGCTCAT CAACATTTGG ATTTTGAATA TTCAATTCAA AAACCTTTATT	3480
AGCTACGTCA ATTGTAAAAT CAGAACCATA GTTGACATGA GCTACTTTTA ATTTTCCATC	3540
TAAATAATAG ATTGCGATTG CAACATCGTA AAATTCGTCA ATGACAAATA AACTCTTTTC	3600
GTTTGTTACA ACCTCATGCT CTCCTGAGTA TACAACGTTA ATTTCCCAAT CATTAAAAAC	3660
CATTTGTTAA CCTCCTTGAA CATTTAAATT GATTCAACTT AAGTTTAACT TATTCATACA	3720
ACTTCGTACA ATATCTAGAT GAACATTAAT TGTATTTCTA GAAATCTTTT TCAATTATAT	3780
GTACTAATTA TACTTTTAAA TTTCTTATTT CAGTATAGTT TTAAAACGAT TTTAAAATAA	3840
TTCTGCAAAT ATATTAACAC ATAATGTGTT CAAAAGTTT TGAACAATTT CAAAACTTTT	3900
ATATAAGGG nTTGACAACA TGGATTCAAA TnTCTTATTT TAAAATTAC CTCATATAGT	3960
GTCATGTTAG CCAATTTTTA AG	3982

(2) INFORMATION FOR SEQ ID NO: 521:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

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AGCTTGgATG ATTTAATaTG GtCCtTTCCC AaCcTTAGAT AATGAAAGAT tTGATAATCC      60
TGAATATAAA GAAGCTATGA AAAAATATcA ACAGAGATTT ATGGCTGmAG ATGAGGCTTT      20
GAAGAAATTT TTTAGTGAAG AGAAAAAAT aAAAAATGGA AATACTGATA ATTTAGATTA      180
TCTAGGATTA TCTCATGAAA GATATGAAAG TGTATTTAAT ACTTTGAAAA AACAAAGTGA      240
GGAGTTCTTA AAAGAAATTG AAGATATAAA AAAAGATAAC CCTGAATTGA AAGACTTTAA      300
TGAAGAGGAG CAATTAAAGT GGGACTTAGA ATTAAACAAA TTAGAAAATC AGATATTAAT      360
GTTAGGTAAA ACATTTTATC AAAACTATAG AGATGATGTT GAAAGTTTAT ATAGTAAGTT      420
AGATTTAATT ATGGGATATA AAGATGAAGA AAGAGCAAAT AAAAAAGCAG TTAACAAAAG      480
GATGTTAGAA AATAAAAAAG AAGACTTAGA AACCATAATT GATGAATTT TTAGTGATAT      540
AGATAAAACA AGACCTAATA ATATTCCTGT TTTAGAAGAT GAAAAACAAG AAGAGAAAAA      600
TCATAAAAAAT ATGGCTCAAT TAAAATCTGA CACTGAAGCA GCAAAAAGTG ATGAATCAAA      660
AAGAAGCAAG AGAAGTAAAA GAAGTTTAAA TACTCAAAT CACAAACCTG CATCTCAAGA      720
AGTTTCTGAA CAACAAAAG CTGAATATGA TAAAAGAGCA GAAGAAAGAA AAGCGAGATT      780
TTTGGATAAT CAAAAAATTA AGAAAACACC TGTAGTGTCA TTAGAATATG ATTTTGAGCA      840
TAAACAACGT ATTGACAACG AAAACGACAA GAACTTGTG GTTTCTGCAC CAACAAAGAA      900
ACCAACATCA CCGACTACAT ATACTGAAAC AACGACACAG GTACCAATGC CTACAGTTGA      960
GCGTCAAACT CAGCAACAAA TTATTTATAA TGCACCAAAA CAATTGGCTG GATTAAATGG     1020
TGAAAGTCAT GATTTACAA CAACGCATCA ATCACCAACA ACTTCAAATC ACACGCATAA     1080
TAATGTTGTT GAATTTGAAG AAACGTCTGC TTTACCTGGT AGAAAATCAG GATCAtGGT     1140
TGGTATAAGT CAAATTGATT CTTCTCATCT AACTGAACGT GAGAAGCGTG TAATTAAGCG     1200
TGAACACGTT AGAGAAGCTC AAAAGTTAGT TGATAATTAT AAAGATACAC ATAGTTATAA     1260
AGACCGAATA AATGCACAAC AAAAAGTAAA TACTTTAAGT GAAGGTCATC AAAAACGTTT     1320
TAATAAACAA ATCAATAAAG TATATAATGG GCA                                     1353
  
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(2) INFORMATION FOR SEQ ID NO: 522:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1987 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

GTCTGAGTCA GGTGCTGTTT GGTTAGATGC TGAAAAACA AGTCCTTATG AATTTTATCA	60
ATTCTGGATT AATCAATCAG ACGAAGATGT AATTAAATTC TTnAAATACT TTACTTTCTT	120
AGGAAAAGAA GAAATTGATC GCTTAGAACA ATTAAAAAT GAAGCACCGC ATTTACGTGA	180
AGCTCAAAAA ACATTAGCTG AAGAAGTAAC TAAATTTATT CATGGTGAAG ATGCATTAAA	240
TGATGCAATC CGTATTTTAC AAGCATTATT TAGTGGTGAT TAAAATCAT TATCAGCGAA	300
AGAATTAAAA GATGGATTTA AAGATGTGCC TCAAGTGACA TTATCAAATG ACACAACA	360
TATCGTTGAA GTCCTTATTG aaACAGGCAT TTCTCCTTCT AAACGACAAG CACGTGAAGA	420
TGTTAACAAAT GGTGCGATTT ATATTAATGG TGAGAGACAA CAAGATGTTA ATTATGCTTT	480
AGCACCAGAA GATAAAATTG ATGGCGAATT TACGATTATT CGTCGCGGTA AGAAAAATA	540
CTTCATGGTT AACTATCAAT AAATATAATT GCATAGCTAA ATAAATTAGA GCCTACTCAT	600
ATTCATTCCT AAGAATGTAA TGAGTAGGCT CTTAATGTAC TTTTCTGTCT GTAAATTATC	660
TAAAGAAATC TCTATCGCCT TGGCCAGGTG ATTGACGTTT TGATCGGCTT TGACGTTTTG	720
GTTGTTCTTT TTGTTGTTTT AATTTCACTT TAACTTCTTTTGTTTTACCA TCACGGATAA	780
CGGTAACAGT GACTGATTCA CCAGGTTTTT TATTTTCATA TAAATAGCTT CTTAAATCAA	840
CATCATCTTT AATTTTCTTG CCATCAATTT CTGTAATAAT ATCACCTTTT TTAAGATCAA	900
TATCACTATC AGCTTTGGCG ACATAAATAC CGTCTTCTCT ATCAGTATGA AGTTGCTCGC	960
GCTCTTCTTC AGGAATATCT TTCAAATTAA TTAAACCAAT ACCAATCGAA GGGCGGTCAA	1020
TTTTACCATG TTTTACAAGT TGTTCAATTG TTACTTTAAC TTCATTACTT GGAATAGCAA	1080
ACCCGATACC TTCAACTTGT GTCGCAGCAA TTTTCATTGA GTTAATACCA ACTAAATTAC	1140
CATTAATATC TACTAATGCG CACCTGAGT TACCTGGGTT AATAGCAGCA TCTGTTTGAA	1200
GAACGCTAAC TTTTGTATTG CCACCAGTTG TCTCAGCGTC AATCGTACGT TCGCTTGCTG	1260
AAATGATACC AGATGTTACA GAGTTAGCAA ATTGTAATCC TAATGGGTTA CCCATTGCGA	1320
ATACGCTATC GCCAGTTTGT ACTTTTGAAG AGTTGGCAA TTGAATGCT TTAATACCTT	1380
TTGTATTTTC AATTTTAAGT ACAGCAATAT CAGTTACTGc ATCTTTACCA ACTAATTTCTG	1440
CTTTAACTTG TTTTTTATTA TGTAATTGGa CTCTAATTTT ATTTGCGCCA TCAATAACAT	1500
GATTGTTTGT AACGATATAA GCTGAATTGT TGTTTATTTG aTAGATAACA CCTGAACCTA	1560
CTCCAGCTTC AGATGGTTTA GATGATTTGC CyTTTAATAA GTCGTCTACA CTTGATGCTT	1620

TTtGCATGtK AATAACTCCA ACAATTGTAG GGGAGACAGA TTTTATCATT TCATGAACGG	1680
TACCGAATTT CTTGCTTTGA CCGTCTAATT GATTGCCACC TTTATTATTT GTTGTCTGAA	1740
CAGTTGAACC ATCTTTATTT AAAATTGT K TATTTAATAC TTTGCCTATA CCAAGTACTA	1800
GAAGTGCACC AATAATTCCA GCAATCAATG CAACGATGAC TGt n TTAAAC CATGGAAATT	1860
TAGGTCTTCT GTATCTAGGT GTTTGGCTAT GGTtTGTTGT AGAATGATCT GTATGATTAA	1920
AATCTGACAT ACTTAACCTC CATTATATGA TTTATATATG CTTTAATTAT GTCTTT n TT	1980
TATAATT	1987

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

TTAGAAGTCA AATCATTAnT GGCGTCnTAT CGAGTATACT ATTAACtTCA ACTATTTTAG	60
CAATTGCATA TATTTTAATG TGGTTTAACG GCCATATGAC aCTAACTTTG ACCTTAACGA	120
CAATAATTAC AAGCTGTTTA ACCTTATTAA TATGTAGTAT TTTTATTAAT CCACTTATAC	180
AAAAAATTAA GCAGTTTAAT ATAAAACTA AGCAATTTGC TAACGGAAAT TACGCAAGCA	240
ATGATAAAAC GTTTAATTCA CCAAAAGAAA TTTATGAATT AAATCAATCT TTTAATAAAA	300
TGGCTTCTGA AATTACGCAA CAAATGAATC AA TTAATC CGAACAACAA GAAAAACAG	360
AACTGATTCA AAACtTAGCC CATGATTTAA AAACACCTTT AGCAAGCATT ATtTCATATT	420
CTGAAGGACT ACGTGATGGT ATAATCACTA AGGATCATGA GATTAAAGAG TCATACGACA	480
TATTAATTAA ACAAGCAAAC AGATTATCAA CATTATTTGA TGATATGACT CATATT ACA	540
CTTTAAATAC AGGTAAAACA TATCCCCCAG AATTAATACA ACTAGACCAA TTACTTGTAT	600
CAATATTGCA ACCATATGAG CAACGTATCA AACATGAAAA CCGCACATTA GAAGTGAATT	660
TCTGTAACGA AATTGATGCA TTTTATCAAT ATCGAACGCC ACTTGAGCGT ATTTTAACAA	720
ACTTACTTGA TAATGCGCTA AAATTTTCAA ATGTTGGTAG TCGCATTGAT ATTAATATTA	780
GTGAAAACGA AGATCAAGAT ACTATCGACA TTGCTATTAG CGATGAAGGT ATTGGCATTA	840
TACCAGAACT ACAAGAACGT ATATTCGAAC GTACATTcAG AGTAGAAAAC TCTCGTAATA	900
CAAAAACGGG TGgTTCTGGA TTAGGCTTAT ATATAGCT A TGAACtCGCG CAACAAAATA	960
ACGCAAAAAT CAGTGTAAAGC AGTGATATAG ATGTAGGAAC TACGATGACT GTAACATT Ac	1020

ACAAATTAGA CATTACGTCA TAATCCGATT TATTTATAAA ATAAAATGCA AAGACTAAAA	1080
AGAAGCTCCC ATTAATGAGG GCTTCTTTTT TTGTTTATTT AGAATAAACT TTATGGGTAT	1140
CCTTCTCATC ATTTTCAAGA CTGAAAGAT TTGTAGCTTG AATAATATAT TTAGGACGTG	1200
CCTTAACTTC ATAATATATC CTGCCAATAT ATTCACCTAC AACACCAATT GAAATTAAC	1260
GTATGCCGCC TAATAATAAA ATAGCTGCAA TCGTTGAAAA ATATCCCGGA ATATTAACAC	1320
CAGATATCAT AATATTGATG GAATAAATAG A	1351

(2) INFORMATION FOR SEQ ID NO: 524:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

TTGTTGTCAG TTTAACGCAA CGTGTTACCG ACTTTTCAAG TACACAACAA TATATATGTC	60
TATTCCATTT TTAGCCCcTG CCATTTTCAT CATTGGTGGT ATTATGTTGT TTATTTCAAC	120
ATTTAATAGC TTAGATGAAA CTGCTGAAAA TAATAACAAA ABAAGAAAC TAATGATTAA	180
AGGACTTATC ATTATTAACA TTTTCATTTAT CGTTATGATG GTTTTAACAC CATATTGGTA	240
CTTGTATTTA ATCGTCTATC TTATTTTCTT GTTGTTTTTA TTGTGGCAAA AGGTTTATAA	300
ATTTTAATAC CAAACTATT AAACACTTCT GATATTCTTA GTTCAAAATA TCAGAAGTGT	360
TTTATAGTGT TATCTAGTTC AGATAAATAT TTCCTTACTT AAAAAACGC CCTCCTCTTA	420
TTTTGACCCC nAT	433

(2) INFORMATION FOR SEQ ID NO: 525:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1845 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

CCCCCACTAT GATATGCTTG GCCTATTGCG TCAATCCCCT TATATTTTCGG CAATAGAGAT	60
GGATGTATAT TCAATATTTT ACCTTCAAAT GAAGCTAATA AGTCTGGACC AATTAGACGC	120
ATGTAGCCAG CTAGAATAAT CCACTCTACC TTATCTTCAT TTAATAATGT TACTAAATGT	180
TGTTCATACG CTGCTTTTGA ATCAAATTGT TTTGGTTCAT TAATATAAAC AGGAATATCG	240
TGCTTTTTTTG CTCTATCTAT ACAAACGCA TTTTGATGAT CCGTAAATAG CGCCGTAAC	300

TCAATATTTT CAAGTTTTCC TGATTCAACA TGCTCAACTA TATTTkCAA GTTACTTCCT	360
GAACCTGATG CAAAATCGC AATTTTAACC ATTGTTATAC CCCCACAAT TCAATTGCAG	420
TTGACTCATT TTTCACAATA TGACCAATTT GATAGGCTTC CACATTTTGT TCTGCTAAAA	480
TCTTCAAAGC GCGTGATACA TCTTTTTTCAT CAACGATAAC CGTATAGCCA ATACCCATAT	540
TAAAAATGTT ATACATTTCA TTTGTGTCTA TATTGCCTTG TTGTTGTAAC CAATCAAATA	600
TTTTTGGTGT TGGAAATGAT GTAGTATCAA TTCTAGCAGC ATATCCGGCT GGCAATGCAC	660
GTGGAATATT TTCATAAAAA CCTCCACAG TAATATGATT CATTGCCTTA ATAGAACTT	720
CTTTTTTCAA AGCAAGTACA GGTTTGACAT ATAATTTAGT TGGTTCTAAA AAGACATCGA	780
TAAATGGACG ATTATCGAAG TTTGATGCCA AATCAATGCC TGATTCATTA ATTAATTTGC	840
GCACTAAACT GTATCCATTT GAATGAATGC CACTTGACGC AAGCCCTATA AEA CT TGTC	900
CCTCTTTCAC TTCTGAACCA TCTACATAGT CATCCTTTTC AACTGCTCCA ACAGCAAATC	960
CAGCTACATC ATATTCGCCT TCGTGATACA TTTCACCCAT TTCAGCAGTC TCTCCACCGA	1020
TAAGTGCAGT ATTCGTTTCA ACACATGCAT CACTAATACC TTTAACAATT TGTTCAATAA	1080
CTTCAGGAAC AACTTTGTTT GTAGCAATGT AATCTAAAA ATATAATGGT TCTGCACCTG	1140
TCGTTAAAAT ATCATTAACA CACATTGCGA CTGCATCGAT ACCTATCGAA TCATGTTTAC	1200
CATAGTCGAT AGCTAGTTTT AATTTTCGTAC CTACTCCGTC TGTTCCAGAA ACTAAACTG	1260
GCGCTGtCAT ATTTAATTGT GATAAATCAA ATGAGCACC GAATCCACCT AAACCACCGA	1320
TAACTTCTTT ACGCATCGTA CGtTTAACaw GaCtAGaCaT TCtTTtACA GCTTCATAAC	1380
CAGCATGAAT ATTTACACCA GATTGTTTAT ATGCTTTAGA CATTTAAATT TCCCTCGCTA	1440
TCAAAAAAGT GTTTGTTTTT AGAAATATAT TGCTTTTGTC GATGACTTAA ATGCGCTTTA	1500
TAATTTGCTT CATAATCATA TAACCCTGCA GGATAATCTC CAGTGAAACT TTCTACACAT	1560
AAGCCACTAT ATGGCGCGTC ATAATCTAAA CCAATTGATT CAATTAACCC ATCTACAGAT	1620
AGATATGCTA ATGAATCAGC GCCAATATAA TCTTTAATTT CTTCAGGTGA TTTGCTTGCA	1680
GAAATTAATT CTGCCGtAGT TGAAACATCG ATTCCGTAAA AACTTGGAAT CATAAATTCC	1740
GGTGATGCTA TACGCACATG CACTTtATTT GCACCAGAAT CkTTTAACAT TTTCACAATG	1800
CGTCGAATTG TCGTACCGCG nACAATGGAA TCATCAACAA GACTG	1845

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

TCATAAA ⁿ G TAAATGTTAA TCGTCATATA ATATTAATT ACAACACCAT TTTGGTTATT	60
TGAAGCTTGT GGCGCTTGTT GTGTGCCACC TTGATTTTGA TTTGAGTTTT GATCTGTAGC	120
AGGTTGTTGT TGATTGCTGG ^{Amt} CACTGTT ATTAGTTG ^{Am} TCACTGTTCT CGTTAGATGT	180
CTTATCTTTA TCTGTCGTAT CATTTTGTTT TTTTCTCAAT AAAC ^T TATTAT CTAAAGGCGT	240
TAATGGTATT AATGAACCAT AATGATTAAT GACACGTTGA TCTAAGAAAT CATTTTTATC	300
ATTAATAGGT GATAATTCTA AGTCTTTACG AAGTAAGTTT GCATATTTTT GAATGCTTTT	360
AACACTTGGA TGATAATAGT AAATACCATT TAACATATCA TCTTTACCTT TTAATTGCGC	420
AGTTTTAATT TCAACATCAT TTGTTaAGTA CATTTTGTCT AAAGCTTTAA TTTCAGAGTT	480
AGTTAAATTA TGCTTTGCAT TTTTACCTAC AATTTGAATC ACGTTATCAA GTTTATCAAT	540
AGAATCAACT TCCTGTGCTT TTTGGAATAA AATCTTAATT AATTCCATTT GACGTTGTCC	600
ACGTTTTAAG TCTGAATCAT GATGTCTAGT TCTAGCAACT GCTAAGCCT CATCACCATT	660
TAATTTTTGG TACCCTTTTT TAATTTTAAT CTTACCAGTA TCATCTGTGT TAGGTTTCATT	720
TAAGTCGTAT GGCACATCAT AGTATATGCC ACCAAGCTCA TTTACAGCCT CGACAAATGC	780
TTTCATATTG ACTCTCACAT AATAATCAAC AGGTACATTC ATGGTAGCTT CTACCGAATC	840
CATTGCGGCA ATTGGACCAC CATATGCATG TGCATGGGTA ATCTTATCGT AATAGCCAAC	900
TTTAGGAATG TAGCTGATAG TATCACGTGG AATACTAAGC ATTCTAATTT GATGTTTTGA	960
TTGATTAAAA GTAGTTAAAA TCATAGCGTC TGATCTAGAG TGTTCAGCAT CCTGTCCTTT	1020
TTTTCTTCTT CCATCGTTAT CATCG ^W ACC TAAGAAAAGA ATAGAGATAG GTTGTTCCTC	1080
GGGATGACTT TATTATCTCT TAAGTTGGAT TGACGTTAGC ATTTTGTGCTG TCTTGAGAAG	1140
A	1141

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

GCACCATTAG CATTGGG ⁿ C ACTGATTGGA GT ⁿ CAGTTG TTGAAA ATC GGCGCCAACA	60
AGTAAAC ^m GG CmCaGGCaGC mAT ^{Am} CCCCa TATTATA ^c TT ATAATGGTTA TATTGGTAAT	120
AATGCTAATT TTATTCTGGA TAAGAATTTT ATTAACGCGA TTAAGTATGA TAATGTGAAA	180

TTCAATGGTA TTAAATTAGC TAAAACGAAT ACGATAAAAA AAGTAGAGAA ATATGATCAA	240
ACTTTTAAAG GTGTTTCTGC AAAAGGAAAC GAAGCAAGTC AATTGCAATT TGTAGTTAAA	300
AATAATATTT CATTAAAAGA TATCCAAAAA GCTTATGGCA AGGACTTGAA AAAAGAAAAT	360
GGTAAAACAA AGGAAGCTGA TAGCGGTATT TTTTACTATC AAAATGCTAA AAAGACATTA	420
GGCATCTGGT TTGTCGTTGA TCATAATAA GTTGTCGAAG TAACAGTTGG ACATACACCA	480
TACAAAACAA GTAAATAAAA TAATGGCATA TTAAGGCTAG AGTGTGAGGA GTGATACCGC	540
ATTCTAGTCT TTTTATTAA ATAATAACGA TTATTGCGTC TTACATAGTT GTTTGAAATT	600
GATAAAAATG TTTATTTGAT TATGATTATT TAAATAGTTA TCTCACATAT TTCAGCATT	660
GATTAAGTAT ATAGAGCACT ATTTTGTATT TGTTAATATT TTCACAAAAA TAAAGCCTTG	720
ATAAATTTTA AAATATAATT AAGCTCAATT TTTAAAATTT TATTTAGCTA CAGATAACAT	780
TTTTAAAAAA GAAAAGAATC AATAAATAAA ATCAACGAAC AAAAAGTATA GAAATAAATA	840
GAAATAATCA TTTACTTTTC TGAAAAATTA AATTAATATT TTATTTATAA GCTGTTTTTA	900
AGATTTTCAGG AGGAATGAAA TGTGaGGAAA TTTTCAAGAT ATGCATTTAC AAGTATGGCA	960
GCATTAACCT TGTTGAGCAC TTTATCACCA GCAGCATTAG CGATTGATTC AAAAAATAAA	1020
CCAGCTAATT CTGATATTAA ATTTGAGGTG ACTCAAGA GTGATGCGGT CAAAGCATTA	1080
AAAGAATTGC CTAAATCCGA AAATGTAAAA AATATTTATC AAGATTACGC TGTTACTGAT	1140
GTAAAACTG ATAAAAAAGG ATTTACGCAT TATACATTGC AACCGAGTGT TGATGGTGTT	1200
CATGCACCTG aCAAAGAAGT GAAAGTACAC GCAGACAAAT CAGGAAAAGT CGTTTTAATC	1260
AATGGGGATA CTGATGCGAA GAAAGTAAAG CCAACGAATA AAGTGACATT AAGTAAAGAT	1320
GACGCAGCCG ACAAAGCATT TAAAGCAGTT AAGATTGATA AGAATAAAGC GAAAAATCTT	1380
aAAGATAAAG TCATTAAAGA rAACAAAGTT GAAATCGATG GTGACAGTAA TAAATACGTT	1440
TATAATGTTG AGTTAATTAC AGTGACACCA GAAATTTTAC ATTGGAAAGT TAAAATTGAT	1500
GCTCAAACCTG GCGAAATTTT AGAAAAAATG AACTTAGTTA AAGAAGCTGC AGAAACTGGT	1560
AAAGG	1565

(2) INFORMATION FOR SEQ ID NO: 528:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2870 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

GGATAGGTAA ATCCATTCAA AATTGGTTGT ACTCATTTA AATCATATTT TTTAATATAG	60
AAACACATAA TTAAAGGAGT GATGATATTA ATGAATAAAC TTCGAGACAC TACTTTTCTA	120
TCATATTTAT TTACTATCAT ATTGTGGGGA TCTGCATTTT CAATGATAAA GATTGCGTTA	180
AATGATTTTA GTGCAGAATC ATTGTGCGCA TTTCGTTTAA TTTTAGCAAC AATAATTCTC	240
TTGCCGTTCG TAATTATAAA GAAATTGCCT ACCCCTGAAC TAAGAGATAT CCCTGTTATT	300
TTTATTTTAG GATTTTGTGG ATTTGTGATA TATCACACAG CTTTAAATTT TGGTGAAaCT	360
TTGATTAGTG CAGGTATAtC TGGrATTcyA GTCTCTACAA CGCCTATTTT TTCTAGTGCT	420
TTAGCTTATA TATTTTTTAAA AGAGCATTTT TCAAAATGGA ATTGGTTAAG TTTACTCGTC	480
GCATTTATAG GAATATCCAT TATTTCAATA AGTAAAGATG ATTACACAAC TATTAATGTA	540
TTAGGTGTTT TTATTATTTT ACTTGCATCT TTTAGTGAAA GTTTGTATTT TACTTTCCAG	600
AAAAAATACA TAGAAAAATA CGGCTTCATC GCTTTCACAC TATaTAAAT AATGGCAAGC	660
TCACCATTTA TGCTTATTTT TATTCCTGAA ATCATCAACG ATATACACGG CGCCACTTTT	720
ACATCAATAG TATCGGTACT TTATTTAGCT ATATTCCCTA CTATAATTCC ATACGTTTTG	780
CTTGCTTATA TTGTGAAGTC AGTTGGTGTC TCTGATGCAA CAATGTCTCT TTATTTAACA	840
CCTATCGTTT CTTTATTATT ATCTTATCTG TTATTAGACG AGCTACCAAC AACCCTTGCT	900
ATTATAGGCG GAATTATCAC TCTACTAGGC GTTAGTTTAA GTAACCTCTT TCAAAATACA	960
TAATTATTCC AAGTCCCGCA CCTCAGAATC CAAAACATT CGAGTGATAA AATTTTAAAA	1020
ATCAAAAATA TAAAATGAT CTAATTTGT CAAATTTACC AATATAAATA CTAATATTTG	1080
CAATTCACAA AGGGGTATAG TCTGAGTGTA TTCTAATACG AAAGGACTTG GTGGATATGT	1140
ATTACAGTTA TGGAAATTAT GAAGCATTTG CGCGCCCTAA AAAACCTGAA AATGTAGAAA	1200
ACAAATCCGC TTACTTAATC GGATCTGGTC TAGCTTCACT TGCTGCAGCT TGTTTTTAA	1260
TAAGGGATGG TCAAATGGAA GGTTCGAAGA TTCATATTTT AGAAGAGTTA CCTAAAGCAG	1320
GTGGTAGTCT TGATGGTGAA AATATGCCTT TAAAAGGCTA TGTTGTCCGC GGTGGTCGTG	1380
AAATGGAGAA CCACTTTGAA TGTTTGTGGG ACTTATTCAG ATCTATCCCT TCATTAGAAA	1440
TCGATAACGC GTCTGTATTA GATGAGTTCT ATTGGCTAAA CAAAGAAGAC CCTAACTATT	1500
CTCGCTGTCG TGTTATTGAG AAACAGGGTC AACGTTTAGT CACAGACGGA GACTTCACTT	1560
TGACTAAAAC GGCGATTAAA GAAATTTTAG ATTTATGCTT AACGAATGAA GAAGATTTAG	1620
ATGATGTCAA AATAACAGAT GTATTTTCCG ATGATCTCTT TAATTCAAAC TTTTGGATTT	1680
ACTGGAAAAC GATGTTTGCA TTTGAACCGT GGCATTCTGC AATGGAAATG CGTCGCTATC	1740
TAATGCGATT CGTTCATCAT ATTAGTGGTC TCGCAGACTT TTCAGCTTTA AAATTCACTA	1800
AATATAATCA ATATGAATCT TTAGTATTAC CTATGGTTGA ATATTTAAAA TCGCATGGGG	1860

TTCAATTTGA ATACGATGTA AAAGTCGAAG ATATTAAAAT AGATGTTACG ACAAGTCAAA	1920
AAATTGCCCC AGAAATATTA ATTGACCGTA ATGGTAATGC AGAATCTATT AAAGTACTA	1980
TAAACGATCT TGTCTTTGTG ACAAACGGTA GTATTACAGA AAGCTCTACT TATGGTGATA	2040
ATGATACACC AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT	2100
TAGCGCGACA AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTAAAA	2160
AAAGTTGGTT TGTTTCAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG	2220
AAAGTATTTG TAAACGTGAC CCACTTGCAG GCAAACAGT TTAGGCGGT ATTATTACAA	2280
TCAATGATTC TGCATGGCAA ATGAGTTTTA CAATCAATCG TCAGCAACAG TTAAAGACC	2340
AACCTGAAAA TGAAATATCT ACATGGATTT ATGCCTTATA TTCAGATGTA AACGGCGATT	2400
ATATTAAAAA GCCAATTACA GAATGTAGTG GTAATGAAAT ATGCCAAGAA TGGCTGTATC	2460
ACTTAGGTGT ATCAACTGAC AAAATTGAAG ACTTAGCAAA ACATGCATCT AATACGATTC	2520
CTGTTTATAT GCCATATATC ACATCTTATT TCATGACGCG TGCTATCGGC GACAGACCTT	2580
TAGTCGTCCC GCATCAATCT CAGAACTTAG CATTTATTGG TAACTTTGCA GAAACAGAGC	2640
GAGACACTGT ATTTACAACA GAATATTCGG TTCGTACTGC CATGGAAGCT GTTTATCAAT	2700
TACTAAATAT AGATCGTGGT ATTCCAGAAG TCATCAATAG TCCATTTGAT CTTCGCGTCT	2760
TAATGGATGC CATATACGAA CTGAATGACC ACCAAGATTT GCGTGAGATT ACTAAAGATT	2820
CGAAAATGCA AAAACTCGCA TTAGCAGGAT TCCTTAAAAA GATAAAAGGT	2870

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

CnGTTTAGCT GCAAAAAGTA AATAACGACA CTGTATTTGG AATTTTGCAA TTAGAAACAC	60
TTTTGGGTGA CATTAAGTCA ATTTTCAGCG AGATTGAAAG CGAATACAAA ATGTCTAGAG	120
AAGAAATTTT AATTTTACTA ACTTTATGGC AAAAAGGTTT TATGACGCTT AAAGAAATGG	180
ACAGATTTGT TGAAGTTAAA CCGTATAAGC GTACGAGAAC GTATAATAAT TTAGTTGAAT	240
TAGAATGGAT TTACAAAGAG CGTCCTGTTG ACGATGAAAG AACAGTTATT ATTCATTTCA	300
ATGAAAAGTT ACAACAAGAG AAAGTAGAGT TGTTGAATTT CATCAGTGAT GCGATTGCAA	360
GTAGAGCAAC AGCAATGCAA AATAGTTTAA ACGCAATTAT TGCTGTGTAA GTTTAATAGC	420

ATAAAAAGAG	GTTTTTCATTA	AGTTGAAAAC	CTCTTTTTTGT	TGTTGGCATT	AATTTTTTCAA	480
ATGTTGACTA	CTCAATCCTA	AATTATAAAT	AGTATAGCGC	aCAAaTGCTT	AAGAAATTTT	540
TTCTATGGCA	CAAATGAATG	GAGCATGATT	ACGTTGGTTT	AAAAATTGAT	ATGCAAAAC	600
TTGCGCATGC	TTTTGATCCA	AAGTACTCAA	GTAATCAAGC	AATGCATGCT	TCTCAATTTG	660
TCCTTCGCTA	TGACCATGAT	ATATAACAAG	TACAATAATA	CCTTCAATTG	ACATTAATGA	720
TAGCAATGAA	TTAATAGCTT	GGATTGTCGT	GTCAGGCTTT	GTCACGATAG	ATTTATCACC	780
TTTAGGCAAA	TAACCTAGGT	TAAAGATGGC	TGCATCAATA	TGACCTTTAT	GTGCATCATT	840
TATATGATGT	TCAATATTTT	CATGTCCATC	TTTTATTAAA	GAAACATGAT	TGAAATCCTT	900
AACTTTATCA	CGTGTATTTT	CCAAAGCTAA	ATCTTGAATG	TCGAAACCAT	AAACATGTCC	960
TTCTGGTACT	TGTTCGGCTA	AAAATAAAGT	GTCATGCCG	TTACCGCAAG	TTGCGTCTAC	1020
AACAATACTT	TCTGGTGTTA	TATGTTGTTT	AATAAGTGTT	TTTGAAAAAG	GGAGTATACG	1080
TTCTAATTTT	ATTGCTTCAC	CTTAGACTTG	TAACGCAAGC	CTTGATAAGA	ATTTCTACGT	1140
GCTAATTCAG	CATCGATGCC	ATTTAATACT	TCCCATTTAT	TAACACTCCA	CATTGGACCT	1200
ACCATGATAT	CTATTGGACC	ATCACCGGTA	ATTCGGTGAA	CGATCATTTT	AGGGGGAATC	1260
ACTTCTAATT	GGTCCACAAC	TAGGTTTGTG	TACTCTTCTT	GAGTCATAAA	AGTTAATAAA	1320
CCTTTATCGT	ATTGTTTTAC	CATCGGTGTA	CCTTTTAACA	AATGAAGTAA	ATGAATTTTA	1380
ATACCTTGTA	CATCCATTG	TGCACTTCTT	TGGCAGTAGC	CATCATCATG	TCATAGTCTT	1440
CGCCAGGTAA	GCCATTAATG	ATGTGTGTAC	ATACATTGAT	ATTATGCTTA	CGTAATTTTG	1500
CCACACCATC	ATAATAAGTT	TTCATATCAT	GGGCACGATT	GATTAAATCA	GATGTTGACT	1560
GATGGATTGT	TTGTAGTCCT	AATTCAACCC	ATAAGTATGT	CGTTGATTG	AAATCTGCTA	1620
AATATTGAC	AACATCGTCT	GGTAGACAGT	CAGGACGCGT	ACCAATAGAT	AATCCCACAA	1680
CACCCGGTTC	TTTAAGTACA	GGTTCGAATT	TTTCTTTTAA	TACTTCAACC	GGTGCATGTG	1740
TATTTGTAAA	TGCCTGAAAA	TAAGCAATAT	ATTTTCCTTC	GTGCCATTTT	TCATGCATCT	1800
TTTCTTTAAT	TTCTTTAAAT	TGTACTGCGA	TTGAATCTGC	ACGATTACCT	GCAAAGTCTC	1860
CGCTACCTGC	AGCAGAACAA	AATGTACATC	CACCATGTGC	TACAGTGCCA	TCGCGGTTAG	1920
GACAGTCAAA	CCCGCCATCC	AATGCAACTT	TAAATATTTT	TTGTCCAAAT	TTATTTTTTA	1980
AATGGTAATT	CCATGTGTGA	TAACGTTTGT	TTTCAAAAGC	GTATTGGAAA	TGATTGCCCA	2040
TATGTCATTT	TCCTTTCTAT	AAAAAAAGAG	TTCTAAGTAC	AGATTTTAAC	ATATTTTAAT	2100
GTTATAGTGT	TTATTATAGT	TTGACAAAAA	AGAGAGAGGA	ACTATGAAAT	ATGAATATAC	2160
CTAAATCAGT	CTGGTGGCTA	GTAATTGGCA	TGGCGTTAAA	TATTACTG	TCCAGTTTTT	2220
TGTGGCCTTT	AAATACAATT	TATATGAAAC	AAGAACTTGG	AAAAAGTTTA	ACTGTTGCTG	2280

GTTTAGTGCT AATGATAAAT TCATTTGGCA TGGTTATTGG AACTTATTA GGTGGTTCAC	2340
TATTTGATAA ATTAGGTGGA TACAAGACGA TTTTAATTGG AACTTTCAC TGTCTTTGTA	2400
GTACAACGCT ACTTAATTTT TTTACGGGT GGCCTTGGA TGCTGTATGG CTTGTAATGT	2460
TAGGGTTTGG TGGCGGAATG ATTATTCCTG CGATATACGC TATGGCTGGA GCAGTGTGGC	2520
CAAATGGCGG AAGACAAACG TTTAATGCGA TATACTTAGC GCAAAATATT GGTGTGGCTG	2580
TCGGTGCTGC AATGGGCGGC TTTGTGCGAGAATTTAGCTT TAACTATATC TTTT TAGCCA	2640
ATCTTATTAT GTATGTTGTG TTTGCGCTTG TCGCGGTAAC GCAATTTAAT ATTGAAATTA	2700
ATGCGAAAGT TAAATATCCA ACTCATTTAG ATATTACTGG TAAAAAGAAT AAAGCAAGAT	2760
TTATTTTATT AGTACTAATT TGTGCAATGT TTGCAATTTG TTGGGTTGCA TATATCAAT	2820
GGGAGTCTAC AATCGCTTCA TTTACACAAT CTATTAATAT TTCAATGGCA CAATATAGTG	2880
TTTTATGGAC AATTAACGGA ATAATGATTT TAGTAGCACA ACCATTAATT AAACCGATTC	2940
TCTATCTGTT AAAAGGAAAC TTAAAGAAGC AAATGTTTGT CGGCATCATC ATTTTTATGT	3000
TGTCGTTCTT TGTACGAGT TTTGCCGAAA ACTTTACAAT ATTTGyTGTC GGTATGATTA	3060
TTTTAACTTT TGGAGaATGT TTGTATGGCC AGCAGTTCCA ACTAT	3105

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

TAATGATTAA ACCAGATGCA GTACAAAGAA ATCTAATTGG TGAAGTAATT TCAAGAATTG	60
AAAGAAAAGG ACTAAACTT GTCGGTGGTA AATAATGCA AGTACCAATG GAACTTGCTG	120
AAACACATTA TGGTGAACAC CAAGGTAAAC CATTTTATAA TGATTTAATT TCATTTATTA	180
CATCAGCACC AGTGTTGCA ATGGTAGTTG AAGGTGAAGA TGCAGTTAAT GTATCTAGAC	240
ATATTATTGG CAGCACCAAT CCTTCAGAAG CTTACCAGG ATCAATTAGA GGTGATTTA	300
GTTTAACTGT TGGTAGAAAT ATCATTCACG GTTCAGATTC ATTAGAGTCT GCTGAACGTG	360
AAATTAATCT ATGGTTTAAT GAAAATGAAA TTACTAGCTA TGCTTCACCA CGTGATGCAT	420
GGTTATATGA ATAAAATATA AACTGTAAAC CTTTACGATT TATTTATAAA GG TAGAAAGG	480
GT TTTGTTAT GTGGTTAGTC ATTATGaTTA TACATAACAA GGCCCGTTTT TTATGTTGTA	540
GTAAATTACT TGAAAAATTT TATAGTTTTT kGGTAACaCG TA tTaAAAaG AGAGGAATAT	600

TCTTTATCAA ATGAAACTAA ACAGAGAGAA GGGGTGTGTTA AAATGAAgAA TATTATTTTCG	660
ATTATTTkGG GGATTTTAAT GTTCTTAAAA TTAATGGAATTACTATATGG TGCTATATTT	720
TTAGATAAAC CACTTAATCC TATAACAAAA ATTATTTTTTA TACTGACTCT CATTTATATT	780
TTTTATGTAT TAGTAAAAGA ATTGATTATA TTTTTGaAGT CAAAGTATAA CAAAAGCGCT	840
TAACATATGT ATATTTTAAT ATCATAATTT TTTTAAACGG ACTGATTAAC TTTATTAATA	Ø0
ATTAACAGTT CGTTCTTTTG TATTAAGAAA TGTAGTCAGT ATATTATTTG CTAAAGTTGC	960
GATACGATTA TATTAAAACG GCTAATCATT TTTAATTAAT GATTATATGA TGCAACTGTT	1020
TAGAAATTCA TGATACTTTT CTACAGACGA ATATATTATA ATTAATTTTA GTTCGTTTAA	1080
TATTAAGATA ATTCTGACAT TAAAATGAG ATGTCATCCA TTTTCTTAAT TGAGCTTGAA	1140
AACAAACATT TATGAATGCA CAATGAATAT GATAAGATTA ACAACATATT ATAATGTTAT	1200
CGTGGAAGTA TGAAAGGAGC GAGTGTGTAT GAGATACCTA ACATCAGGAG AATCACATGG	1260
ACCTCAATTA ACAGTTATTG TTGAAGGTGT ACCTGCAAAT ATAGAAATA AGGTTGAGGA	1320
TATTAATAAA GAAATGTTTA AGCGTCAAGG CGGTTACGGA CGTGGACGTC GTATGCAAAT	1380
TGAGAAAGAT ACAGTAGAAA TAGTATCAGG CGTTAGAAAT GGTTATACAT TAGGTAGTCC	1440
AATTACTATG GTTGTAACCA ATGATGACTT TACGCATTGG AGAAAAATTA TGGGAGCAGC	1500
TCCAATAAGT GAAGAAGAAC GTGAAAATAT GAAACGTAAT ATTACAAAAC CAAGACCTGG	1560
TCATGCAGAT TTGGTTGGAG GTATGAAATA TAATCATCGT GATTTACGAA ATGTGCTAGA	1620
GCGATCATCT GCTAGAGAAA CAGCAGCTCG AGTTGCAGTC GGTGCCTTAT GTAAAGTGTT	1680
ATTACAACAG TTAGATATCG ATATATACAG TCGTGTTGTT GAAATAGGTG GAATTAAAGA	1740
TAAAGATTTT TATGATTCAG AAACATTTAA AGCAAATCTT GATCGTAATG ATGTTCTGTG	1800
AATTGATGAC AGTATCGCAC AAGCAATGCG AGATAAAATT GACGAaGCTA AAAATGAAGG	1860
AGATTCAATT GCGGGTGTCTG TTCAAGTTGT AGTTGAAAAT ATGCCTGTTG GTGTaGTAG	1920
TTATGTGCAT TATGATCGTA AGTTAGATGG TAAGATTGCA CAAGGTGTTG TCAGCATAAA	1980
TGCTTTTAAA GGTGTAAGCT TTGGTGAAGG ATTTAAAGCA GCTGAAAAGC CAGGTAGTGA	2040
GATTCAAGAT GAAATTCTAT ATAATAGTGA AATTGGTTAT TATCGTGGAT CTAATCACTT	2100
AGGTGGTTTA GAAGGCGGTA TGTCAAATGG AATGCCAATT ATCGTTAATG GTGTAATGAA	2160
ACCAATTCCA ACGTTATATA AACCATTAAA TTCAGTAGAC ATTAATACTA AAGAAGACTT	2220
TAAAGCAACA ATTGAACGTT CTGATAGTTG TGCTGTTTCT GCAGCAAGTA TCGTCTGCGA	2280
ACATGTGCGTA GCATTTGAAA TAGCAAAAAGC ATTATTGAA GAATTCCAAT CAAATCATAT	2340
TGAGCAACTT AAACAACAAA TTATTGAGCG CAGACAATTA AATATTGAGT TTTAACAACA	2400
AGAACAATTG AGGTGTAATC ATGAAATTAC AAACAACATA CCCTTCAAAT AATTATCCAA	2460

TATATGTTGA	ACACGGTGCA	ATTGACCATA	TTAGCACGTA	TATTGATCAG	TTTGATCAAA	2520
GTTTTATATT	AATTGACGAG	CATGTAAATC	AATATTTTGC	TGATAAATTT	GATGATATTT	2580
TATCATATGA	AAATGTACAT	AAAGTTATTA	TTCCAGCTGG	TGAAAAGACG	AAAACATTTG	2640
AGCAATATCA	AGAAACATTA	GAGTATATTT	TATCCCATCA	TGTAACTCGT	AATACAGCAA	2700
TTATTGCTGT	TGGTGGTGGT	GCAcTGGTGA	TTTTGCTGGG	TTTATTGCGG	CGACACTTTT	2760
ACGAGGCGTG	CACTTTTATAC	AAGTGCCAAC	GACTATACTA	GCGCATGATT	CTAGTGTTGG	2820
CGGTAAAGTG	GGTATTAAC	CAAAGCAAGG	TAAAAACCTT	ATCGGTGCAT	TTTATCGTCC	2880
AACTGCTGTG	ATTTATGATT	TAGTCTTTTT	AAAGACGTTA	CCATTGAGC	AAATATTAAG	2940
TGGCTATGCA	GAAGTTTATA	AGCATGCGTT	ATTGAATGGT	GAATCAGCGA	CGCAAGATAT	3000
CGAACAGCAC	TTTAAAGATA	GAGAGATATT	ACAGTCATTA	AATGGTATGG	ATAAATATAT	3060
TGCTAAAGGT	ATTGAAACGA	AGCTGGATAT	TGTTATTGCA	GATGAAAAAG	AACAAGGTGT	3120
ACGTAAATTT	TTAAATTTAG	GTCATACATT	TGGTCATGCT	GTTGAATACT	ATCATAAAAT	3180
ACCTCATGGT	CATGCAGTGA	TGGTTGGCAT	TATCTATCAA	TTTATAGTTG	CGAATGCTTT	3240
GTTTGATTCT	AAGCATGATA	TTAATCATTA	TATTCAATAT	TTAATACAAC	TCGGCTATCC	3300
TTTAGACATG	ATAACTGACT	TGGATTTTGA	AACGTTATAC	CAATATATGC	TAAGTGATAA	3360
AAAGAATGAT	AAGCAAGGTG	TACAAATGGT	CTTGATTAGA	CAATTTGGAG	ATATCGTTGT	3420
ACAACATGTT	GATCAACTAA	CATTACAACA	TGCATGTGAA	CAATTAAAAA	CATATTTTAA	3480
GTAGGTGAAT	GAAATGGTAA	ATGAACAAAT	CATTGATATT	TCAGGTCCGT	AAAGGGCGA	3540
AATAGAAGTG	CCGGGCGATA	AGTCAATGAC	ACACCGTGCA	ATCATGTTGG	CGTCGCTAGC	3600
TGAAGGTGTA	TCTACTATAT	ATAAGCCACT	ACTTGGCGAA	GATTGTCTGC	GTACGATGGA	3660
CATTTTCCGA	CTGTTAGGTG	TAGAAATCAA	AGAAGATGAT	GAAAAATTAG	TTGTGACTTC	3720
CCCAGGATAT	CAATCTTTTA	ACACGCCACA	TCAAGTATTG	TATACAGGTA	ATTCTGGTAC	3780
GACAACACGA	TTATTGGCAG	GTTTGTTAAG	TGGTTTAGGT	ATTGAAAGTG	TTTTGTCTGG	3840
CGATGTTTCA	ATTGGTAAAA	GGCCAATGGA	TCGTGTCTTG	AGACCATTGA	AACTTATGGA	3900
TGCGAATATT	GAAGGTATTG	AAGATAATTA	TAACCATTA	ATTATTAAGC	CATCTGTCAT	3960
AAAAGGTATA	AATTATCAAA	TGGAAGTTGC	AAGTGCACAA	GTAAAAAGTG	CCATTTTATT	4020
TGCAAGTTTG	TTTTCTAAGG	AACCGACCAT	CATTAAAGAA	TTAGATGTAA	GTCGAAATCA	4080
TACTGAGACG	ATGTTCAAAC	ATTTTAATAT	TCCAATTGAA	GCAGAAGGGT	TATCAATTAA	4140
TACAACCCCT	GAAGCAATTC	GATACATTAA	ACCTGCAGAT	TTTCATGTTC	CTGGCGATAT	4200
TTCATCTGCA	GCGTTCTTTA	TTGTTGCAGC	ACTTATCACA	CCAGGAAGTG	ATGTAACAAT	4260

TCATAATGTT GGAATCAATC CAACACGTTT AGGTATTATT GATATTGTTG AAAAAATGGG	4320
CGGTAATATC CAACTTTTCA ATCAAACAAC TGGTGCTGAA CCTACTGCTT CTATTCGTAT	4380
TCAATACACA CCAATGCTTC AACCAATAAC AATCGAAGGA GAATTAGTTC CAAAAGCAAT	4440
TGATGAACTG CCTGTAATAG CATTACTTTG TACACAAGCA GTTGGCACGA GTACAATTAA	4500
AGATGCCGAG GAATTAAAAG TAAAAGAAAC AAATAGAATTGATACAACGG CTGATATGTT	4560
AAACTTGTTA GGGTTTGAAT TACAACCAAC TAATGATGGA TTGATTATTC ATCCGTCAGA	4620
ATTTAAAAACA AATGCAACAG TTGATAGTTT AACTGATCAT CGAATAGGAA TGATGCTTGC	4680
AGTTGCTTCT CTACTTTCAA GCGAGCCTGT CAAAATCAAA CAATTTGATG CTGTAAATGT	4740
ATCATTTCCA GGATTTTTAC CAAAATAAA GCTTTTAGAA AATGAGGGAT AATATAAAAT	4800
GGAAGATATC TATAAATTAA TAGACGATAT CAATCTACAA AACTAGAAA ATTTAGACTC	4860
TCGTGTTAAT GAAGCAATAA CTAAGTACAA CGATGACGCA TTATTTATTC TAGGAGAGAC	4920
ACTTTACAAT TTTGGATTAA TCCaCAAGG TTTGGAAGTA TTCCGCGTGT TATATCACAA	4980
ATATCCAGAC GAAAGTGAAT TGCTGATTAA TTTTATTGAA GGTTTAATGT CTGAAAATCA	5040
AACTGACGAA GCGTTAGAAT ATTTAAGTTA TGTGTAACCA TCACCTGAAA AGTTGATGTT	5100
AGAAGCAGAT TTATATCAAC AAATTAATAT GATGGAAGTT GCTATTGAA AATTACAAGA	5160
AGCACTTGAA CTAGAGCCAA ATGATCCAAT AATCCATTTT GCATTGGCTG AAATGTTATA	5220
TTATGATGGT CAATATTTAC GTGCTACCTC TGAATACGAA ACCGTTTTAG AAATGGTGTA	5280
ATATCAAGTT AATGGTGTA ACTTATTCTC TCGTATGGCA GATTGTAGTT TACAAAGTGG	5340
kAACTATAGT GATkCcGATt CgCTTATACG ATGrAATTAA TGAAGATGAA ATGACTTCAG	5400
AAGATTATCT CAAAAGAGCC ATTTCTnACG ATAAAAATGA CATCACTCAA GAAGCAATTA	5460
AAATAATGAC TACATTACTT TCTAAAGATC CTGATTATAT TCAAgGCTAC TTGTATTTAC	5520
aATCaTTATA TG	5532

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 942 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

AATTGGGTTA TACTATAGGT AAATTTAAGG AGGTAAGAAA ATGGATAAAA AAGAATTAGC	60
GAAATTTATA GGCAATAAAA TCAGATACTA TAGAACCaaa TTGaACTTAA CTCAAGATCa	120
ACTTGGAGAA AAACtCmACa CTAAAAArGC TACTATTTCA AATTATGAGA EGGGTACAG	180

AACTCCTAAA CAAGATGATT TGT TTGAAAT TGCTCATATT TTAAATATCA GATCGATGA	240
TTTGTTCCT ACAAGAAATA ATAAAAAAAA CGACATCACT TCCATATACA ACAAACAC	300
ACCTCCCGC CAAGAAAACG TACTTAACTA CGCAAATGAG CAATTAGATG AACAGAATAA	360
AGTCACTTCT ATAGATGAAT ATAAAGAGTC TAACTAGTA TCGTATATTG CATGTGGTGC	420
AACTGGTGCT GGCATAGGAG AAGAATTATA TGATGACATA TTGCATGAAG AAGTATTTTT	480
TAAAGAAGAC GAAACGCCAT CAAATGCTGA TTTTGTATT TTAGTTAATG GTGATTCAAT	540
GGAACCTATG TTAAAACAAG GAACATACGC TTTATTAAG AAAGAAGATT CTATTAAGA	600
TGGTACAATT GCACTCGTTG TATTAGATGG AGTAAGTCTT ATCAAGCGTG TAGATATATG	660
CGAAGACTAT ATTAATTTGG TATCTCTAAA TCCGAAGTAT GATGATATCA AAGTCGCTTC	720
GTTTAGTAAT ATTAAAGTAA TGGGCAAAGT TGTATTGTGA TTAATAGCGC CTATATG	780
CTTTAATATA AAAGACGTCT ATTTCAGCAG TGTTTAAAG GAGTTTATAA TGAAAATAAC	840
TAATTGCAAA ATAAAAAAG AACTATAGT ATATGAAGTT TTAAGTAGTG GTAATCAACC	900
ATTCACCTAT GAGTTACCTA AAGATTTATC GTCACATAAT GC	942

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

TGGnAAATGC AAACCAAAT ATGaTCCTCG TGcAAGTTGA AGCGGGACGT TATGAAGAAT	60
GGGTAAAGAA TGGTTATTTT AAACCGTCAG AAGATAAATC AAAAGAAACA TATACAATTG	120
TTATCCCGCC ACCAAATGTA ACTGGTAAAT TACATTTAGG ACATGCATGG GATACGACTT	180
TACAAGATAT CATTACACGT ATGAAACGTA TGCAAGATA CGATACGTTA TACTTACCAG	240
GTATGGATCA TGCTGGTATT GCGACACAGG CAAAGGTAGA AGCTAAATTA AATGAACAAG	300
GAATAACTAG ATATGATCTT GGTGCTGAAA AGTTTTTAGA ACAGGCATGG GATTGAAAG	360
AAGAGTATGC GTCATTTATT CGTGCGCAAT GGGCTAAATT AGGTCTAGGT TTAGATT	417

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ D NO: 533:

GATCCTGAAC CCGCATTTGT TTCCACTAAA ACAGTATGCC CACTTTCTAC TAAAGCGTGC	60
ACACCACTTG GTGATAAACC AACACGATTT TCATTATTTT TAATCTCCCT TGGTATACCA	120
ATTTTCATAC CATCCACCTC CATAATCATC TTAACGCGAA CATTTTGAAA GCGCAATCAA	180
AAATCCACAA AATTGTAAAG GTTATTACAC TGACTTTTCC GAAAATTGTG GTAAAATATA	240
ATTAAGAAAAG AACAAAGGAGG CACTTACTAT GATTACTTAC AAAAAATATTT TAATCGCAGT	300
TGACGGTTCA CATGAAGCGG AATGGGCATT TAACAGAGCA GTTGGTGTTG CTAAACGTAA	360
CGATGCGAAG TTAACAATTG TGAATGTAAT TGATTCAAGAACGTATTCTT CTTATGAAGT	420
TTATGATGCT CAATTTACTG AAAAACTTAA GCATTTTGCA GAAGAATTAT TAAATGGTTA	480
TAAAGAAGTA GCTACTAACG CTGGTGTTAA AGATGTAGAA ACGCGTCTAG AGTTTGGyTC	540
TCyTAAATCT ATCATTCTTA AAAAGCTTGC ACATGAAATT AATGCAGACT TGATTATGAG	600
TGGTACATCA GGCTTAAATG CCGTGGAAAg ATTTATTGTT GGTTCGTAT CAGAATCTAT	660
CGTTTCGTCAT GCGCCATGTG ACGTGTTAGT TGTTCGTACT GAAGAGTTAC CAGCAGACTT	720
CCAACCACAA GTT	733

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

TGATGATCCT GAAGCGCTAT TGGATAATTA CAACACTGAA GATGTTGATG CACACAATTA	60
CAATAATATA AATCATGTTA TTTTGCCTG CGATGCGGGT ATGGGTCTTA GTGCAATGGG	120
TGCArgCATG TTACGTAATA AATTTAAAAA GCGGGGCATT AATGATATTA CAGTTACAAA	180
TACTGCGATT AATCAATTGC CAAAAGATGC TCAATTAGTT ATACTCAGA AAAAATAAC	240
TGATCGTGCT ATTAAACAAA CACCAAATGC CATCCATATT TCAGTGGATA ATTCCTTAA	300
TTCACCAAGA TATGAAGAAC TTTTAAATAA TCTAAAAAAA GATGATCAAG CATAATAATT	360
AAATAAATTA AAAAATGGAG GATACCGCCA TGTTATTGAG TACACGTGAA AAAGAAATGA	420
TAGCCCTAtT GATTAAGTAC CACGGtCAAt ATATCACTAT ACACGACATT GCTCAGCAAC	480
TTGCGGTGTC CTCTCGTACT ATTACCGTG AATTTAAAGG TGTTGAAGCA TATTTAACTT	540
CATTTTCATT AACTTTAGAA CGCGCAAACA AAAAAGGGcT ACGCATTGCT GGCACAGATT	600

CTGATTTAAA CGATTTGAAG CAATGATTG CACAACATCA AACCATTGAC TTATCTGTTG	660
AAGAGCAGAA AGTAATTATT ATATACGCTT TGATACAAGC CAAGGAGCCA GTTAAACAAT	720
ATAGTTTAGC GCAAGAAATT GCGGTTTCTG TCCAGACTTT AGCAAAGATG TTAGATGATT	780
TAGAGCTTGA TTTAAATAAG TACCAACTAT CTTTATCTCG AAAGCGTGGCGAAGGCATTT	840
ACTTGGTAGG TACTGAATCA AAGAAACGTG AATTTTAAAG TCAATTAATG GTGAATAACT	900
TAAATAGTAC TAGCGTTTAT TCAGTAATTG AAAATCATTT TGTCTTTCAT TCATTAAATC	960
AAATCCACAA AGACTTTGTT GACTTAGAGC GCATTTTTAA TGTTGAAAGA CtATTaATGG	1020
ACTACCTAAG TGCCTTACCC TACCAACTTA CCGAATCAAG TTATTTAACT TTAAGTGTCC	1080
ATATCGTGCT CTCCATTTCA CGTATAAAAA ATGGAGAGtA TGTCGCATTA AACGATGATA	1140
TTTATGATTC TGTACAAAAC ACATTTGAAC ACAAAGTaGc AAGCGAACTT GCTGATAAAC	1200
TTGGTCAAAT ATATGACGTC ACGTTTAATC A@cAGAAAT TGCTTTCATT ACTATCCATT	1260
TACGTGGAGC TAAACGAAAA AATCTTAATG ATACATCATT AAATAATCGT TGTGAAGAAA	1320
ACAAAATTAA AGCGTTTGTG AACAAAGTAG AAATGATTTT CCGTATGACA TTTGCAGATT	1380
TGGATACTTT AGTAGATGGA CTGACGCTAC ACCTTAATCC TGCAATCAAT CGTTTGcAG	1440
CTAATATCGA GACCTATAAT CCGTTAACAG ACATGATTAA GTTCAAATAT CCAAGACTAT	1500
TTGAAAATGT AAGATTAGCT TTAAATGATT GTTGGCCTGA TTTGATTTTT CCAGAGAGTG	1560
AAATTGCTTT TATAGTtTTA CACTTTGGTG GCTCGATTAA AAACCAAGGT AATCGATTTT	1620
TAAACATATT AGTcGTTTGC AGCAGTGGTA TGGGAAGTAG TCGTCTATTA TCAACTCGTC	1680
TAGAGCAAGT TTTTAGTGAG ATTGAGCGTA TTACACAAGC ATCAGTCAGC GATTTGAAGT	1740
CACTAGATTT AAGTCAATAT GATGGCATTa TTTCTACTGT GAATTTAGAC ATCGACTCCC	1800
CCTATTTAAC GGTAACCCA TTATTACCAG ATAGTGATATCAGTTATGTC GCACAGTTTT	1860
TAAATACAAA GTCTACGTTT CAAGAGACGC ATGATAAATC ATCAAACATG ATTGATAAGG	1920
ATGATGTTCA TGTTGAAACG AAAGATGTTG ATGGCAACAC ATCTTTTGAA AATGAACAAA	1980
CTTCATACTT AACTTCAGTT TTCGAAAAAC ATTTAAGTGA CGAAAAATCA GAACAATTAT	2040
TGCATCATAT GCGTTCGGGT TTAACCTTGC TTGATTCAGT GAAAATAGTT AGTACCGAAG	2100
TTAAACAGTG GCAAACATAT ATCGCAGATT ATCTATATCA ATGCGATGTA ATAAACGATC	2160
CAACGTCATT CGCTGAACTA CTAGAGCAAC GATTGATTGA CAATCCAGGA TGGATATTAA	2220
GTCCATATCC TGTTGCAATA cACACCTAA GAGACAATAT GATTAAACAC CCTATGATTC	2280
TAATCACAGT TTTAGAAGAA CCGTTAACAT TGCCTAGTAT TCAAAATGAC AATCAAACAA	2340
TTAAATATAT GATTTCATG TTTATTTCTG ACAATGATTT TATGGCATCA CTGGTAAGTG	2400

ACTTGTC CGA	ATTTTAAAGT	TTGAAATTAG	AATCTATTGA	TACTTTTGTG	GAAAATCCAC	2460
AGGAACTTGA	AACATTATTA	AGAAACAAAT	TTTTAGAACG	AATTAAAAAA	CAATTTATTT	2520
AGGAGTG TAC	AAAATGAGCG	AATTATTTAG	TAATGACAAT	ATCTTTTTTA	ATGTAAATGT	2580
TAACAGCCAA	AATGAAGCAA	TTGAAAAAGC	AGGTAAAGCC	TTAGTTGATA	GTGGTGCTGT	2640
AACAGATGCT	TATATTCAAG	CAATGAAAGA	TCGTGAGCAA	GTCGTATCAA	CATTTATGGG	2700
AAATGGCTTA	GCAATTCCTC	ATGGCACAGA	TGAAGCTAAA	ACAAATGTGA	TTCACTCAGG	2760
TTTAACATTA	TTACAAATCC	CTGAAGGCGT	TGACTGGGAT	GGCGAAGTAG	TTAAAGTTGT	2820
CGTGGGAATT	GCTGGTAAAG	ATGGCGAAAG	TTTAGACTTG	TTATCTAAAA	TTGCAATTAC	2880
ATTTAGCGAA	GAAGAAAATG	TGGATCGTAT	CGTTCAAGCA	AAATCTGCAG	AAGAAATTAA	2940
ACAAGTATTC	GAGGAGGCAG	ATGCATAATG	AAAGCAGTTC	ACTTTGGTGC	TGGTAACATA	3000
GGTCGTGGTT	TCATTGGTTA	TATTCTgCAG	ACAACAATGT	TAAAGTAACA	TTTGAGACG	3060
TCAATGAAGA	AATCATTAAT	GCTTTAGCTC	ATGATCATCA	ATACGATGTT	ATTTTAGCTG	3120
ATGAGTCTAA	AACAACGACG	CGCGTGAAtA	ATGtTGATGC	AATTAATTCA	ATGCAACCTT	3180
CTGAAGCGTT	GAAACAAGCA	ATTCTAGAAG	CTGATATTAT	TACAACAGCT	GTTGGTGTTA	3240
ACATACTACC	TATTATTGCT	AAATCTTTTG	CGCCTTTCTT	AAAAGAAAAA	ACAAACCATG	3300
TTAATATTGT	TGCTTGTGAG	AATGCTATTA	TGGCAACTGA	TACATTGAAA	AAAGCAGTAC	3360
TTGATATTAC	TGGCCCTCTT	GGTAACnaTA	TTCATTTTGC	TAAC TCAGCA	GTTGATAGAA	3420
TTGTACCATT	ACAAAAGAAT	GAAAATATAT	TAGACGTAT	GGTTGAGCCA	TTTTACGAAT	3480
GGGTTGTTGA	AAAAGATGCA	TGGTATGGTC	CAGAACTAAA	CCATATTAAA	TATGTTGATG	3540
ATTTAACACC	ATATATTGAG	CGTAAATTAT	TAAC TGTA	TACAGGACAT	GCATATTTAG	3600
CGTATgCTGG	tAAATTTGCA	GGTAAAGCTA	CAGTTTTAGA	TGCAGTTGAA	GATAGTTCAA	3660
TTGAAGCTGG	CTTACGCCGT	GTTTTAGCTG	AAACTAGTCA	ATATATTACT	AATGAATTTG	3720
ATTTTACTGA	AGCGGAACAA	GCTGGTTATG	TTGAAAAAAT	AATAGATCGT	TTCAACAATT	3780
CTTATTTATC	TGATGAAGTA	ACACGTGTCG	GACGAGGTAC	ATTACGTAAA	ATTGGCCCTA	3840
AAGATAGAAT	TATAAAACA	TTAACATATC	TTTATAATAA	AGATTTAGAA	CGCACTGGTT	3900
TATTAAATAC	AGCTGCATTG	TTATTGAAGT	ATGATGATAC	AGCAGACCAA	GAACTGTTG	3960
AGAAAAATAA	TTACATTAAA	GAACACGGTT	TAAAAGCGTT	TTTAAGTGAA	TATGCTAAAG	4020
TTGACGATGG	CTTAGCCGAT	GAAATAATTG	AAGCGTACAA	TTACTTTCA	TAATTTATTG	4080
AGCTTTGTTT	GAAACAAGAA	GTTTCCAACG	TTATTCGTTA	ACAATCAGTA	ATAATGTAGT	4140
AGTTCCCTTG	AATTAACAAT	ATTAAATTTT	TGAACATAAA	AAATACTCCC	TTCAACATAG	4200
ACACTTAACT	TGTGTTATGT	ATGAAAGGAG	TATTTTTGCG	TTAATAATTT	GTTTTATTTT	4260

CGAGCCACAG	CCACCTATTC	AATGGCTATT	GGTCATTACT	AAAACAAATT	CATATTAACT	4320
GTTAGACTTG	GTTACTTAGT	AAGGAATATT	TCCCTATGAA	ATAACTAGAT	GTTACATTC	4380
TTGAATAAAT	TTTATTCTTC	AGTTTGTTGG	TCTTTCTTAG	TGAATCTTCT	AATTAAGAAT	4440
GCCATACCTG	CACCTAGAGC	TAATCAGCA	TATGGTAAAT	CGTCATTATG	TGACATACCA	4500
GTATCTGGTA	AAGTTTTAGC	TTGTTGTTTA	GCTTTATTAA	CTTTTCCTTG	TTGAGCTGAT	4560
TTTGTCTTAG	CTTGGTGGTC	GTCAGTGTTA	GTTACATTAA	GCATATCTTG	ATTAGCACTA	4620
TTGCTTCCAT	TTGAAACTGT	AGCTGGAGAT	GCATTGGCAC	CGTCGTTTTGCGTA	gyTTTA	4680
TTGTTTGCAG	CTGAACCAAC	TGATTTTTGC	GTATCATTAG	TATCTGCTGT	TGCCGTATCA	4740
TCTTTTTGGC	TAACATTAGT	TGAAGTCATT	TTTTCTTTTG	CTTCAGAAGA	TGCAGATGTT	4800
GATGGTTTAT	TCGAAACTTC	AGTATCAGCT	TTGCTTGGCG	ATTTATCTGC	TTCGTTAGAT	4860
GCAACGTTAG	TTTCAGACTT	AAGTTGTCCT	GCATCAGTTT	GATTTGTCGT	ACTTTCTTCT	4920
TTATCTTTTG	ATGTATTAGA	AGGTACATTT	GGTCTGTGTA	TGTCTGCTGA	AGGCAATGTT	4980
TCAGTTGtG	ATTCAACCAT	ACTTTGATTT	GTTGAATCAC	TACCATCTTT	TTCTGCCTTA	5040
GCTTTATTTT	CAGATTTTGG	TTGTGCAACC	TETCATTAG	TTGATTGAGA	TTCAGCACTA	5100
TTATTTACTT	CAGCATTTTG	TTTTGAATCA	TTTACAGATG	CATTATCTTT	GCTATCAGCA	5160
GATGATGCTG	CTTCTGTGCT	CGCAGTTGTT	GGAGCCGTTG	CTGTTGATCC	TGTTGGTGCA	5220
TTCTCGTTTG	TTGCTGTAGT	TGTACTATTG	TTATTTGTTG	TGCTTTCTGC	TGGCGTTGA	5280
TTATCAGTTT	CTGTTACAGG	TTTATCAGTT	GTGCCGTTAT	TAGTTGATTC	TACTTCTGGT	5340
TTACTAGTTA	CATCGTTATC	CATTGTCGGA	CTGTTTGTTG	ATGCATCTAC	ACTAGAATTG	5400
TTATTAGCTT	GCGGTTTATC	ATTTGCATCA	TCAGTTGCTG	ATGTTGCTGT	TGTTTCACCT	5460
GTTGCCGCAT	CATATTATT	TGGTGTTGTC	GGAGAAGCGT	CTGCTTTGCC	ATTAGCTGTC	5520
GTCTCAGATA	CGTTAGGTTG	TCCAGTATTT	TCTGGTGTTG	CATTAGCATT	TGAATTTGCT	5580
GTTGCATCAT	TATTATCTAT	ACCATTATTA	GTATCATTAG	CATCTGGATC	ATTCTGAGGC	5640
ACAATCGCTT	CAATTGCAGG	TATCGTTACA	TTTTGTAATTCAGCA	AACTTC	TGCATTTGTT	5700
TGTGTTTTAT	CTAATTTATC	AGCAAATCTG	TCAAATATC	TACCTAAATC	CGTACGTGCA	5760
ATTTCTTTTCG	CCGATGCATC	TGCATCTGCA	TTTTTAATTA	TTTCTATTTG	CTTGTTAACC	5820
ACTTCTCTGA	TTGCTTCCAA	AGCATTTTTTC	TTAACTTCAG	GATTAATACG	TTGTGCTTTA	5880
AGTTGTTCAA	GCGCACTATT	TTTGACAGTA	GCGATTTCTG	CATTTGTAGT	TTGATCAGAA	5940
ATATCTTCAG	TTGCTTTTGA	TAAAATGTCT	TCTAAAGCAT	TCGTAAACGC	TTCTTTTTCT	6000
TCAGTTGTAG	CATCAGCGTT	GACATTTACA	CCTGCTTCAA	TCTGGTCTAG	TGCAGTTTCT	6060

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 977 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

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AACAAAGCCT TCCAATTATC TGCGTCGGTA GAACAAGTAT TAGCAACTTT ATCACCTACG      60
CTAAACAGTC CTTACGATTT ATACGGCAGC ACAAAAATGC TAGATATTAC ATTCGATTCA      120
TTTGAACATG ATGGTACAAC GTACCCTGTC GACTATGCTA CGTTTGAAAA TGATTATGAA      180
GATAATAAAG ATCCTGAGTT TAGACGTAAA AGTTTCAAAT CGTTAGCGA TGGGATTCTGA      240
AAATATCAGC ATACTACCGC GGCTACATAT AATATGCAAG TACAACAAGA AAAAATTGAA      300
GCTGATTTAC GTGGATTGGA ATCAGTCATC GATTATTTAT TACATAGTCA AGAAGTAACG      360
CGTGATATGT TTGACCGTCA AATCGATATG ATTATGCGTG ACTTGGCACC AGTTATGCAG      420
AAATATGCTA AACTTTTACA ACGTATTCAC GGATTAGATA ACATGCGTTT TGAAGACTTG      480
AAGATTTCTG TAGACCCTGA TTATGAACCA GAGATTTCAA TTGAAGACTC AAAAAATTAT      540
ATTTTCGGTG CGTTAAGTGT TTTAGGTGAT GACTATACAA ACATGTTACG TGAAGCATAC      600
GATCAGCGAT GGaTTGATTT TGCAGAAAAT AAAGGTAAAG ATACAGGCGC ATTTTGTGCA      660
AGTCCATACT TTACACATTC ATATGTGTTT ATTTCTTGGA CTGGTAAAAT GGCTGAAGCA      720
TTTGTCTTAG CACATGAATT AGGTCATGCA GGTCATTTTA CATTAGCTCA AAAACATCAA      780
CCATATCTTG AATCAGAAGC ATCAATGTAC TTTGTTGAAG CCCCTTCTACAATGAATGAA      840
ATGTTGATGG CCAATTATTT ATTTAACACA AGTGATAATC CAAGATTTAA GCGTtGGGTT      900
ATTGGCTCAA TTTTATCTAG AACATATTAT CATAATATGG tACCCmTTTA TTAGAAGCnG      960
CTTATCCACG GGGAGTG                                     977
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(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

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AGACAGTGAT yGaATTTTCAT TTACAGTACA CAAATCATCG AAAAATTGGT AACATTCTTC      60
TCTATTTTCT AACGTTAgwA TTgCATCAAA CAATTCATCT AACGCTGCAC CTCGTAATTT      120
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TTCAATTTGC ATATCGAAAC AACCCCTATA ATTTTATTCT TTATGTCATT TTAACGCATT	180
AATCTATTAA AGTGTAGCGa TTTATATTT ATTAAATCTG AATCGTTACT TTATTTAATT	240
TTATGCTAAT CCAGCGCGTT CGAAAATAGT GTCAACTTGa TTCAAATGAT GTTTAGGATC	300
GAAACATTCA TCCAATTCTT CTTTTGTAA AACACTTGTA ATAGACTCAT CTTGTTTCGAT	360
TAATTCACGG AACGGTGTTT TCGTTTCCCA AGATATCATC GCTTTTGGTT GTATTGTC	420
GTATGCTTCT TCACGAACCA TACCTTTATT AATTAATGCT AATAAGACAC GTTGTGAGAA	480
AATCAGACCA AATGTTTTAT CTATGTTATT ACGCATATTA TCTTCAAATA CAGTTAAACG	540
GTCCACAATA TTTGTGAACG ATTCAATGCA TAATCTAGTG CtATTGTAAC ATCTGGAAC	600
ATAATACGCT CAGCAGAAGA ATGAGAAATA TsTCTTTCAT GCCATAATGG CACATTCTCA	660
TAAGCTGTAG TAATATAACC ACGAATGACT CTTGAAATAC CTGTGATATT TTCAGAACCA	720
ATTGGATTTT GTTTATGAGG CATTGCAGAT GAACCTTTTT GGCCTTTTGC AAATGCTTCT	780
TCAACTTCTC TCGTTTCGGT TTTTTGAAGG TTACGATTT CAACGGCAA TTTTCTAGT	840
GATGTCGCGA TTAATGCTAA TGTCGCAATA TAGTATGCAT GTCGATCGCG TTGCAATGTT	900
TGCGTTGATA CAGGCGCTGT GCCAATACCT AAATGTTTAC ACACATAACT TTCTATTTCA	960
GGAGGAATGT TAGCAAAAGT ACCTACTGCA CCACTCATTT TCCCTACTTC AATTTCTTCT	1020
CTTACTTGTT TGAAACGTTG TAAGTTACGT TGCATTTCCG TGTACCACAA TGCCATTTTG	1080
ACACCAAATG TAGTTGGTTC TGCATGCACT CCATGTGTAC GTCCCATCAT CAATGTATAT	1140
TTATAATTTT TTGCTTTTTT AGCTAAAACG TCGATAAATC TTTCTAAATC TTTTCAATA	1200
ATGTCATTTG CTTGTTTAAAT AACGAACTT AAAGCTGTAT CTACAACATC AGTAGAAGTT	1260
AAACCATAAT GTACcACTTA CGTTCTTCAC CTAGCGTTT AGAAACTTGT CTAGTAAAGG	1320
CTACAACATC ATGGCGCGTT TCTTGTTCAA TTTCTTGTC ACGTTGACA TTTACCTTTG	1380
CGTTTTGACG AATTTTTTGT ACGTCAGCTT TCGGTATATG TCTAATTCA CTCCATGCTT	1440

(2) INFORMATION FOR SEQ ID NO: 537:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 784 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

GATAAATCTA TnCAGTTTCC GTCCAAATAT CtGCaCCTAA AGCTTTTAaG TGTTCTACAA	60
TATCTgTATA ACCTCTATAA ATATGTTTAA CATTGTAAAT TGTAGTTACA CCCTCAGCAA	120

TTAAACCAGC AATAATTAAA CAAGCTCCTG CTCTTAAATC GCTAGCATAA ACTTCAGCAC	180
CATGTAATGT TGATGGTTTT ATCGTTGCTG TGCCTTCGTC AACTTCAATA TTTGCACCCA	240
TGCGCTTTAA TTCTTCAACA TGTTTAAAAC GCTCCGGATA AATCGTATCA GTTACAAATG	300
AAGGACCATT TGCCATAAAT AATAATGGTG TAATAGGCTG TTGCAAATCA GTAGCAAAAC	360
CTGGATATAC TAGTGTTTTA ATATCAACAA ATTGATATGG CGCATTATTA TTGATGCGAA	420
TTCTTTCGTC TCTTACATCA ACATTCACAC CTAATTCACT AAATTTAGCA GTTAATGTTT	480
CTACATGTTT CGGAACAATA TTATTTAATA TAACATTTTC TCCACATGCT GCAGCGATAC	540
ACATATATGT GCCTGCTTCA ATTCTATCAG GTATAACTTG ATACTEGAA CCATGTAATT	600
CTTTGACGCC ATTGATTTTA ATTGTTGATG TACCCGCTCC CTTAATATTA GCTCCCATAC	660
TTGTTAAGAA GTTAGCAACA TCAACTACTT CCGGTTCTTT AGCAGCATTT TCAATTACAG	720
TTTGTCTGTG TGCATAAACT GCAGCTAGCA TAATGtnAAT TGTTGCACCT ACGCnAACCA	780
TATC	784

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

CAATCTCCAC CAATGACACG TCGTCATTCG TGACCTCATA CCArACAAAA AACAGTCTCG	60
CAATCAAGAC TGTTTTCCAC TCAATATATT CATCCATTAG CGTAATAGAT TATTTGACTT	120
CTGTAGCTAC AAAGaTTTTA CGTTTTTCCC AAACGCCTGT cTTTTTCATTG TAATCATCAC	180
AAGTAATTAA TGTTAATTGT TTATCTTTAC CTTTTTGTTT ATCTAGAAcT CCTACATCTG	240
TAGGCTTAAC ATCTCTTATA CTTGTCATTT TATACTTACG TGTTTCATTA CCAACTTTAA	300
AGTACACCAT ACTACCTTTT TTGGCTGCTT TAAGATTTGT AAATTGATg TTCGGACGGT	360
CAATGAAAGT GTGTCCTGCA ATTGAAATAT TTTGATCATC TAGTGATTCA TTTTCTTCTG	420
CAAAGCTTAC ACCTCTATTT AATTGTTTCTG GTGTTGCTGG TCCTGGATAT ACTGGTTCTT	480
TAATATCAGC ATCTGGAATT TCAATATAGC CTGCCACTTT CGATTTATCT TTCGGAATTT	540
GAGGTTTAGC TTGCTGCTTT TTATCTTTAC TCGCCTGTTT TTTTACATTT TTATCATATT	600
GTTCAATCTT TTCATCTTTA TCTTTATCGT GAAGATAATT ATCGATATGT GGTTTAGCAA	660
ACAAATATGC TGCCACTAGG aTAAGTACCA CACCAGCGAT TGTCATTAAT CGATTTGTCC	720
ATTTTTTCAT ACGTTAAGGC TCCTTTTATA CATTTACAA TGCCTGTTAA CATTTCATAT	780

AGTATACCAT TAATTTCAAA ATGACTCATA GCAATTCATT TTATACTATA AAATTTACAT	840
GTATACTTTT ACGTTAGATT TCATTACACA TATTTGCATT CAAATAACGA AACGCTTTTA	900
ATAATTACTA AGGGGGAATT GATATGATTA GATACGCTAA AAAAGAGGAT TTAAAGCTA	960
TATTAGCGAT ATACAATGAT GCCATTATCA ATACTACAGC TGTTTATACT TATGAACCAC	1020
AAACCATAGA CGAACGTGTC GCATGGTTTG AAACGAAACA ACGTAAGCAT GAGCCTATCT	1080
TTGTATTTGA GGAAAATGGA AGTGTCTTAG GGTTCGCGAC GTTCGGTTCA TTTAGACCTT	1140
GGCCAGCATA CCTATATACA ATCGAACATT CTATTTATGT CGATGCTTCA GCTAGAGGAA	1200
AAGGTATTGC TAGTCAATTA CTACACCATT TAATTGTGGA AGCAAAAGCT AAAGGTTATC	1260
GTGCGCTAGT TGCAGGCATT GATGCTTCCA ACAAAGCGAG TATTCAGTTG CATCAAAAGT	1320
TTGCTTTTAA GCATGCCGGC AACTGACCA ATGTAGGTT TAAATTTAAT AGATGGTTAG	1380
ATTTAGCATT TTACGAATTA GATTTACAAG ACTAGTAATG TTTGAATCAC ATAATATAAA	1440
CAAGACAACC ATGTTAATTC CCTTAACATA ACAAGCCAAC ATATAAAATT TTAAACTTCT	1500
CAGGGGAGTG GGACAGAAAT GATAAAGAGC CACTAATGAT TTATTATGTA GTGGTTCTTA	1560
CACATTAGCC ACAGCTAATG TGTAcTTAAA AATAGGAATA CATGAGTAAA ACTCATGCAT	1620
AAGAAATACT AATTTCTATA GAAAAAGTAT TTCTTTATCG TCGTCCCACC CCAACTCGCA	1680
CATTATTGTA AGCTGACTTT TCGTCAgCTT cTGTGTTGGG GCCCAAAAAG CTTGTTACAA	1740
GCGCATTTTC GTTCAGTCAA CTACTGCCAA TATAACTTTG TAGAGCATAT TACATTGATT	1800
TACATTGTCC CTTTTATTTA TTCTTTTCAA ATACTATCCC CATAGCTTTG ATTTAACGCT	1860
TTTTCTCAAT AACAAAACGA ATATAGTAGA ACATGAAAAC GATAATCATG CTGAGCGATA	1920
AAGATTTAAA TAATAGATTG ACCCACGTTC CCTCAGTCGT ATATCATAT GTAATCGTTG	1980
TGTTAATGAT GAATGCTATA AAGATGATTG ATAGTCTTAG CATATCATCA CTCCTTTTAA	2040
GTTATTTTAG ATATACGGGG GCGCTTTTGC AATCACTATT TTGATTAGTA TGCATTTTCC	2100
ATAAATCTTT CAACTTCTTC AGAGATAATT AAGAAGCATC TATCTGGTAC TAATGATCCA	2160
GACAGATGCT TCTTTTTTAT CAATATTTTA TTGTTATCTC ATTAATTATT TTTAACCATA	2220
TCTTCAGCTG TGCCAAAGAT TTTACGTTTA ATTGCTTCGC CAGTTGGTGT GCCTGCTAGT	2280
CCACCCAATC CAGTTTCACG TAATGATGCA GGAAGGTTAC GACCAACCTT ATCCATTGCT	2340
TCAATAACTT CATCAACAGG GATTCTACTT TCAATACCTG CTAATGCTAA ATCTGCTGAA	2400
ATTAAAGCGT TACCCGAACC AATTGCATTT CTCATAACAC AAGGAATTTT ACAAGTCCG	2460
GCTACTGGAT CACAACTAA ACCTAATAAA TTAATTATCG CTAATGCCAT AGCGTGCCCC	2520
GATGCTTCTG GTGATCCTCC GAATATAGCT ACTGCTGCAG CTGCGGCCAT TGAGATGCT	2580

GAACCAACTT CAGnTTGGCA GCCACCTGTT GCACCAGCTA CACTTGCATT GTTTGCTACG	2640
ACACGCCCAA ACAATGCTGA AGTGAATAAG AAATCAATCA TTTGCTCTTC TGTTAAATCA	2700
TGTGTTTTTT CTAATTTAAA AAGTGCACCG GGAATGGTAC CCGAGGAACC AGCTGTTGGC	2760
GtGCACAAA TAATACCCAT CGCAGCATTG ACTTCATTTG TTGCAATGGC AcCtTTGcTG	2820
CGTCAATCAT TTCATATCCA GACAAAGCAT GATGTGTTTC ATTATAATCA CGTAGTTTAG	2880
CAGCATCATG ACCAGTGTAG CCCGTTACAC TTTCAACCCC ATCACCTGTC GTCCCTTTGA	2940
TTACTGCGTC TCGCATGACA TCTAAATTTT GTTTATTTG CGCTCGCACT TCATCACGTG	3000
ATTTACCGCT TAATTCATT TCTTCTTTAA CCATGATATC CGCAAATGAC ATATTATTTT	3060
CTACGGCATA ATCTATAGTC TCTCTAATTG AATCAAACAT GTTTATTCCC CCTCTAATTT	3120
ATATAGGAAA CGTTTACGTC ACTGTATTTT TCTTTAATTG TATTTAATGT TGATTCTGAG	3180
ATTGCTTTAT TTAATGGTAT TACAACCAAG CATTTATCTT CATCTATCTT AATAAATTCA	3240
TCTTTACAGT CTAATTTTCA ATCGTTGATA TCATTGATGA AATGATTTAC TTGTGCTTTA	3300
GTCATATTTT CGTCAACAAC TAAAATTGGT AATCCATGAT TTAAATCTAC TTCTAGTCCA	3360
TTTATATGAA TACCTTTAAT TTTAATTGTA CCACCACCGA TTGAAATACC GATAATTTCA	3420
ATGTAGCGAC CATCATTACG AGATGATTTG ATATAAGCAC AGTTTGGATG TTGACCAATA	3480
CTATCGCCTT CTTCTTCGAT GATATCTATT TTAATACCAT CATCAGCTGC AATTTCTAAT	3540
GAAGATTTAA TTCGGTTATC AAATGTTGAA TATCCCATTG CCCACCCAC AATAGCGACA	3600
TCTGTACCAT GTCCTTGGTG TGTTTGAGCA AATGATTCAT AATAATGTAT TTCAATATTT	3660
TTATATCTCC CAATATTGCG CGTGCTGAAT TCCCCTTTAC TGCACCAGCC GTATGAGAAC	3720
TTGAAGGGCC CAT	3738

(2) INFORMATION FOR SEQ ID NO: 539:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

TGGCTGTCTT CTCTATGAGT GTAGTAAGTA AGTTAACGGA TTTAACGCCA AGGCAAATAC	60
GTTACTATGA AACACATGAA CTCATCAAAC CTGAAAGAAC AGAAGGTCAA AAACGTCTGT	120
TCTCACTCAA TGATTTGGAA AGATTACTAG AAATTAAATC ATTATTAGAA AAAGGATTTA	180
ATATCAAAGG GATTAAACAA ATCATTTATG ACTCACAAGA GCATTTAACA ACAGATGAAC	240
AAGAGATAAG AAAAAAGATG ATTGTAGATG CCACGCAAAA GCCTATTGGA GArACTTTGC	300

CAATAAATCG TGGTGATTTA TCCCGATTTA TTAAATAAAA TTTGGAGGAT TTTAAAATGC	360
CAAAACGTAC TTTCATAAA GACGACATTC GTAAATTTGC AGAaGGAA AaTGTAaGaT	420
ATTTAAGATT ACAATTCCT GATATTTTAG GAACAATTAA AAATGTTGAA GTGCCTGTAA	480
GCCAATTAGA AAAAGTACTT GATAACGAAA TGATGTTTGA CGGTA	525

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

TTGATTTGCT ACAAAGTATC TnCTCATTTT TGTATCCTGA AAAATCTTTA GTGTAATAAT	60
GTTGTTCACT TTTAATATTT TCAGTCATAG TTGACTACCT CCGTATATTT TGATTTAATT	120
AAGTTGTATA TTTTGATGAA CACTTATTGT TACTTGTTGG CGCAAGTAGC AGTTTTTTCA	180
TTCTTCATAA AAGTATTCCT TATAGAATAT GAATGTTGCG AACTTGCGA ATCCTGCAAT	240
TGaCCATGCT GtAGTGAAGT ATAGAAACGG CATAAGTACA ATCGCTAAGA CTGTGAAGCA	300
TAGTACTGCT ACTAGGTAGC TTTTATAAAT GTTACTCATT TTCTTTTTTC AACTCCTCCA	360
TTATTCTCTG GTCTGATAAG TCGTGATAAG GGAATTTTTT CcTAGCTAAT TGGACTGGTA	420
TTCTGCCTCG TATCGCAATG TATCCTTCAT CTTCAAGCTC TTTATTCT TCTCTTATTA	480
TTTGTCTGCT TTTGGATTTA GAAACAGATA AAATTACCgC AAGTTCTTTA GCTTGCAAAC	540
TATTTTTTCAT CATATCTTTT CCTCCTTTAA AATAACTGTT GATTCTCTGG GTTATCTGCT	600
TCGTAAATTAT CTGCAATAAT ACTTTTAGCG AAAAAGTCCA AACTGACCTT ATATAGGTTG	660
TTCATAGATT TCTTTACGTT AACCCCTTCC TCAAGTACAT AAGGCACCCCT AAAATCATTT	720
ATAAACAGTC CGTTTTTCGTC TAAAGTAACG GTTGGAATT CAGGTTTGTT CCGTCTATAA	780
ACTTCTCCTA GTGTAGGTTT TTGCTTTTCA GCTTGTTTAG TGAAGTCGGA AAATGCCTTA	840
AGTAGTTTTA TTCCTGAATC AGGATCACTG TGTCGCTCAA TCGTTTCTGC TGTAGACTCT	900
TTACTAAAAT CATTTCTATT GATTACAGGC TTTCTCGTAT TTCGTTCAAT CTTCCAAACC	960
TTCCACGTCA CAACTGCCAT TGTGGTGAGG AGGGTTGTTT TGTATAGTGC GTTCATTTGT	1020
AATTCCTCCT ATTAAGTTGT TTGTTCAATT GTGTGTGTTA TTCTTCTTCG TCTAAATCAA	1080
AGTGCTGTTT GATTGGTCA ATTGCCCACT CAATCATTGA TTCAAGGTGT TTCTCTCTGT	1140
CGACTTCGTA AGTGTGCTCA ATCTCGCCTG cATATGTCAC AGTAAGAGTA TCTTTGTGTG	1200

TGTATGTTTG ACTTTTGTTy TCTtTAACTG CATAAAGTGT TAATACTATA TTGTTTAGCT	1260
TTyCTTTTTTG TTCTGGTGTC ATTTACGCTC CCCCTAmATT AGCyTCATAA CCGAATTCAG	1320
TCATGATTTT ATGTATTTTC AATCTGCCTT TTTGTGTCCA TCTAGTTTGT AAAACTGTGT	1380
CTTCTCTGCC ATCAGAACGC ACAATTGT	1408

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

GTTTCGTCAAT GATTTTTATC CGATGCTATG AGATTaTCA AATACAAAAT GCTCTCTTAA	60
AAGCAGTTAT TGACTGAAAA TCTACTTCTA AGAGAGCACT TTATTTAATT ACTTAAGAAA	120
TCTTGAAATT TCAATATACG ATGTTTATGA TAAGTCGCTT ATTTTCATCTT TAGGCTTGTT	180
ATTAGTAAGT AGTTTAATAC CACTGATTAA CCATAAAGCA AATGTAATTA TGTTACCAE	240
TATTACAGCT CCAATAATCA ACAATATACC ACTCATTTTT TTGTTTTTAG ATGCTTTAAA	300
CATACCGATT GCACCTAAAA TAATTGAAAT GATTCCAAAT ATGAATAGGG ATAAGAATAA	360
TACAGTGAAA ATTGCTGCTG CTGTTTCTGc ATCAACTGGG nCAACCTCAC CATTAAGTGT	420
TGTTGGACAC AT	432

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

ATAATCATGA AGTnGCTAAA nCGCCAAATA ATGATGGTTC TGGACATGTT GTGTTAAATA	60
AATTCCTTTC AAATGAAGAG AATCAAAGCC ATAGTAATCG ACTCACTGAT AAATTACArG	120
GAAGCGATAA AATTAATCAT GCTATGATTG AAAAATAGC TAAAAGTAAT GCCTCAACGC	180
AACATTACAC ATATCATAAA CTGAATACGT TACAATCTTT AGATCAACGT ATTGCAAATA	240
CGCAACTTCC TAAAAATCAA AAATCAGACT TAATGAGCGA AGTAAATAAG ACGAAAGAGC	300
GTATAAAAAG TCAACGAAAT ATTATTTTGG AAGAACTTGC ACGTACTGAT GATAAAAAGT	360
ATGCTACACA AAGCATTTTA GAAAGTATAT TTAATAAAGA CGAGGCAGTT AAAATTCTAA	420

AAGATATACG	TGTTGATGGT	AAAACAGATC	AACAAATTGC	AGATCAAATT	ACTCGTCATA	480
TTGATCAATT	ATCTCTGACA	ACGAGTGATG	ATTTATTAAC	GTCATTGATT	GATCAATCAC	540
AAGATAAGTC	GCTATTGATT	TCTCAAATTT	TACAAACGAA	ATTAGGAAAA	GCTGAAGCAG	600
ATAAATTGGC	TAAAGATTGG	ACGAATAAAG	GATTATCAAA	TCGCCAAATC	GTTGACCAAT	660
TGAAGAAACA	TTTTGCATCA	ACTGGCGACA	CGTCTTCAGA	TGATATATTA	AAAGCAATTT	720
TGAATAATGC	CAAAGATAAA	AAACAAGCAA	TTGAAACGAT	TTGCAACA	CGTATAGAAA	780
GACAAAAGGC	AAAATTACTG	GCAGATTTAA	TTACTAAAAT	AGrAACAGAT	CAAATAAAAA	840
TTTTTAATTT	AGTTAAATCG	GCATTGAATG	GTAAAGCGGA	TGATTTATTG	AATTTACAAA	900
AGAGACTCAA	TCAAACGAAA	AAAGATATAG	ATTATATTTT	ATCACCAATA	GTAAATCGTC	960
CAAGTTTACT	AGATCGATTG	AATAAAAAATG	GGAAAACGAC	AGATTTAAAT	AAGTTAGCAA	1020
ATTTAATGAA	TCAAGGATCA	GATTTATTAG	ACAGTATTCC	AGATATACCC	ACACCAAAGC	1080
CAGAAAaCGt	TAACACTTGG	TAAAGGTAAT	GGATTGTTAA	GTGGATTATT	AAATGCTGAT	1140
GGTAATGTAT	CTTTGCCTAA	AGCGGGGAA	ACGATAAAAAG	AACATTGGTT	GCCGATATCT	1200
GTAATTGTTG	GTGCAATGGG	TGTACTAATG	ATTTGGTTAT	CACGACGCAA	TAAGTTGAAA	1260
AATAAAGCAT	AATTATATTG	GGGGAAGAGC	ATCTATATAT	TTTTTTAAGT	ATATAAGACG	1320
TCTTATTTCC	CCTTAATTTA	TTGTGAAGTA	TATGCAAAT	GCAATGAATAGATT	GTCCAT	1380
CATTTTAACG	TTATAATGAA	TTTAACGACT	TAGAACTACA	CAAGTAAAGG	AGAATGAAGA	1440
TGTCTCGAAA	AACGGCGCTA	TTAGTTTTGG	ATATGCAAGA	AGGTATAGCG	AGTAGTGTAC	1500
CTAGAATAAA	AAATATTATT	AAAGCGAATC	AGAGAGCAAT	TGAAGCAGCA	AGACAACATC	1560
GAATACCAGT	CATTTTCATA	CGTTTAGTGT	TAGATAAGCA	TTTTAATGAT	GTCTCCTCGA	1620
GTAATAAAGT	GTTTTCAACA	ATTAAAGCTC	AAGGATATGC	GATTACTGAA	GCAGATGCAT	1680
CTACACGAAT	ACTTGAAGAT	TTAGCACCAC	TAGAAGATGA	GCCGATTATT	TCTAAGCGAC	1740
GCTTTAGCGC	ATTTACAGGT	AGTTACTTGG	AATTTATTT	ACGTGCAAAT	GATATTAATC	1800
ATTTAGTATT	AACGGGTGTC	TCTACAAGTG	GAGCTGTATT	GAGCACGGCA	TTAGAAAGTG	1860
TAGATAAAGA	CTATTATATT	ACTGTTTTAG	AAGATGCTGT	TGGTGATAGA	TCAGATGATA	1920
AACATGACTT	TATTATTGAA	CAAATTTTAT	CACGCTCATG	TGACATTGAA	TCCGTAGAT	1980
CATGGAAAAG	TAGTTTATAG	TTAATATAAC	GTCAATTAAA	GCTCGGCAGT	AATGTTTGAG	2040
AATAAGTACA	TTTGCTCATA	TTTATAAAAT	GTGTGAGATG	GCAATTGAAA	CGGATATGAT	2100
GAGGAACATT	TGAACATAAA	ATAATATATT	TATATAAAAC	GACCgAGGCG	TTCGAACTGA	2160
ATGtCCTCGG	GTTAATTGA	ATAGAAATCG	GACTTATGAA	CGAAATATGT	TTAAGTCGAA	2220

CTCCTTGTTT ATACTTATAA ATTTTACGGG TTTAATATAA TACTTATTTA CCTGTAATAT	2280
ATGCATAATT nCTTCAGTCG GTCAGCCTGT CGTTGCATAG TTCCTATGCA GCAAATGCAT	2340
ATCCTAATCC TTTAACATTG GCATTnCTGC AAATGAACGCATAGAATCCA TTTACTGTTA	2400
ACTTTTTnCA ACAAATGTCT nACATG	2426

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

GAGTTGGGGA ATGTGCTCAA AATATGCGGA CTTTATGCAT TyCGGAATTG sCCaATTGCA	60
GCTTTAAGCT ATGGTCAAAA AAAGAGGGTC ACTATAGCAT CTGTTTTAGT CTAAATCCG	120
GAAATAATCA TATTGGATGA ACCGACTGCT GGTCAAGATT TCTATCATT TAATGAGATA	180
ATGTCATTTT TAATTGAACT AAACAGACAG GGAAGACGA TTATTATGAT TACGCATGAT	240
ATGCATTTAT TGTCTGAGTA TAGTTCAAGA ACAGTTGTAT TATCAAAAGG TCAAGTCGTT	300
GCTGATACCA CGCCAgTATT GGTTTTAAAT GATAAAAAAA TCTGTGAGAT TGCATCATTG	360
AGACAAACAT CGCTATTTGA AATGGCCGAA TATATAGGGA TTAGCGAGCC ACAGAAATTA	420
GTACAATTAT TTATTAACCA TGATAGGAAG GTGAGACGcC AATGAATCAA TATAATACTA	480
TAGGTTTTCA CCCGGGAAAT AGTCGTATTC ATCAATTAAA TGGACTGTT AAACTTTTAT	540
TCTTATTAGT TGTTTCTATT TCTGCAATGG TGAATTATGA CACAAGATAT TTAATTTTAA	600
TTAGTGCTTC ATCTATTTTA TTGGTCAAAT ATGCTCATAT TGAATGGAAA CAAGTTCGCT	660
TTGTTGTTAA ATTCATTCTG TTTTTCACAA TAAtTAAATAT TATTGCCGTG TACATATTTG	720
ACCCTGAATA TGGTGTGAAG ATTTATAATC AGCGTACAGA GTTAGTCAAT GGTATTGGTC	780
GATTTACGCT AACATCACAG GAATTATTCT ATCTTTTTTA TCTAATATTA AAATATATTA	840
GTACAGTTCC TTTAGCGTTA ATATTTTTAT TCACAACGAA TCCGAGTCAT TTTGCTGCAA	900
GTTTAAATCA GCTAGGTGTG AATTATAAAA TCAGTTACGC AGTCTCACTA GCATTAAGGT	960
ATATTCCAGA TATTCAAGAA ACATATTtTA ATATTTTACA AGCGCAACAA GCAAGAGGAT	1020
ATGATAATTC GAAAAAGCA AAATTTACTA GCCGTGTTAA AGGTATCAAA CGCATTGTGT	1080
TACCTTTAAT ATTTTCTAGT ATCGAAAGAA TTGACACTAT TAGTACTGCTATGGAGTTAA	1140
GACAATTCGG ACAGTATAAA AGGAGAACCT GGTACGTCAA AAAACAATTA AAAAAAGATG	1200
ATTATGTTGT TTTGTGTTTG ACGTTAATAC TTCTGATGTT AGTAGTTACA TTATTCTTTT	1260

TAAATAATAG TCGATATTTT AACCCGTGGC ATTAGTATTC ATATAAATAG TCTTTAAATA	1320
GAAATAGGAG GGAGACATTT AATGATAAAT ACTGAAAGAT TAAATTTAAT GATTCCAAGT	1380
TCCTCGCATT TAATTGAACT TTATAATATT TGTAGTCATC CACAAGCAAA TATATACACT	1440
CCCAAAGGTT TACATAATTC CAAATTAGAC ACACAACGGT GGATTGAAAA ATGGCGAAAC	1500
CATTGGCAAC AATATCAATT TGGTTACTTT GATTGGTAA AAAAAATAGA TTGTAGTGTT	1560
ATTGGTATTT GTGGATATGA ATATCGACAA TTAAAGCAAG AaACAGTATT AAATTTATTT	1620
TATAAATTAC ATCCAAGTTT TGAAGGACAA GGGTACGCAT GTGAGGCTAT TACAGCAATC	1680
ACAAATTTTG TGAATTATAT CGATCAAGAA ACAGTAAAAG TTATCAGGAC AAATAAGT	1740
AACCAACGTT CAATAAATTT AGCAGAAAGG CTTAAATTCA AGCGAGACGA TACTATGGAC	1800
GACATTATCA ATCAAGGAGA TATTGTGTTT TAAaAATAAA ATACTATGAC ATTATCTAAA	1860
AAATAAAATT AAAA	1874

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

TCAACATTTT TAACACCAAT GTGAAAATGA TCTATGTGAT TTGCAATGGC TTGATTTGTA	60
ATATGTGTGC CTAAATGACC TGTAGCACCT GTTAACATAA TATTCATTCA CTTCATCTCC	120
TAATCTTTAT ATACATAACA TAATACTTAT TTGATGGTTT TCAAAACATT TGATTTTATA	180
AAAAATTCTA ATCTGTATTT ATTGTCGACG TGTAGTAA ATACGTAAAT ATTATTAATG	240
TTGAAAATGC CGTAATGACG CGTTTTAGTT GATGTGTATC ACTAATATCA TTGAAAATTT	300
TAATCaGGTA CTACGACAAT ATGATGTCTG TTTTGTGTCT GAAAGTTTTA CAGTTTTTAA	360
AATAAAAATG GTATAAAGTG TGATTTGTAT AAAAAAGAGT CTCGACGGAT AAGAATTGAT	420
TAATAACAGT TAGCATTTTA TTAATTACCT TAACAATGAT TCAAGTTTAG TTAAATGAGG	480
TTTAATTTGA AAGGGGATAG CGCCTCAATA TAATGTAGGT AGATTGTTCA TATTACGTAA	540
TTGAAAAATC AAATTTAAAT AGATTGGGGC TAAAAATTAT GAAATTTAAA GCGATAGCAA	600
AAGCAAGTTT AGCATTGGA ATGTTAGCAA CAGGTGTAAT TACaTCGAAT GTACAATCAG	660
TACAAGCGAA aGCAGrAGTT AAaCAACAAa GTGAaTCAGA GTTAAACAC TATTATAATA	720
AmCCAATTTT AGAGCGTAAA AATGTGACTG GATTTAAATA TACTGATGAG GGTAACACT	780

ATTTAGAAGT CACAGTAGGG CAACAGCATT CTCGAATCAC TTACTTGGA TCTGATAAAG	840
ATAAATTTAA AGACGGAGAA AACTCAAATA TAGATGTGTT TATCCTTAGA GAAGGTGACA	900
GTAGACAAGC AACAAATTAC TCAATTGGTG GCGTTACAAA ATCAAATAGT GTGCAGTATA	960
TTGATTATAT CAATACGCCA ATTTTAGAAA TCAAGAAAGA TAATGAAGAT GTACTTAAAG	1020
ATTTTTACTA CATTTCAAAA GAAGACATCT CATTAAAAGA ACTTGATTAT AGATTAAGAG	1080
AACGTGCGAT TAAACAACAC GGCTTGTATT CAAATGGTCT TAAACAAGGT CAAATTACAA	1140
TTACAATGAA TGATGGCACA ACACATACAA TCGATTTAAG TCAAAAACCTT GAAAAAGAAC	1200
GTATGGGTGA GTCAATCGAC GGACTAAGA TTAATAAAAT TCTAGTAGAA ATGAAATAAT	1260
ACTTTCTAAC AACAAAGCGC TATGTTGAAT AGTGCTTGTT ATGGAAATAT ATGGAAGTTA	1320
AGCGACGTAC TGTGCTTAG CTTCTTTTTT TGAGGGGAAA AGTTACAAAA CTCACACAAA	1380
CAGTCGCACC ACGCATTATC TTTTGCTTAA ATAGCTTAAT CATATTTTGA GAATAGTTAA	1440
AAACAGGTTA ATGTGAATAT CCGAATACAG CTCCTATAAT ATGGGTGTAT GATTCAAATT	1500
ACGTAATAAA ACAATCTAAT TATAATAGAT TGGAGCATAC AACTATGAAA ATGAAAAATA	1560
TTGCAAAAAAT AAGTTTGTTA TTAGGAATAT TAGCAACAGG TGTAAACACT ACAACGGAAA	1620
AACCAGTTCA TGCCGAAAAG AAACCTATTG TAATAAGTGA AAATAGCAAA AAATTAAAG	1680
CTTATTATAA TCAACCTAGT ATTGAATATA AAAATGTGAC AGGTTATATC AGTTTCATTC	1740
AACCAAGTAT TAAATTTATG AATATCATAG ATGGTAATTC TGTTAATAAT ATTGCTTTAA	1800
TTGGCAAAGA TAAGCAACAT TATCATACGG GTGTACATCG TAATCTTAAT ATATTTTACG	1860
TTAATGAGGA TAAGAGATTT GAAGGTGCAA AGTACTCTAT TGGGGGTATC ACGAGTGCAA	1920
ACGrTaAAGC TGTCGACCTA ATAGCAGAAG CAAGAGTTAT TAAAGAAGAT CATACTGGTG	1980
AATATGATTA TGACTTTTTTC CCATTTAAAA TAGATAAAGA AGCGATGTCA TTGAAGAGA	2040
TTGATTTTAA ATTAAGAAAA TACCTTATTG ATAATTATGG TCTTTACGGT GAAATGAGTA	2100
CAGGAAAAAT TACAGTCAAA AAGAAATACT ATGGAAAGTA TACATTTGAA TTGGATAAAA	2160
AGTTACAAGA AGACCGTATG TCCGATGTTA TCAATGTCAC AGATATTGAT AGAATTGAAA	2220
TCAAAGTTAT AAAAGCATAA CACATATACT TGATGACGAA ATAAGTTGAA ATTGAAATAG	2280
AGAGGTTAAG TGACGATCAA ACGTTGCTTA ACTTCTTTTT AATGCTTAAA AATTATTTCA	2340
AAGGCACATA GAAACGCTAT ATTAATCTCA TACTCACTCA TTATTTTTTG CTTAAATTAC	2400
TTAATAATAC TTCAATAATT GTTAAAAGGG GTTTAATGG ATTATCTTAG AACGCCATCT	2460
ATAATGATGT TGTATGATTC AAATTACGTA AAAAGACAAT CGAATATAAT ATAGATTGGA	2520
GCATACAATT ATGAAAATGA GAACAATTGC TAAAACCAGT TTAGCACTAG GGCTTTTAAAC	2580
AACAGGCGCA ATTACAGTAA CGACGCAATC GGTCAAAGCA GAAAAAATAC AATCAACTAA	2640

AGTTGACAAA	GTACCAACGC	TTAAAGCAGA	GCGaTTAGCA	ATGATAAACA	TAACAGCAGG	2700
TGCAAATTCA	GCGACAACAC	AAGCAGCTAA	CACAAGACAA	GAACGCACGC	CTAAACTCGA	2760
AAAGGCACCA	AATACTAATG	AGGAAAAAAC	CTCAGCTTCC	AAAATAGAAA	AAATATCACA	2820
ACCTAAACAA	GAAGAGCAGA	AAACGCTTAA	TATATCAGCA	ACGCCAGCGC	CTAAACAAGA	2880
ACAATCACAA	ACGACAACCG	AATCCACAAC	GCCGAAAAC	AAAGTGACAA	CACCTCCATC	2940
AACAAACACG	CCACAACCAA	TGCAATCTAC	TAAATCAGAC	ACACCACAAT	CTCCAACCAT	3000
AAAACAAGCA	CAAACAGATA	TGACTCCTAA	ATATGAAGAT	TTAAAGCGT	ATTATACAAA	3060
ACCGAGTTTT	GAATTTGAAA	AGCAGTTTGG	ATTTATGCTC	AAACCATGGA	CGACGGTTAG	3120
GTTTATGAAT	GTTATTCCAA	ATAGGTTTCT	CTATAAAATA	GCTTTAGTTG	GAAAAGATGA	3180
GAAAAAATAT	AAAGATGGAC	CTTACGATAA	TATCGATGTA	TTTATCGTTT	TAGAAGACAA	3240
TAAATATCAA	TTGAAAAAAT	ATTCTGTCGG	TGGCATCACG	AAGACTAATA	GTAAAAAAGT	3300
TAATCACAAA	GTAGAATTAA	GCATTACTAA	AAAAGATAAT	CAAGGTATGA	TTTCACGCGA	3360
TGTTTCAGAA	TACATGATTA	CTAAGGAAGA	GATTTCTTGG	AAAGAGCTTG	ATTTTAAATT	3420
GAGAAAACAA	CTTATTGAAA	AACATAATCT	TTACGGTAAC	ATGGGTTTCT	GAACAATCGT	3480
TATTAAAATG	AAAAACGGTG	GGAAATATAC	GTTTGAATTA	CACAAAAAAC	TGCAAGAGCA	3540
TCGTATGGCA	GACGTCATAG	ATGGCACTAA	TATTGATAAC	ATTGAAGTGA	ATATAAAATA	3600
ATCATGACAT	TCTCTAAATA	GAAGCTGTCA	TCGGAAAAAC	AAGAAGTTAA	GAACAACGG	3660
TTTACATGTT	GCTTAGCTTC	TTTTATTATG	CGTAATGATG	TAAAAAGACG	AATATTCATT	3720
TGTTTGTAAT	AGTGGCATT	CTATGTCTTA	AAAGTGACGA	AACTTCAAAT	GTGCCAAGTG	3780
TTGAATCACA	TCAAATCAT	TTTTATTTAA	CGAACATTAT	GGATTTCTTA	ATTTACTTAA	3840
CGATGATTCA	AATATAGTTA	AACAAGGTTT	AATGTGAATG	GAGCAATACG	CCATCTATAA	3900
TAAAGCTGTA	TGATTCAATG	AATGTAATCG	AACAAATCTA	ATAATTACGA	ATGGAGCATA	3960
CAACTATGAA	AATAACAACG	ATTGCTAAAA	CAAGTTTAGC	ACTAGGCCTT	TTAACAACAG	4020
GTGTAATCAC	AACGACAACG	CAAGCAGCAA	ACGGACAAC	ACTATCTTCC	ACTAAAGTGG	4080
AAGCACCACA	ATCAACACCG	CCCTCAACTA	AAATAGAAGC	ACCGCAATCA	AAACCAAACG	4140
CGACAACACC	GCCCTCAACT	AAAGTAGAAG	CACCGCAACA	AACAGCAAAT	GCGACAACAC	4200
CGCCTTCAAC	TAAAGTGACA	ACACCTCCAT	CAACAAACAC	GCCACAACCA	ATGCAATCTA	4260
CTAAATCAGA	CACACCACAA	TCGCCAACCA	CAAAACAAGT	ACCAACAGAA	ATAAATCCTA	4320
AATTTAAAGA	TTTAAGAGCG	TATTATACGA	AACCAAGTTT	AGAATTTAAA	AATGAGATTG	4380
GTATTATTTT	AAAAAAATGG	ACGACAATAA	GATTTATGAA	TGTTGTCCCA	GATTATTTCA	4440

TATATAAAAT TGCTTTAGTT GGTAAAGATG ATAAAAAATA TGGTGAAGGA GTACATAGGA	4500
ATGTCGATGT ATTTGTCGTT TTAGAAGAAA ATAATTACAA TCTGGAAAAA TATTCTGTCTG	4560
GTGGTATCAC AAAGAGTAAT AGTAAAAAAG TTGATCACAA AGCAGGAGTA AGAATTACTA	4620
AGGAAGATAA TAAAGGTACA ATCTCTCATG ATGTTTCAGA AT CAAGATT ACTAAAGAAC	4680
AGATTTCCCTT GAAAGAACTT GATTTTAAAT TGAGAAAAACA ACTTATTGAA AAAAATAATC	4740
TGTACGGTAA CGTTGGTTCA GGTAAAATTG TTATTAAAAT GAAAAACGGT GGAAAGTACA	4800
CGTTTGAATT GCACAAAAAA TTACAAGAAA ATCGCATGGC AGATGTCATA GATGGCACTA	4860
ATATTGATAA CATTGAAGTG AATATAAAAT AATCATGACA TTCTCTAAAT AGAAGCTGTC	4920
ATCGGAAAAA CAAGAAGTTA AGTGACAACG GCCTACATGT TGCTTAGCTT CTTTTGTTAT	4980
GTTTCGATGAT TTGAGAACCC GAATTTTCGA TGGGTCCAAA TATGACGTGG AAGAGACCTG	5040
AATTTATCTG TAAATCCCTA TCTATCGGGT GTGAAGCACA ACGGGATCAG TTTTATTTAA	5100
CGAACATTAT AGATTCCTTA ATTTACTTAA TAATGATTCA ATGATTATTA AACATGGTTT	5160
AATGTGAAAG GTCAAATACG CTAACATAA TAAAGCTGTA TGATTCAATA GACGTAAGCG	5220
AACAAATCTA ATAATTACGA ATGGAGCATA CAACTATGAA AATGACAG E ATTGCGAAAG	5280

(2) INFORMATION FOR SEQ ID NO: 545:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 886 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

AGTAA A ATTG CCGGTATGAT GGACACAAAC GGTGACCTTG GTCAAGGTGA ATTAGCGATT	60
AATCCACc t A AATCAGATTT gAACGAATTA CCTTGGGCTA CACGTAAAAA TAAACAGCCA	120
GCTTCATCCG AAAA A gGTTT AAGTGGTCAT CATGGTAATG CAGCAATGCC TCAAACCmA	180
TTAGATTATC AAATATCTAT TGATAAGGTC GTTGAACAGG CGCAAAAAGC TGGTATT A AAA	240
AAGCCGTTTT CAATCGTATA TCCAAGTGAT AAAAATGGTA CCTTTATTGT ATCTAATACT	300
AGTAATTCAG GTGTTACTGG GCTAGATGTA TCACCATAA AGGAACAAAC ACTTTATTTT	360
GATCAATATA GCGGTAAAAA GCTAGG T ACG ATTAAATATG ATGACTACGG TATTATTGCT	420
AAATGGTTTA CATGGGGCAT TCCGCTTCAC GAAGGTCATT TATTCGGCAT TTAAATAAA	480
ATCATTAATT TATTTGTATG TATCGCTTTA TTAGTAGCCA TTGGCATGGG GTTTGTCTCT	540
TGGATAAAGC GTACAAAAAA TACTGCAGTA AAAGTACCAC ATCGCGTAAA AA A CCAGCA	600
TCTATATCAC TCATAATATG TTTAATTGTA TTAGGATTAT TAATGCCATT ATTTGGATTA	660

TCACCTTATCC TTGTATTTAT AATTGAATTA ATATTATATA TTAAAGATCG TCGTGCTAAA	720
CAATAATGCA CTAAAGTTT TGAAGTGACG AAATTTACAA AATGgATTCT CGTCTCTCTA	780
ATTACTTAAA ACGGGgTtCy AaTAATAAAT CgTACTGaTG GgAAAGTTTT TACTTTTTTAt	840
CTGtCCGAtT TTTTnGAAwT TGAAGATAAA AAAGCATCTA AAACGC	886

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GGCATTGTG TCCTTATATA AGGAAGTG tTAAATACAT TACTGTTGTT AAGTTGTTTT	60
TGTAATTCAA AGAGCAGAAC AGAGTAACAT CATCAGTTGT AGTAAACGAT AATCCGGTAA	120
AACAACATAA TGAAATAATG AAAGTCATTT AACCTGAACA TAAAAATATA TTTGTTTTTC	180
ATTAAGAATA ATTCAAGTAT ATTTAAATCG AGGTTAATTA TCGTATGAAA CGATGCACGT	240
TATAATAAAA ATGTATGATT CAAATTACGT AATGAAAACA ATCCAATATA TTAAGTTGG	300
AGCAAATAAA TATGAAATTT ACAGCATTAG CAAAAGCGAC ATTAGCTTTA GGAATTTTAA	360
CAACAGGAAC TTTAACAACA GAAGTTCATT CAGGTCATGC AAAACAAAAT CAAAAGTCAG	420
TAAATAAACA TGACAAGGAA GCATTATACC GATACTACAC TGGAAAGACT ATGGAAATGA	480
AAAATATTAG TGCTTTGAAA CATGGTAAAA ACAACTTACG TTTTAAGTTT AGAGGTATTA	540
AGATTCAAGT TTTACTGCCT GGAAATGATA AAAGTAAATT TCAACAGCGT AGTTATGAGG	600
GGTTAGATGT TTTCTTTGTT CAAGAAAAAA GAGATAAGCA CGATATATTT TATACTGTTG	660
GTGGTGTAAT ACAGAATAAT AAAACATCTG GAGTTGTAG TGCACCAATA TTAAATATTT	720
CAAAAGAAAA GGGTGAAGAT GCTTTTGTGA AAGGTTACCC TTATTACATT AAAAAAGAAA	780
AAATAACACT AAAAGAACTG GATTATAAGT TGAGAAAGCA TCTAATTGAA AAATACGGAC	840
TTTATAAAAC AATCTCAAAA GATGGTAGGG TCAAAATTAG CTTGAAAGAT GGCAGTTTTT	900
ATAACCTTGA TTTAAGATCT AAATTAAAAT TTAAATATAT GGGGGAAGTC ATAGAAAGCA	960
AACAAATTAA AGATATTGAA GTTAACTTAA AGTAAATCAT TACGAATAAT TAAAAGTAAT	1020
TGAAGCGGCT TAACGGTGAA ATGTAAATTG GTGCGCATAG CTTATACAAA AAGGATGCAT	1080
CAATCGATAT CGTCGTAA GCGTTTTGGT TTGTGTGTCA TGAATCCTAT CCCAATCTCC	1140
ATAAAGGTAA AATTTCCACC ACCAACATCA AAATTCTCCA CATCGCAACA TAACCAAATG	1200

TTATAATAAA	TCTATTACAC	AAAGAGATAA	ATTACTTATT	CAAAGGCGGA	GGAATCACAT	1260
GTCTATTACT	GAAAAACAAC	GTCAGCAACA	AGCTGAATTA	CATAAAAAT	TATGGTCGAT	1320
TGCGAATGAT	TTAAGAGGGA	ATATGGATGC	GAGTGAATTC	CGTAATTACA	TTTTAGGCTT	1380
GATTTTCTAT	CGCTTCTTAT	CTGAAAAAGC	GGAACAAGAA	TATGCAGATG	CCTTGTCAGG	1440
TGAAGACATC	ACGTATCAAG	AAGCATGGGC	AGACGAAGAA	TACCGTGAAG	ACTTAAAAGC	1500
AGAATTAATT	GACCAAGTCG	GTTACTTCAT	TGAGCCAGAA	GATTTATTCA	GTGCGATGAT	1560
TCGTGAAATT	GAAACGCAAG	ATTTTCGATAT	CGAACACCTG	GCGACGGCAA	TTCGTAAAGT	1620
TGAAACATCA	ACATTAGGTG	AAGAAAGTGA	AAATGACTTT	ATCGGTCTGT	TCAGCGATAT	1680
GGATTTGAGT	TCAACGCGAC	TAGGTACAA	TGTCAAAGAA	CGTACTGCTT	TAATCTCTAA	1740
AGTCATGGTT	AATCTTGACG	ACTTACCATT	CGTTCACAGT	GACATGGAAA	TTGATATGTT	1800
AGGTGATGCA	TATGAATTCC	TAATTGGGCG	CTTTGCGGCG	ACA _g CGGGTA	AAAAAGCAGG	1860
CGAGTTCTAT	ACACCACAAC	AAGTATCTAA	GATACTGGCG	AAGATTGTCA	EGACGGTAA	1920
AGATAAATTA	CGTCACGTGT	ATGACCCAAC	ATGTGGTTCA	GGTTCACTGT	TGTTACGTGT	1980
TGGTAAAGAA	ACACAAGTGT	ATCGTTATTT	CGGTCAAGAA	CGTAACAATA	CTACATACAA	2040
CTTAGCACGC	ATGAATATGT	TATTACATGA	TGTGCGTTAT	GAGAACTTCG	ATATCCGTAA	2100
TGATGACACA	TTGGAAAACC	CAGCCTTTTT	AGGCAATACA	TTTGATGCGG	TTATTGCGAA	2160
CCCACCGTAT	AGTGCGAAAT	GGACTGCAGA	TTCAAAGTTT	GAAAATGACG	AACGATTCAG	2220
TGGTTACGGC	AAACTTGCGC	CTAAGTCTAA	AGCAGACTTT	GCCTTTATTC	AACACATGGT	2280
ACATTACCTA	GACGATGAAG	GTACCATGGC	CGTGTACTC	CCACATGGTG	TATTATTCCG	2340
AGGTGCTGCA	GAAGGTGTCA	TTCGTCGTTA	TTTAATTGAA	GAAAAGAACT	ACTTAGAAGC	2400
TGTGATTGGT	TTGCCAGCGA	ATATTTTCTA	TGGGACAAGT	ATTCCAACAT	GTATTTTAGT	2460
ATTTAAAAAA	TGTCGCCAAC	AAGACGACAA	CGTACTATTT	ATCGATGCAT	CCAATGATT	2520
TGAAAAGGA	AAAAATCAAA	ATCATTTAAG	CGATGCCCAA	GTCGAACGTA	TTATAGACAC	2580
ATATAAGCGT	AAGGAAACAA	TTGATAAATA	TAGCTACAGC	GCGACACTAC	AAGAGATTGC	2640
CGATAACGAT	TACAACCTAA	ATATACCGAG	ATATGTCGAT	ACATTGGAAG	AAGAAGCACC	2700
GATTGATTTA	GATCAAGTCC	AACAAGATTT	GAAAAATATC	GATAAAGAAA	TCGCAGAAAT	2760
TGAGCAAGAA	ATCAATGCAT	ACCTGAAAAG	ACTTGGGGTG	TTGAAAGATG	AGTAATACAC	2820
AAAAGAAAAA	TGTGCCAGAA	TTGAGGTTC	CAGGGTTTGA	AGGCGAATGG	GAAGAGAAGC	2880
AGTTAGGGGA	TCTTACAGAT	AGAGTAATTA	GGAAAAATAAA	ACTTAGAA	TCGAAAAAGC	2940
CTTTAACAAT	ATCCGGACAG	TTAGGTTTAA	TTGATCAAAC	AGAATATTTT	AGTAAATCAG	3000
TTTCGTGCGA	AAATCTAGAA	AATTATACAC	TAATAAGAA	TGGAGAATTC	GCGTATAACA	3060

AAAGTTATTC TAATGGATAC CCATTAGGGG CTATTAAAAG ATTAAC TAGA TATGATAGTG	320
GTGTATTGTC CTCTTTGTAT ATTTGTTTTT CTATTAAAAG TGAAATGTCT AAAGACTTCA	3180
TGGAAGCATA TTTTGATTCTG ACACACTGGT ATAGAGAAGT TTCTGGAATT GCAGTTGAGG	3240
GTGCAAGAAA TCACGGATTA TTAAATGTTT CTGTGAATGA TTTTTTTACT ATTCTAATTA	3300
AATATCCAAG TTTAGAAGAA CAGCAAAAAA TAGGCAAGTT CTTCAGCAA CTGACCGAC	3360
AAATTGAATT AGAAGAACA AAGCTTGAAT TACTTCAACA ACAGAAAAA GGCTATATGC	3420
AGAAAATTTT CTCACAGGAA CTGCGATTCA AAGATGAGAA TGGTGAAGAT TATCCAGATT	3480
GGGAAAATAG CAAAATAGAA AAATATTTAA AAGAGAGAAA CGAACGTCT GACAAAGGGC	3540
AAATGCTTTC AGTAACTATA AATAGTGGCA TTATAAAATT TAGTGAATTG GATAGAAAAG	3600
ATAATTCAAG TAAAGATAAA AGTAATTATA AAGTAGTTAG GAAAAATGAT ATTGCATATA	3660
ATTCTATGAG AATGTGGCAA GGGGCTAGTG GTAAATCAAA TTATAATGGG ATTGTTAGCC	3720
CTGCATATAC TGTGCTTTAT CCAACACAAA ATACTAGCTC ATTATTTATT GGATATAAGT	3780
TTAAAACACA TAGAATGATT CATAAATTTA AAATTAATTC ACAAGGATTA ACATCAGATA	3840
CATGGAACCT AAAATATAAA CAATTAmAAA ATATAAATAT AGATATACCT GTATTGGAGG	3900
AACAAGAAAA GATAGGTGAT TTCTTTAAAA AAATGGATAT ATTGATAAGT AAACAGAAAA	3960
TGAAAATTGA AATATTAGAA AAAGAGAAAC AATCCTTTTT ACAAAAAATG TTCTTATAAC	4020
TTTGATAAAT ACATAGATTG CATAAGAATA AAATTTGTAT AATTTAACAT AAAAGTTGTA	4080
AAAGTAAAGT GAATTAAAA CGAACATTAA ATTTAGGCAC TGTGAAAGCG CAGTCTTT	4140
TTTGTGTCGA AATTGTGTAC AGAATAAGTA GTTAAATAAA GATTAAGTTG AGATAAAGTG	4200
TTATTCGTAA ATAAAAGAGA GTAGATCGAT AGGAATTGAA TGATATTAGT TAACTATTTA	4260
TTAAATTACT TAATAATGAT TAATTTTTAG TTAAAGTAAG TTTAATGTGA AGCACGACCA	4320
TTGCTCATTA TAATGA	4336

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

TAAGCTATCT GAGATAATTG CTGATAACAT TAAACCGGCA ATTTAGGTT TAATTTCAA	60
GCCACGTTCT CTAAACATTT TGTATAAAAT TGTAGCTGTA CAACCAACTG GTTCAGCAGC	120

ATAACATAAA GGACCAGCAG TTTCGAAATT TGaATTCTG TGATGATCAA TTACATGCTT	180
AATTGTAGCA GAGGCAATCG TATCAGAACT TTGTTGGaAT TCGTTATGAT CAACTAAGAT	240
AACATCTTGA CCATCTAAAT CATCTGTAA TAATTCCGGA GCAGGTACAT TAAATGTATC	300
TAACGCGAAT TGAGTTTCTG CACTCACATC ACCTAAACGG TATGCTTTGG CTCCTGAAT	360
ACCTCGAAGT TGTTCaAATT CTGCCaTAAT AATCGCAGAT GAAATTGCAT CAGTGkCTGG	420
aTTCTTATGT CCGAAAATAT ATGTTTTAGC CAnTGTCAAA TATCTCCCTT GTAAATTGTA	480
TTCTTTA	487

(2) INFORMATION FOR SEQ ID NO: 548:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

TTGGTGGTGC AGCAGTTATA GCAATTGTTT TAGCATTTCAT TGGTAAGTTC ACTGCATTAA	60
TTTCTTCTAT ACCTACmCCA GTTATGGGAG GAGTATCTAT ATTACTTTTC GGTATTATTG	120
CAGCAAGTGG CTTAAGAATG TTAGTTGAAA GCAAAGTAGA TTTTGCGAAC AATCGAAATT	180
TAGTTATAGC TTCTGTAATT TTAGTTGTAG GTATCGGAA TTTAGTATTT AACTTAAAAG	240
AAATTGGTAT CAACCTTCAA ATTGAGGGGA TGGCATTAGC TGCACTTTCA GGAATTATTT	300
TGAACTTAAT CTTACCTAAA GAGAAAAAAC AAAACAATTA AGATTTACAA ATTAAGGAGG	360
GCGCTTTTAT GAATCATTTA TTATCAATGG AACATTTATC TACAGATCAA ATATACAAAC	420
TTATCCAAAA GGCAAGTCAA TTAAATCTG GTGAACGTCA ACTACCAAAC TTTGAAGGGA	480
AaTATGTCGC AAATTTATTC TTTGAAAATT CTACTCGrAC AAAATGTAGT TTTGAAATGG	540
CAGAACTTAA GCTAGGGTTA AAAACGATTA GCTTTGAAAC ATCAACATCA TCTGTTTCAA	600
AAGGTGAATC TTTATATGAC ACATGTAAAA CTTTAGAAAG TATTGGCTGT GATTTATTAs	660
TCATTAGACA TCCGTTTAAT AACTACTATG AAAAATTAGC GAATATTAAC ATCCCAATTG	720
CGAATGCTGG TGATGGTAGT GGACAACATC CAACACAAAG TTTACTTGAT TTAATGACGA	780
TATATGAAGA ATATGGATAT TTTGAAGGCT TGAATGTATT GATTGTGGA GAcATTaAAA	840
ATTCACGTGT CGCACtAGTA ATTACCAAnAG T	871

(2) INFORMATION FOR SEQ ID NO: 549:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

TCAATCTAAT ATATACTTCA TGACTTCCCG CCAAAGGCGC AATCGTAGGA TTAGTCTGTT	60
TATCGATAAG ATCTATTAAT ATTGTTTCTA CTTTAGATTC ACCTATTCCC GCAAATCTTA	120
ATAGTTCAGA ATGTATAATT CGATTATGGT TTATAAAATG TGACAACAAT TCATTTTTCA	180
CCATTGGTTG CATTCTTTTC GGTGGACCTG GTAATAAAAT AATTTGTTTG TTTTCAAAT	240
TCACCATCAT TCCTGGAGCC ATGCCATGAT GATTTGTTAA TACAGTTGAA CCTTCAATTA	300
CTAAAGCCTG TTGTcTATTA TTAGGTGTCA TTTCTtGTCC TTGTTCTCA aAAwAGCTTT	360
CAATATATTG AAAGAAGGCT CATCAATAAC TAAATCTnTA	400

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

ATACCTCCAG CTAGAATACC AGCGTATTTT ATAAAATACT TCCTCCATTC AACTATATCT	60
ATATTTAATT ATTTAAATTT CGTTGCATTT TCCAATTGAA AATCATTTT AAAATCAAAA	120
CTCTAAATGT CTGTGTATTA CTTAAAATTA TACATATTTT GCTTATATTT TAGCATATTT	180
TGTTTTAAACC TATATTACAT TATATCAGAC GTTTTCATAC ACAAATAATA ACATACAAGC	240
AAACATTTTCG TTTATTATTT ATATCACTTA ACTAATTAAT TTATAATTTT TTATTGTTTT	300
TAAGTTATCA CTTAAAAATC GTTTGGCaAA TTCGTTGTGA CGCTTGTCCA TCTTCTAATG	360
AACAGAATTT TTGATAAAAT ACCGTTTCGTG CTTCAATATA CTCATTTGCA GTCTCATCGA	420
TTTGTTTTTAA TGCATCAATG AGTGCTGTTT GATTTTCAAC AATTGGACCT GGCAACTCTT	480
TTTTATAATC CATGTAAAAA CCTCTAAGCT CATCGCCATA TTTATCTAAG TCATATGCAT	540
AGAAAATTTG CGGACGCTTT AATACACCGA AGTCGAACAT GACAGATGAG TAGTCGGTAA	600
CTAACGCATC GCTGATTAAG TATAAATCCG AAATGTCTTC ATAAatCTGAA ACGTCTTTCA	660
CAAAATCATC ATGTTTCATCA ATACGTGTCA CAACTAAATA ATGCATGCGTAAkAAAATAA	720
CATArTCATC ATCCAGCGCT TGACGCAAAG CTTCTATATC AAAGTTAACA TTAAATTGAT	780
ATGAACCTTC TCGAATCGCT TCATCGTCAC GCCAAGTTGG CGCGTACATA ATCACTTTTTT	840

TATCTAATGG AATATTTAAT CTTGTCTTAA TACCATTAAT ATATTCAGTA TCATTGCGTT	900
TATGTGATAA TTTATCATTT CTTGGATAAC CTGTTTCCAA AATCCTTATCT CGACTAACAT	960
GAAATGCATT TTGAAATATC GATGTCGAAT ATGGATTAGG TGACACTAGA TAATCCCACC	1020
GTTGGCTTTC TTTTTTAAAG CCATCTTGGT AATTTTGAGT ATTTGTTTCCT AGCATTTTAA	1080
CGTTACTAAT ATCCAAACCA ATCTTTTTTTA ATGCGTGCC ATGCCATGTT TGTAAGTACG	1140
TCGTTGCGGG TGATTTATAT AACCAATCTG GTGTACGTGT GTTAATCATC CwCGCTTTTCG	1200
CTCTTGGCAT CGCTAAAAAC CATTTTCATTG AAAACTTTGT AACATATGGT ACATTGTGCT	1260
GTTGGAATAT GTGTTCATAT CCTTTTTTCA CACCCCATAT TAATTGGGCA TCGCTATCT	1320
CAGTTAAGTA TTCATATAAT GCTTTGGGGT TGTCGCTGTA TTGTTTACCA TGAAAGCTTT	1380
CAAAATAAAT TAGATTCTTG TTTGGCAATT TTGATAGTAA TTTAAAAGTC GTATATATAC	1440
TATGTTCTAT CAATTTTTTTA ATTGTATTTT TAATCATGTC GTACCTCCGA CGTGTTTTTG	1500
TAATTATATT AATATGTATG AGC	1523

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

CAGTAAGAGA TTTTCTTAAT TGAAAATAAT CTTACTGCTT TTTTAAATTT AATTTGAGA	60
TTCAATATTA GTTTATCTCA TTGTGGCATT AATTGATAAA ATTGTTTTAA TGTTATAAAT	120
CAAAGTCtTC TTCAACAATT TCAATGTCTG CATCtATCT ATGATATGTG AAAAAGCTAA	180
TTCTTATGCG GTCTAAATGC TCTAAATGGT GTCGATACTC TTCGATGGCT GCAACAATTT	240
GCATAACATT GGCAAACGAA TATTCCGTTT GATAAGGAnG ATTTATTAAAC TCATGCTGAA	300
ATGTGGACAA TAAATCTTTT TTCTGCGGAT TATCTAACTC ATAATCAACA TGTGTCACAT	360
TATAACGTGC TTTTTTAGAA AGGCTAGCTA AAATTGCTC GTGAAAAGCA GTTAATGAAT	420
CTAAATCTAA TTTGATTTGT AATAGGAAAT TGTATTAAAG TAAATATAAG TCGTTTTGAT	480
AACGCGACAA TTTGTTTAAAT ACTTCATAAG CTTGTCTAGT CGTCTGAACT ACTTCTCTGA	540
AAAGTATTTT CTTTCTtTC TGTTGGTGAA TATGTTTTTT TGTAATAGGA CGTTCTTCGC	600
TATAGTAATC ATAAATTTTC TCTAACTTTT CGACACGTTG TTTTAAATTA TGACTATCTT	660
GTTTAATATT ATTAACTCC GTCGTATCAT TTAATACTAA TTTAAACCAC ATAAAAATAT	720
CTGAGGATAT ATTTAATGAA TTATAGTAAA TTTTGTTC AATTTAGGT GGTAGAAACA	780

CAAAGTTAAC TAGAGATGAA CTTATGACAC CAATCATTAC AAGTACAAAC CTGTAAAAGG	840
CGGTAATATA GAAAGAACCG GTATGTTGTC CCATAATGAT TAATGCTGTT ACACTCGCCA	900
AAGTAGCAAC ATGTGCTAAA TTAAATTTAA ATAAAATAGC AATAAGTACT ATGACGGTAA	960
CACCCATAAT GATAAAATTA TCACTAAAAA TTGTTACCAT TGTAACAGAT AGTATGGCAC	1020
CTATAATGTT ACCCAATGCT TGATCAGAAA CTGTTTTTAA TGAACGATAA ATACTAGGTT	1080
GCATTGCACa ACAGCACTGA CACCAGCTAA GGCTTTCAGA CCAACATCAT CCGGTAGTAA	1140
AGAAGCGATA GACATAGCTA AAATAATGGC TATACCAGTT TAAAAAATCC GAGCTCCTAG	1200
TCTCAAAAAT AATGACGCCC CTTTTAAGTT TATTGAATAT CTAATATTCG TATTCATTAC	1260
TGTTATACAC TTACTAGTTA CAAAATTCAA GCTTATTTAT AGTTGTAAA ATAAATCATA	1320
CATAATACTG ATAGCGATGT AAAACTTTAG TCAGAGATTA AAATAGTATAAATTTGTAAA	1380
ATAAAAACTC ACATAGTGAC ATATCAAGTT AACGTTAAT AGTTAACGAT ATAAAATGAA	1440
TCTACTATGT GAGCATTTGC TTTATTTTAA TTCAATTAAA AATATACTTC CTTAAAAGTT	1500
ATTTCATTTG ACTAAAAGCA TAGTCTGCAG CTTTTAAAGT TTGTTTAATA TCTTCTTCTG	1560
TATGTTCAAGT TGTTAAGAAC CAAGCTTCAA ACTTAGAAGG TGCTAAATTG ATACCTTGAT	1620
TTAACATTAA TTTGAAAAAT TTACCGAACG CTTGCGCGTC AGAATGTTCA ACTTGATCAT	1680
AATGTGTGAC TTTTTCATCT GTAAAGTACA ATGTTAAAGA TCCATAAATA CGATTAATTG	1740
TAGCTGTGAT ATTATGTTTT TCGATTAATT AAGTAAACC TTCTTCTAGT TGTTGGCCTA	1800
AGCTGTCTAA TTTTTCATAA ACACCGTCTT GTTCTAGTAC TTCGAGTAAT GCAATACCTG	1860
CTTTCATAGA TAACGGGTTA CCAGCCATTG TACCAGCTTG ATATGCAGGT CCTAGAGGTG	1920
CTACTTGTTT CATAATATCT TGACGTCCAC CATAGCCTCC AATTGGTAAA CCACCGCAA	1980
CAATTTTACC AAATGCAGTT AAATCAGGGA TAACACCTAA TAAATCTTGA GCGGCACCGT	2040
AATGGAAACG GAATGCAGTA ATTACTTCAT CATAAATCAC TAGGGTCCCA TTGTTATGTG	2100
AAATTTCATT AACCTCTTCT AAAAATCCAG GTTGAGGCAT TACCATTCCA AAGTTACCAA	2160
CAATTGGTTC TACIAATACT GCGGCAATTT CATCACCCCA AAATTCAATT GCTTCTTTAT	2220
AGGCGTTAAT ATCATTGAAA GGTACAGTAA TGACTTCACG TGCGACGCTT TCTGGAACAC	2280
CAGCTGAGTC TGGAGAACCG AGCTGAGATG GGCCGCTACC TGCTGCAACC AATACTAAAT	2340
CAGAATGGCC ATGATAAGAT CCAGCAAATT TTATAATTT ATTTCTTTTA GTATATGCAC	2400
GTGCAACACG AATTGTTGTC ATGACTGCTT CTGTTCCAGA ATTTACAAAG CGAATTTTCT	2460
CAAGAGATGG AATTGCATCA CGTAATTTTT TGCTGAATTC AATTTCTAAT TCAGTCGGTG	2520
TACCAAATAA AACACCTTTA GCAGCTTGTT CTTGAATTGC TTTAGTAATA TGAGGATGTG	2580

CATGCCCCGT	AATAATTGGA	CCGTATGCTT	GAAGGTAATC	AATAAATTTA	TTGCCATCGA	2640
CATCATATAA	ATATGCACCG	TGTCCTTCTT	TCATAACAAC	AGGTGCACCG	CCTCCTACAG	2700
CTTTATAAGA	ACGAGAAGGG	GAATTGACAC	CGCCTAGAAT	ATATTCGTTT	GAAAGTTGTT	2760
GTAAACG TTC	ACTTTCAC TA	AAATTCA TTT	ATATCAACCT	CTTTTAATTT	AATATTTTCA	2820
TCTAATATCG	TATCATAAAA	TTATTATAAT	GAAGAAAAAG	GTGATTATAT	GTTGCAAAAA	2880
GGAGAACAAT	TTCCAATATT	TAAATTAGAA	AATCAAGACG	GAACTGTCAT	TACAAATGAT	2940
ACATTAAAAG	GTAAAAAGGC	GATTATATAT	TTTTATCCTA	GAGATATAC	ACCTACTTGT	3000
ACCACAGAAG	CTTGTGACTT	TAGAGACAAT	TTAGAAATGT	TCAATGATTT	AGATGTTGCA	3060
GTATATGGTA	TAAGCGGTGA	TTCAAAGAAA	AAACACCAAA	ATTTTATTGA	GAAACACGGA	3120
TTGAATTTTCG	ATTTATTAGT	AGATGAAGAT	TTTAAATTAG	CTAAAGAAA	GGCGTATATC	3180
AGTTAAAAAA	ATCATTTG GC	AAAGAAAGTA	TGGGCATTGT	AAGAACGACT	TTTATAATAG	3240
ATGAACAAGG	TAAAGTATTA	GATGTTATCG	AGAAGGT TAA	GGTTAAAACA	CAAATAGAAG	3300
AACTTAAAAA	CATTTTGGGG	TGACATATAT	GAAAGTTGTT	GGGT TAAATC	GTATGCGTGA	3360
AGTTGAAACT	GAATTACAAC	AACGCTTTC	AGATTTAGAT	TTTAAATTTT	ATAAAAAAGC	3420
ATCAGAAATA	CCTGAGAGCG	ACTTGGCTGA	TTTAGATATA	TTAGTTGGTT	ATGATGGCGG	3480
TATCAATGAG	GCATTTTTAC	GACGTTGCCC	GAATTTAAAA	TGGATTGCAT	GGTTTGCAAC	3540
GGGTGTAAAT	ACATTGCCGT	TAGATTATAT	TGCAGATCAC	GGCATACTTT	TAATAATGG	3600
AAAAGGTGTT	CAAGCTAAAC	AATTATCTGA	ATACATTTTA	GCTTTCATTT	TAGATGATTA	3660
TAAAAAGATG	AAACTATCAT	ATGATAACCA	ACGACAACAT	ATATATGATT	CGAAAATAAC	3720
TGGTAAACGC	CTATCAGGAC	AAACAGTTTT	ATTTTTAGGT	ACAGGTGCAA	TTGCTACTAG	3780
AACTGCGAAG	TTAGCAAAGG	CTTTTAATAT	GAATTTAATT	GGTCTGAGCA	AGTCAGGTCA	3840
GAACAAAGAT	GAGTTTGACG	AGATATATAC	TATCGAATCA	CTTGAAAGCA	CATTACCAAA	3900
TGCTGACATT	ATTATAAATG	CTTTACCAGA	AACGCAAGAA	ACGATTCaTT	TaCTAAAGAA	3960
AAAACATTTT	GAATTAATGA	AAGATGAAGC	ACTTTTATA	AATATAGGAC	GAGGTAGCAT	4020
AGTTAAAGAA	GCGCTCTTAA	TAGAAGTATT	AAAAAGTAAA	GTTATTTCGAC	ATGCATATTT	4080
AGATGTGTTT	GAAAATGAAC	CTTTGAAACC	TAATCATGAA	TTATATGAAT	TGGATAATGT	4140
AACTATAACA	GCGCATATAA	CTGGTAATGA	TTATGAAGCA	AAGTATGACT	TATTAGATAT	4200
TTTTAAAAAC	AATCTAGTTA	ATTTTCTCAA	TAAGAATGGT	CTAATTGAGA	ATGAAGTTGa	4260
TGCTAAAAAA	GGCTATTAAA	TGA rATCATC	ATGTAAATAT	TGACACGCGC	GCAATACTAC	4320
AGTTATATTT	aTAGTAAgTt	AATaATgATT	ATATAAGAAa	GATGGTgATA	TAGATGAGTG	4380
TTGAAATAGA	ATCAATTGAA	CATGA ACTAG	AAGAATCAAT	TGCATCATTG	CGACAAGcAG	4440

GCGTAAGAAT TACACCTCAA AGACAAGCAA TATTACGTTa TTTaATTTCT TCACATACTs	4500
ATCCAACAsC TGaTGaAATT TATCAAGCAC TTTCACCTGa TTTTCCAAAT ATAAGTGTTG	4560
CGACAATATA TAATAACTTA AGAGTGTTTA AAGATATTGG AaTGTA AAA GAATTAACAT	4620
ATGGAGACTC ATCAAGTCGA TTCGACTTTa ATACACATAA TCATTATCAT ATTATATGTG	4680
AACAATGTGG TAAGATTGTT GATTTTCAAT ATCCACAGTT AAATGAAATT GAAAGATTAG	4740
CTCAGCATAT GACTGACTTT GACGTAACAC ATCATCGAAT GGAAATTTAT GGAGTTTGTA	4800
AAGAATGCCA AGATAAATAA TTAACTTTG GTAGTATGAC AAATTAAAAA AGCGTTACTw	4860
ACTTCATATA AGTAAGCGTA ATATTTAAGA nGTTAAACGA CATGaAAGTt GTTTAACTTT	4920
TTT	4923

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

TCCGGCTTTA AAAACTTTTC CCAATTCCAG CTTGGGCCTT TGGCATTAAAT ATTAACCTCC	60
TGGTTCGGAT TAATTGGGAA CCTAACnTT TAGGCAATAA TTGGTTTAGG CAACTTCCAA	120
ATTGGTGGTT CAACCAACGT CTTTGGATAC CyTGcTCATT TAATTCTAAA ATGgTyrGAA	180
CGCATTTTGG TACCCAAAAt GgTGACGTTT GTTTGCACGG TCTAAaAAT TGTCTAAGTT	240
GTGATTGGT TTCATTAATT GAaCACCATT TTGCTCTTCA GCAAGACCTT TGTCTACTTT	300
TAAGAACGGA ACAACACCTT TATCAGCTAA GTAATCTGCA GTGTATTTGC TTTCTACTTC	360
GCGATCCATT GTTTGTTCGA AAAGAATAGC ACCCAAATT TTATCTGGTG AGAATGAAGG	420
TGAAGTTACC ACACGTGTAC GCATATCGTG AACAAGTTGG AACATTTCTG CTTCAATTGCT	480
ATATTGATCT TCGTTTACAC CATATTCTTT AAGTGCTTTT GGTGTACTAC CACCACTTTG	540
GTCTAATGCG GCAATAAAGC CTTTTCCATT TTTCATTTTT TCTAATTGCT CTTTATTCAT	600
ACTTTCCACT CCTTAACTTT TCAATACaC TCCAGTATGA TAAAAATGAG AACATTTCTC	660
AAGTCATAAA CCTTGAAAAG TGTATAAAAT GTGAAAAATA ATTGTCAGTT TAATTAAAAA	720
TATTATTTTA TTCTAGGTAT GACTAACGCC ATTAATGACA TAAAGAAAAT ATGTGTAATA	780
ATCCAACCGA TTAATTCTGT CACACTAAAT TGAAAAATTG GACGTTGCGC AAaAATACT	840
AAAAGGGAT ACAATGCTAT AAATAAGAAA AATAAAGGGA TATAACATAG ATAGTAAAGC	900

CTTTTAGAAG TATGAAA

917

(2) INFORMATION FOR SEQ ID NO: 553:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 432 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```
ACTCCCATAT CCACTGGCAA GATTTATAAT TTGTAATTCT AAAGTATAAT AGCCTATATT      60
TTTCAAATC TCTTTTTTTA TGATTAACAT CCCTCTAAGT GCACCTAAAG GTTTTTATGT      120
AATGTATTAA ATATTTCCAT TTATACATAT ACATCTTGTA TAAAAAGAAA GAACTCCATA      180
TATACTCAAA AGGTATACTG AAGCTCTATA TATTATATAA AATTATTATA CTATTTTGAA      240
AAACATAAGT AAATCACTAA ACATGATTTC TTCACTTTT AGAAAACTTT TAATACTATA      300
AAAGCACCCA CTCAGTCACT AGTTTGGGCA GTTATTGTAT GCCTATTGaa CTCAATGCgT      360
ATATTACAAT ACCTTTTTtCG CATATTCATA TAAGacTTTG CATCTTTAAG CTTAATTGCT      420
ATCTCTTTCT CT                                                                432
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(2) INFORMATION FOR SEQ ID NO: 554:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

```
TTTTGCTTTA TGTTAAATGG ATTATTaTTA GAATAAAAAA TCGGTGATGA GCTAAAAAAG      60
TGTGTAGGAT GTTTCCKAA CCAATTTTTT ACATCCGAAG ATATCGAACA ATATCTTCCT      120
ACTTCTACAT TATTAAAATC ACTACCAAAT CCAATATAAC TGTATTCACC AATGTGAGAA      180
TTCCTGATTT TACACCATCT ATCTATATAG TTATTGCCAT CAAATTTTGA GTTTGTAATA      240
TAGCCAAGC GATGAATCTT AACATTCGAT TCTTTAGAGG ACTGGTTTTT CAGCAAACCA      300
ATTATCTTTT CAATCGCTAT CCTCATCGTC ATTTCTCCA AGTATTTTGA TTGATAATAT      360
CTTTATAGCT TTGAATAATT TTAACACCT TTGTGAAAC GTTAGTGTCT TTATAATCAA      420
TAGCATCAAT CATCGGTTTCG TTATTGTTTT GCATCTCTCT TGCTAGTTCA ACGGATTGGA      480
TTAGATTGTT ATAGGTAATA CCACCTACAA TAACCGTACC TTTATCTAGT ACTTCCGGTC      540
TTTCTGTGGA AGTTCGAATA AGGACACCAG GGAACCTCAA AATAGACGAC TCTTCTGACA      600
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ATGTTCCACT ATCTGATAGC ACAACAAATG CATCTTTTGT CAATGCATTA TAATCAAAGA	660
AACCAAATGG CTTTAACTGT TTAACATAATG GATCAAATTC AAATTTACTT TCTTCAATTT	720
TCTTCCAAC TCTTGATGC GTTGAATAAA TCACAGGCAT TTTATACTTT TTGGCAATAT	780
CATTTATCGC ATTCATTAAT GATTTAAAAT TCTTTTCATT ATCGATATTC TCTTCTCTAT	840
GCGCAGATAC TAAAATGTAT TGTGCGGTT CTAATCCTAG TTTATTTAAA ACGTCACTGT	900
GATTAATTTT ATCTCGATGC GCTTCTATCA CTTCTGTCAT CGGTGATCCT GTyACAAAGA	960
TATTCGCTTT ATTGAAGCCT TCATCTAATA AATAACGTCT GTATGTTCC GTATAAGGTA	1020
GATTCACATC ACTGACATGG TCAACAATTT TACGATTGAT TTCTTCAGGT ACATTCTGAT	1080
CAAAGCATCT ATTACCCGCT TCCATGTGGA ACACAGGAAT CTTTAATCGT TTAGCAGATA	1140
CTGCTGCTAA ACAACTATTT GTATCACCAA GAATTAAAAG TGCATCTGGT TGTTGCGGTA	1200
ATAAAACATC ATATGTCTTC GCAATAATAT TCCCCATCGT TTCTCCAnGt TACTTCCAAC	1260
TGCCTCTAAG TAGTGGTCCG GTTGTCTTAA TTCCAAATCA TCAAAGAAAA TTTGATTCAA	1320
TGTATAATCA TAATTTTGAC CAGTGTGTAC TAATATCTGA TTAnAAATAT TGAT	1374

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

TGCATTTCTG CCGACTTCGA GAAGTTGCAA TGTTTATAAT ACTGTGGACT TCAGCTCCGT	60
TTACCTCTAG GCATGTCCCT TTCACGTTT GCTTATGATA ACGTTATCGA CATTGTTAAA	120
TTGTCCTTTT TGAAAAAATA ATTCTGGTGA GATAGACGCT ACTTGGaTTT CaTCaGTTTG	180
TAAaACGCA GtATAAtTAC CaTTACTAAA tTGaGTTAAT CGTtCaTATA AAGTACTAAT	240
AGGATAATAA ATGTTATCCG TTAAgCGCGC CGTATAGTTC ACTTGATACG TTTCGCCTTC	300
AACAATTGCT TGTTGGACAC GTTTAATATT AGTCATCATA ACCTCAGAAG ATTCAACAAA	360
TGAAAAATGA TACTTTGATA CATAAGAAGT TTGATGTTCA TATGTTGAAT TTATGCTTTC	420
CGCTTTTTCA AAACATAAG CTGCTGCATA AATATCATCT TTAGCTAATG AATGTGTACA	480
CATAGCATGA TTAAATACT TTGCCGCTTC GTAACCTAAA TATAACGAGA CATATCTACC	540
TTGTCGtKgt GCGCTGTGC AAAGTGTATC ACTTCTCCCA CATCAGCCAA CTTAGTAGCA	600
ACATACTTCT TTATAAATCC CTTTAATGA ATATGGTATT GCTTATATTC ATTTTCAGTT	660

AAATAGTAGC GATAATTATA TTCTATTCTC ACAGTAATCA CCTACCTTCG ATAAAAATAA	720
TTCAACTTGT CGATAACCGT ATTCACTCAA AATAGATTCA GGATGATATT GCACACCAAA	780
AACCGGAAAT CTAATATGCT CAAATGCCAT AATAATCGCT TCATCGTTTT TGCTGTAAT	840
CTTTAAGCAA TTTGGAAAAG TCGCTCCGTC AGCAATTAAT GAATGATAAC GCATTACATT	900
GAAATTTTGA GGCAGTCCTT GAAAAATACC TTCATTGGTA TGGCGTAACT GTGTAGTATG	960
TCCGTGTACA GGATGATAGC CGTGAATGAT ATTTCCACCA AAATAAGACA CGATACATTG	1020
AAATCCTAAA CATAACCTA GTATAGGTAC ACGCTGATAA AATTGTTCTA ACACTTCATT	1080
CAAGATAGGA TAATCATCCG GaTTACCCGG CCCAGGCGAA ATAACAATTG CTTTTGGCTT	1140
CATATTAATG ACGTCTTCTA TCAGCAGATT ATCAATACCA ACAACTTGAA CTGTTAGTTT	1200
CGTTTGAGTC TTAATATAGT CTATTAAATT ATAGTAAAT GaATCATTAT TATCTATGAC	1260
TAGAATCATT GTATACTCCG TTCTAAATGT GTTTTATTTT TATAATATGT ATTGGATGTA	1320
GCTAAAACTT TAAAAGCATT GTCATTATCC TGACCTTGAT TTTAACTAAT ATATGGTATA	1380
TTCTATTTCAT CGTACATAAA TGAATATCAG AGGTTCCTAG CTGAAACCCT CTATAAA AA	1440
CTAGGCCATT GAAATTTCAA ACATTCGTTG GG	1472

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

AGAACAGCAA GGATTACTTA CTGAGGAATT AAAGAAGGAT ATTTTAAAAC AGAACAAATT	60
ACAACGTGTT GAAGACCTAT ATAGGCCTTT TAAACAAAAG AAAAAGACAA GGGCAACTGA	120
GGCGAAACGT AAAGGGTTAG AGCCATTAGC GATATGGATG AAGGCACGTA AACATGAAGT	180
CTCAATTGAA GAAAAAGCAC AACAATTTAT AAATGAAGAA GTGCAATCGG TTGAAGATGC	240
TATCAAAGGT GCACAAGATA TTATTGCGGA ACAAATTTCA GATAATCCTA AATATAGAAC	300
AAAAATTTTA AAAGATATGT ATCATCAAGG TGTGTAACT ACATCTAAAA AGAAAAATGC	360
TGAAGATGAA AAAGGTATTT TTGAAATGTA CTATGCATAT AGTGAGCCAA TTAAACGCAT	420
TGCTAATCAT AGAGTTTTAG CTGTTAATCG TGGTGAAAAA GAGAAAGTAT TATCTGTAAA	480
GTTTGAATTC GATACGACAT CAGTAGAGGA TTTCATTGCA CGTCAAGAAA TCAATCATAA	540
TAATGTAAAT CGCAGTTATA TTTTAGAGGC GATTAAAGAT AGCTTGAAAC GCTTAATTGT	600
CCCTTCGATA GAGCGTGAAA TCCATGCTGA TTAACTGAA AAAGCTGAAA ATCATGCAAT	660

AGATGTTTTT AGTGAAAACT TAAGAAATCT ATTACTGCAA CCTCCAATGA AAGGTAAACA	720
AATATTAGGC GTAGATCCAG CATTTAGAAC AGGTTGTAAA TTAGCAGTCA TTAACCCATT	780
CGGTACTTTT ATAGCAAAAG GTGTGATTTA TCCGCATCCA CCAGTTTCTA AAAAAGAGGC	840
AGCAGAGAAG GATTTTGTAC AAATGGTTAA AGCGTATGAT GTGCAATTAA TTGCAATTGG	900
CAATGGTACT GCAAGTCGTG AAACAGAACA ATTTGTTGCA GATTAATTA AAAAGCATCA	960
GTTGCCAGTA CAATTCATCA TTGTCAATGA AGCGGGCGCT TCAGTATACT CAGCATCAGA	1020
AATTGCTAGA GATGAATTC CTGATTTTCA AGTG	1054

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

AAATGTCAGA ATACAAGAAA AAAATAATTG AATTAATTGA AAGTAATTTA ACAGGATATG	60
AAATTTCTAA AAAAAGTGGG GTTTCTCAAT ACGTACTTTC ACAATTAAGA CAGGGCAAAC	120
GCGAAGTAGA TAATCTAACC CTGAATACAA CAGAAAAATT ATATGAATAT GCCAATAAAG	180
TTTTGTAATT TAACTAATGT ATAAATTAAT CAAGCTATGT TTATTTGATT TAACTATTAA	240
TAAAAATCAT ATGGTGAATG GATATTATAA TAATTAAAAT AAAAAATAG TAGATTCCAA	300
TTTGTGAAAA AGGAGTATGT CGTTTCATTT AGAATTTATT GCACGAAATT AGCATCGAAT	360
AAGGGAAAAA AAGTGTTAAG TTTTAAATGA TAAAAAAGAT TGGAATGGAT CGTCTTGAAA	420
TGCTCCCTTC AAAGTTTTCA TTTTTTCAAT GTCGACTTCG AAGGGGCAT TTTCATTAAA	480
TTGTTATAGC TTTTATATT TGTATAATGA ACATATAAGT TTAAGAAGGT GCGAGTGAAG	540
GAAATAAAAA AGCTCAAATG TACCAAATTG TTAATCTTAA TAAATCTCTA CTTTATAAAG	600
ATTGAATGGA CATTCGAGCG TTAATCAGTC AGGAGGGACT TTCCCTCCTA CAATTTAATA	660
ATAATACTTG CTTCACTACT ATACAAGGAG TGAGTTGTTA TGTTCAAAGT GAATTATTCG	720
ATTTTAAGTT ATTATCCAGA ATATAATATC GCAGTAAGTT GGCAACGTTT AAGAGAAGGA	780
AAAACAATAA AAAACAAGAT TTAATACTGC TCGTCATGA GGCGCTTGAA CATTATTTGA	840
TGAATAAGTA TAATTTCAAC TATGATTATG CACATAAAAT TGTATCAAAA AAATACGATT	900
ATTCAATTTT TATAAAAAAG AAGGTGGATT AAATGCTTAC ATTAATAAAA TTGGAAAGAA	960
GATGaACAGG tTATAATATA TGraTATATa CCTGaAGATG aTATAAGTAC CGGGTAAAGG	1020

GTCCCGTACC TTTTAAATTA AAAAAGTTCC AGGGGGT

1057

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

CTGTGCTGTA TTTACTTTAA TTTGACGACA TTTGAGAAGT ATTATGATGG nTGTAGTTAT	60
TTTATGAAAG TAATGTATTA ACAATCGAAT TACTAAGTCT ATATTGGTAG GAATATCGAT	120
GTTTAGTTTA AATGGAATGC ACTATTTAAG TTTTAAATAT GGAGATGTTT GTGACTTTTC	180
GATGATTAAG ATTTTTATAG GTGTGCATCA TTTCAAATAA ACTTTGTGTT TAAAATTGAG	240
CTTAGGAAAT CGATAGGTTT AGATGAGGAT ATTGTTGAAG TTATGTGTCT TGTATCCTTA	300
GTTGTTATAA AAGCGCAAAA AATAGCACCG CTTTCTCTTT ATCTGTGTAG AAAGGATGCT	360
ATTATTGTAA AACAAAGTT TTAATTTnAT TTTCTGATaT ATCATATGT _r ATT _c TACCTG	420
TATCAATTTT TATCGAATTA TAACCATCAA AATTATCAAC TTTATCATCA AAGTCTATCA	480
CTTTTCCAAT TAATATTTTA TTATTAGTAA GCGTTAATTT GACTAATTTG CCTATGTATG	540
ACTGTAAATT CATATTTAAT CACTCCTTTT TAATATACGG AACTACATGA AAAC CA TTT	600
TAGAATAATG AACCTTACCT AATTTTCGTTT CAATATATTT ACCATTCACA TAAGATTTAC	660
CTATTATCTT TTTATAATCT ATAACTTGTT TTATTCTAAA ATTCCCTTCA TCATCAAACA	720
AAACTGGAAT ATCAATAAAT TCTTTTTTAG TCATCTTTTC ACTTTCATTA GAATCTATTA	780
TAGTATAACT TGTAATAAAA GATGAATTAT TTTTCTTATT ATTATATTCA TTTGTGCATA	840
AAATATGACG CTTTGTCTTA ACATTATTCA ATTTCA _r TCGT CATTTTACCA TTACTTATCA	900
TTTCAAGCAT TTCTTTTTTA GCTTTTTGTA GAAAGGATGC TATTTTGTA TTTATTTAAT	960
AATCTAATAC TTTTATCTC AGTTTCATCA AACGAAT AA CAGCAAAATC AGTCTGTATA	1020
TCTACAACAA GATTTCTGT TTCGCTCTCG AATTCATTTT CATAGTCAGT TACAAACCTT	1080
TCGTATTCTT CATTATTCAA AAGCGTGATA ATAACATCTT TACGATATGC ATCT _n CAATT	1140
CTCAATACTT TTCACCTACT TATCAATATA AGGTACTATA TGaG _c ACCTG GTCTTCGAAT	1200
AATGGCACTT cCCTTTCTGG TTTCAATATA CACATTTTCG ATATGTATTT TTCCAATAAT	1260
TTGATTAAAA TTAATAATCT CTTTCAAATC AAATCGCTCA TCACTTAATA TTAGATTGCC	1320
TGTTGACATT TTTTCTCTTA ACAATTCATT CAATAAATCT ATAGAAAGTA TTGTATAGCT	1380
AGGCAATTTT TTATTATTTA AAATGGCTCT TTTTTTATTT TCATTATATA GGTGATGACC	1440

TAACATATAT CTATTTTATT TTCCGCAATT TATTTCTATT TTTATTTTAC CATTTTTAAT	1500
CATTTCTTTT ATCTGGTTTT TAGCTTTTTtC CTGtAATTAT GCTTCTTTTA CTTCTACTTG	1560
ATATTTACct TCACGCTCTT TAAAGAACTT GTCCCGCCAA TTGC CA ACAT GTGGCACTGT	1620
GGTACTTCTA CACCAAGGAT GCATAGGTGG CGCATTCACA CCTGGTATCA TATCTTTAAC	1680
TTTAAATATT TTTCCGTTAA GTGAATGACA TAATTTAGAT GTTTTACTAT CTATTTTGGC	1740
AACATATTTA TATTCGCCAT CTTACCAAG TTCTTTTAAA TATGTTAAC TTTGTGCTTC	1800
TGCATTTTCA GTAAATAGTT AAAAAAGCGT ATAAAAATAG CACCACTTTC TCTTTAkCTG	1860
TCTAAAAAGG ATGCTATTTA TCTTTTGAAT TTGAATTCTT TTTGCTTTT TCTATACTTT	1920
CAAATTCTTC AACTAATTCT TTAAAAGATT CACTCAATTC TTTTGCAGTT ACATTTCCAT	1980
CTAATTGTGA ATCTAACATA ATTAAATCA TCTCACTTTA TATTTAATCa TATTTATACT	2040
ATAAAGTTTT TTCAATAATT TTTCAATATG GCTATCATTA ATGATATTAA TATGCGTAAA	2100
ATATTTAGCA CAAAATTTAC TCACTATTTT ACCATGAAAC CTATTTGACT TGGTAATAAA	2160
TTTTACTTGT CCCTTATTAG TAACGATTGT CATTGATTTT ATTGATGGAT G CT AAAAAA	2220
TGTAAATAAA TCATATTCTG AAAATCCTGA CTGTCCAGGA TGGTTATGTA ACATAACAAT	2280
TGAATTCGGT TTAGTGTTAA ATAATAATTC GGTTGCTTGT TACCCTGGCA CAAAAGATAC	2340
ACTATCTTGA TTGACATATA CTTTTGTAAA TTTACCATCT TTTAACAAAT AAGCTACTTC	2400
ATTGCTATCA TTGTTTTCCA TGAGATATAC CTCCGTTTAT AGtCTGTCGA CTGATATTCC	2460
ATACTTGCTT TTAAAATGTC ATCAGCACGT TTTGGACAAT AAAAAATAAC CTTACATTT	2520
GAAGGTAAA ATTTTTAAAG TAAACTTTCT TTATCCCCAT GCTACGAGTT CAGATTCAGG	2580
AAATAGCCCT TTACTAGTAT TTATGTATAT TCT CT ATG GCATGAATAA AATAATTATC	2640
TCTTGTATTT tTTTCTAAAC TAGATTTTTT AGCATTGATA ACTTCAAGAC TATCTATATC	2700
CATTTGAATA ATACCAGGCT TAATATTTTC ATCATTATTA GGAAAATATT TATATGTAAC	2760
ACTTTTATCA TTAATTTCTT TTATTTTTAA TATTAGCAAT CATTTCCACC TCTAATTAAT	2820
TAAAATACTA TAATTATATT TTATTTCTGT AAGTTTATGT GCCTCTATAT AGTGTAAT	2880
ATACTTATTC ATTAGATAGT GTTCAAGAGC TTCATGTTTC TACATTATTA TATCCATTTT	2940
TTTAATATTT TTCCCTTCTC TTAAACGTTG CCAACTTTGA GCCATATAAA AGTCAGGATC	3000
AAATTGTTTA AATCCACTTT CTAATAAATA CTTATTTTCA AATATATGTT CATAAACTCT	3060
TTGAATTAAA TTTTATTTA TATTAgTATT TTTAGCAATT TTAGAAATCT CTATCTGTTT	3120
ATCTCGATTT CTAAGTGAAT TATAATAAAT TTGAGCATGT CTGTTCCCTT TGATACCGTA	3180
TTCATCACTT TTATTATTAA GTGCACCTGA TTCAATAAAA A ACCTTCTA CTTGATATTT	3240

ACCTTCACGC TCTTTAAAGA ACTTGTCTCG CCAATTGCCG ACATGTGGCA CTGTGGTACT	3300
TCTACACCAA GGATGCATAG GTGGCGCATT CACACCTGGT ATCATATCTT TAACTTTAAA	3360
TATTTTTC CG TTGAGTGAAT GACATAATTT AGATGTTTTA CTATCTATTT TGGCAACATA	3420
TTTATATTCG CCATCTTCCA CCAAGTTCyT TTAAATATGT TAACTTTTGT GACTCtTCyT	3480
TTTCAACGAA TAATGAAAAA AGCATATAAA AATAGCATCG CTTTCTCTTT ATCTGTGTAG	3540
AAAGGATGCT TTAATACCaT GCTATTTTAT AATTTTcGGG AAATTcTTGC TTCTCGATAA	3600
AGTCTCTTAC TACAGAAAAA GACTTATTAC GATATAACAT AAAATATTCT TCATTTTCTA	3660
TTTCAGATAA TGAGAAATCT ATAACCTCTG CATCTTTTTT ATTAAAAGTT ACTGAACCTT	3720
TACCGTTACT TATATCATCT TCAGGTATAT ATTC	3754

(2) INFORMATION FOR SEQ ID NO: 559:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

ATTTAACTAA AACTATAaAT AATCAAATGA TATTGGAAGA TATTcCATA GATATCGAAA	60
AAGGTAAATT GACTTCTTTA ATTGGACCTA ATGGTGCGGG TAAGAGTACT TTACTTTTCAG	120
CGATATGTAG GTTAATTCGT TTTGAGAACG GTGAAGTGAA AATAGATGGA CAGCTCATGT	180
CTGATTATAA AAATAATGAC TTGTCGAAAA AAATATCTAT ATTAAAACAA ACAAACCATA	240
CTGAAATGAA TATTACGGTA GAGCAGTTGG TAACTTTGG ACGATTCCCT TATTCTAAAG	300
GTCGTTTGAC GAAAGAGGAT CATGATATTG TCAATGATGC GCTAGATTTG TTGCAACTAC	360
AAGATATCAG AAATCGTAAT ATTAAGTCAT TATCTGGTGG ACAACGTCAG CGTGCATACA	420
TTGCAATGAC AATAGCACAA GATACTaAT ATATTTTGCT AGATGAACCA TTAAATAATT	480
TAGATATGAA GCATGCTGTT CAAATTATGC AAACGTTAAA AATGTTAGCG CATAAAATGA	540
ATAAAGCGAT TGTCATTGTG TTACATGATA TTAACCTTGC GTCCTGTTAT TCAGATCAGA	600
TTGTAGCATT GAAAAACGGA CAACTAGTTA AGTCAGATTT GAAAGATAAT GcATTCAAA	660
GTAGTGTTTT AAGTGATTTA TATGACATGA ATATTCAAAT TGAACATATA AGAAATCAAA	720
GGATTTGTTT ATATTTTAAG GATTGATAAT TTGGAGaCAC TTTAAAGGGG TGATGCGCCA	780
ATTAAAGAAG GGTAAACGT AAAGCATTTA TTTAT	815

(2) INFORMATION FOR SEQ ID NO: 560:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 919 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

GAAACGAATA ATAAATTTAC TGAGTTATTA GTTGAAAAAG CTAATAAACA TGATGATGTT	60
CTCGATAmGT TGATTAATAT TTTAAAATAA GCGATACACA CTAATAAAAT TGTATTATTA	120
TTATGTTnAA TTGACnCCTC CTAAATTTGC AAAGATAGCA ATTTAGGAGG CGTGTTTATT	180
TTTATTGACG TCTAACTCTA AAAGATATAAATTAGACATT TACAAATGAT GTAAATAACG	240
CAATTTCTAT CATCGCTGAT AACAATTCAT GGTTTAATAT GCAATGAGCA TATACTTTTT	300
AAATAGTATT ATTCACTAGT TTTAACAATC AATTAATTGG TATATGATAC TTTTATTGGT	360
TATTTTTATC CCATAGTGTG ATAATTACTA TTTTTCATTC ATAATAAAGG TTTAAACAT	420
GTTAATAGTG TGTAAGATTA ACATGTACTG AAAAACATGT TTAACATAAT GATATAAGGA	480
GTGACGTACA TGATCCGTCT AGGTAAAATG TCAGATTTAG ATCAAATCTT AAATCTAGTA	540
GAAGAAGCAA AAGAATTAAT GAAAGAACAC GACAACGAGC AATGGGACGA TCAGTACCCA	600
CTTTTAGAAC ATTTTGAAGA AGATATTGCT AAAGATTATT TGTACGTATT AGAGGAAAAT	660
GACAAAATTT ATGGCTTTAT TGTGTGTCGAC CAAGACCAAG CAGAAATGGTA yGnyGACATT	720
GACTGGCCAG TAAATAGAGA AGGCGCCTTT GTTATTCATC GATTAACCTGG TTCGAAAGAA	780
TATAAAGGAG CTGCTACAGA ATTATTCAAT TATGTTATG ATGTAGTTAA AGCACGTGGT	840
GCAGAAGTTA TTTTAACGGA CACCTTTGCG TTAAACAAAC CTGCACAAGG TTTATTTGCC	900
AAATTTGGAT TTCATAAGG	919

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

ATCATATAAA CCGGCTGCTT CTAAAAACGA AAATACTGTT ACTGGACCTA AAAATTTAAA	60
CCCGTATTGT TTTAAATCTT TAGATAGTTG TGTTGCAGTA TCATCAACTG TGATACGATC	120
AGAAGCATGT TCATACTGCA AATCTTTAGG CTTACCATTT ACATATGACC ATAAAAATTT	180
ACTAAAACTA CCATATGCTT GTTCAATTTT TAAATACCCT TGAGCTTGAT TAACAATTGC	240

TTCTAATTTT TTACGATGAT GAACGATATT TGGAAAAGTC ATTAAGCGGT CGATATCTTG	300
AGCGGTCATT TGTGCTACCT TTTCTGGTTC GAAATCATAA AATGCTTCTT CATAGGCTTC	360
TTTCTTTTTT AAAATAGTTA ACCAAGATAG CCCAGCATGT TGTGaTTCTA ATGCTAAAAG	420
TTTAAACAAT GCCTTGcAT CATAGAGCGG TTGTCCCCAT AATGGATcm TGATAGTCTA	480
AGTAGACTGG GATCTTTAGT ACCAAATGCG CATTCATT	518

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

CTTATTTAAA AGTAAATCAA TCAATGTATT ATAATCCGAA TAGTCCGCAT AAAGCTGGTT	60
TGCaGGCAAA tCAATTACTA CAACAAGCAA AAACCCAAAT TAATGCAATG rTTaATTCAA	120
AAACAAATTA TGATGTTGTA TTCACTAGTG GTGCAcTGAA TCCAATAATC TTGCTTTAAA	180
AGGTATTGCC TATCGTAAAT TTGATACAGC GAAGGAAATA ATTACATCCG TGTTAGAGCA	240
TCCGTCCGTA TTAGAGGTTG TAAGATATTT GGAAGCACAC GAAGGATTTA AAGTTAAATA	300
TGTTGATGTA AAGAAAGATG GCAGTATTAA CTTAGAACAC TTCAAAGAAT TAATGTCAGA	360
CAAAGTCGGT TTAGTAACAT GTATGTATGT AAATAATGTA ACTGGACAAA TACAGCCTAT	420
TCCACAAATG GCTAAAGTTA TAAAAAATTA TCCTAAGGCA CATTTTCATG TAGATGCGGT	480
TCAAGCATTC GGCAAAATTT CAATGGATCT CAATAACATA GATtTATTA GTTTAAGTGG	540
ACACAAGTTT AATGGTTTAA AAGGACAAGG CGTCTTACTT GTAAATCACA TTCAAATGT	600
TGAACCAACT GTCCATGGTG GTGGTCAAGA ATATGGTGTT AGAAGTGGA CAGTTAATTT	660
GCCAAATGAT ATTGCAATGG TTAAAGCGAT GAAGATAGCT AATGAAAAC TTGAAGCATT	720
GAATGCATTT GTTACTGAGT TAAATAATGA CGTCCGTCAA TTTTAAATA AATATCATGG	780
AGTTTATATT AATTCTTCAA CTTCAGGTTC ACCATTCGTT TTAAATATTA GTTTTCCTGG	840
CGTAAAAGGT GAAGTATTAG TTAATGCTTT TTCAAATAT GACATTATGA TATCTACGAC	900
AAGTGCTTGT TCATCTAAAC GTAATtAATT AAATGAAGTA TTGGCTGCAA TGGGATTATC	960
AGACAAATCT ATTGAAGGTA GTATAAGATT ATCATTTGGG GCTACTACAA CTAAAGAAGA	1020
TATAGCGAGG TTAAAGAAA TATTTATCAT CATTTATGAG GAAATTAAGG AGTTGCTAAA	1080
ATAATGAAGT ATGATCACTT GCTTGTTAGA TACGGGGAGT TAACATTAAA GGTTCAAAT	1140
AGAAAGAAAT TTGTAAATCA ATTAAGAAAT AATGTAAATA AGTCaTTAAA AGGACTTGAT	1200

GGGTTTGTCTG TTAAAGGCaA ACGAGATCGT ATGTATATTG AACTTGAAGA CCATGCaGAT	1260
ATAAATGAAA TAACATATCG ATTATCAAAA ATTTTCGGTA TTAAATCTAT TAGTCCAGTA	1320
TTAAAAGTAG AAAAAACAAT AGAGGCAATA AGTGCAGCGG CAATTAAATT gCGCAGaATT	1380
TGAAGaAAAC AGCACATTTA AAATTGATGT GAAGCGTGCC CGATTAAAAT TTCCCCAATG	1440
GATACGGTAT GGAATTACAG CGTGGAATTG GGGTGGTGCC AGTATTGGAG CACTTCGCCA	1500
TATTTCCAGT GGATGTCCAA CGTCCCAGnC CCA G GAATT	1539

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

ATAnCGTATA CATGTGTTCT TTAAAATTGT GATAAGGAGT TTAGGATGGT TTATTTAAAA	60
TCAATAGATG CCATTGGATT TAAGTCTTTT GCAGATCAAA CCAATGTTCA ATTCGATAAA	120
GGTGTAAGTCA CAATTGTTGG TCCAAATGGA AGCGGTAAAA GTAATATTAC AGATCTATT	180
AAATGGGTGT TGGGTGAACA ATCGGCTAAA TCATTACGTG GCTCAAAAAT GGAAGATATT	240
ATCTTCTCAG GTGCAGAACA TCGCAAAGCT CAAAATTATG CTGAAGTACA GTTAAGATTA	300
GATAATCATT CTAAAAAGCT CAGTGTGAT GAAAACGAAG TTATTGTAAC AAGAAGATTG	360
TATCGAAGTG GTGAAAGTGA GTACTACATA AATAATGACC GTGCAAGATT AAAAGATATT	420
GCCGATTTAT TTTTAGATTG TGGATTGGGA AAAGAAGCGT ATAGCATTaT CTCGCAAGGT	480
AGAGTTGATG AAATACTAAA TGCTAAACCA ATTGATAGAC GTCAAATTAT TGAAGAATCG	540
GCTGGTGTAC TTAAATATAA AAAACGTAAG GCTGAATaT TAAATAAACT TGACCAAACA	600
GAAGATAATT TAACGAGAGT AGAAGACATT TTATATGATT TGGAAGGTCG CGTAGAACCT	660
CTAAAAGAGG AGGCAGCTAT AGCTAAAGAA TATAAGACAC TTTCACATCA AATGAAACAT	720
AGTGACATTG TAGTTACAGT sCACGATATT GATCAATATA CAAATGACAA TAGACAATTA	780
GATCAACGTT TAAATGATTT ACAAGGCCAA CAAGCAAATA AAGAAGCTGA CAAGCAACGT	840
TTAAGCCAAC AAATTCAACA ATATAAAGGT AAACGTCATC AACTTGATAA TGATGTTGAA	900
TCgCTTAATT ATCAATTAGT AAAAGCTACG GAAGCCTTTG AAAAATATAC GGGACAATTA	960
AATGTTTT	968

(2) INFORMATION FOR SEQ ID NO: 564:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

TTGTGTGTAT GCATTCAATG TGCTCTGTTT GTAAATGGCT AGCTATATAA TTTAgGATTC	60
GAGGATCGTC ATCGACAACA AGACATTGCA CCATAGCTAT AAACCTCCCTT ATCTTTTTTCA	120
TTTATTATAC ATGTAAAATA TTTTTCGTA AAAAAACAATTGTTTCATATT GAGTTCATAT	180
TTCAACCTTA TACTGACGCT AAAGAAGAAA TAGGGAGAAG TGAATCGATA TGAAATTAGC	240
GATAAAAGAG ATTATGTTTT ACAAATTTTCG TTATATTTTA ATCACATTAA TCATTCTTTT	300
ATTAAGTATT ATGGTGTTAT TTATTAGTGG TTTAGCTCAn GGGCTTGGTA GGGaGAATAT	360
TTCGTwATTT GAACACTTTG GATAATGATG aaTATGtTGT TCaAAAAATG AAAGAGCCGC	420
aAATTGaGAA ATCGCA	436

(2) INFORMATION FOR SEQ ID NO: 565:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

ATGTTTTGTC AATATCAATT GTTTGAGATA AATCCGCTTG TATAAACGA ACTTTATCAT	60
CATTAAATTT GCTAGTTAAT TCATTTATAT CAGTACGATA ATATTGCACA TAAACTTCAA	120
ATCCATCAGT TAATAATTGT TTGACTATCT CAGAACCAAT TGAACCAGAA CCACCTAATA	180
CTAATGCTTT CATTACTTTT TAATCTCCAA ACGACTATCG ACTTGCTGAT CTAAATTTAA	240
ATATAACGAT GACGTTTCGT TAATACTATC TAACGTGATA TTTCAACAA TGTCTAACAT	300
GTCAAACACG CTAACACCTT CAAAATACAA TTTAGTATAT TGATTAGCAA TATATTCAGG	360
TGAGTTTAAA CTTGATATGA ATTCACCTAT AAATTGCTTT TTCAAAAGTT CAAATGCTTC	420
TGCATCTTGG AAAATGCCTT TTTTATCACG CAACTCATCT AATAATAATT TTTTAAATTT	480
ATCTGGTTCT TCAGTAGCAC TTGTCACGAT TGAAAACTA TACGTCGGCT CTAGTACAAA	540
TTGATAACCA AATGTATCAT CGATAAGTCC TTCGTTTAAT AAATTCTGAT AAAAATCTGT	600
TTCTTCCCCA AAAATTAAC CAAAGAATAA TGACATTTCT AAATCACGTT GTACATATTT	660
TTGAGGCGCT TCTTGTAATG GTTTATTTTT AAAACCAAGC ATTAGTCTTG GTGATTGAAT	720

TTTCATAGAT TCAGTAACAA ATGCTTCTTT AACATCctTCC GGTTCATCAA CAAGTCCTCG	780
TTCGATTTTG GGTTGGTTAA CTTTATTACG AGCATCCTCG TGTGTGTTTA CTATTCgACA	840
TATTGCTTCA GGATCCACAT CGCCAACAAC AAATAAAACC ATATTTGATGGATGATAAAA	900
CGTTTCATAA CATAGATACA AATCATCTTT TGTAATATCG TATATACTTT CTACACTACC	960
GGCAATATCA ACACGTATTG GATGTTGTTG ATACATTGCA CGCAAtGTAT TaAACATTAA	1020
TTTATATCCA GGTTGCTCTT GaTACATTTT TATTTCTTCT GCAATAATAC CTTTTTCTTT	1080
ATCAACAGTT TCTTTTGTA AATAAGGCGT TTCaACCATT GTAAGTAAAC GTTTAATGTT	1140
GTTTTCAATA TtATCAGTTG CACTGAACAA GTAGCTTGTA CGATCAAAGC TTGtAAACGC	1200
ATTTGCTTGT GCGTTATCTT CAGCAAACGC AGTAAATAAG cTTCTTCTTC TTTTTCAAAT	1260
AATTTATGTT CcTAAAAAGT GAGCAACTCC ATAGGTACA GTAACAAATT GGTCTTGTCC	1320
AAGGGGTTTG AATTGATTAT CTAATGAACC AAATTGTGTA GTGTAAGTGA CAAATGTCTT	1380
TTGAAAACCT GGTTkGGGGA TAATAAATAA TCGTAAACCA TTTTCTAATt CTTGTTTCGA	1440
tACTCTTTCG TCTATTAATT CATAATAACG CTCTTTCATT ATTTATCCCC TCCTTTTtEC	1500
AACACATAGA TtGTATCTAA AAATGCTTTT TCAGCAACAG AAACAATATC TTCGCGACTT	1560
ACCTTCTGTA TATCATTTAT AAATGTTTCT TTGCTTTGTG GTTGCTCTAA TAATATTTGG	1620
TTATGCATAA TCTCTATAAT ACTTTTCGGA CGATCTTCAG ATTCATATCG ATGAGAAATG	1680
ATTACTTTTT TAGCTAACTC TAATTTTTCT TCAGTGAAAT CTCCTGCTTT TATTTTTTCA	1740
AATTCACTTA TAATAGTGTC TTTTGCAGTT TCGTACTTAT CACTTGAAAC CCCACTCAAA	1800
ACAAATAAAT AGCCATTTTT GCCATCAATT TGTGAATGTA TAGAGTACGC TAAACTTTGC	1860
TTTTCTCGCA CTTCATTAAA TAAAACAGAT GAAGGATCTCCTCCAAACAT CATGTTAAAT	1920
ACAACAAAGG CAGCATATCC ACTTTGTCCA TATTGTGTTG GAAAACGGTA TCCCATATTT	1980
AATTTAGCTT GATCCACGTC ATCATATTCA ACAATATAAT CAACTTCTTC ATCGTGTA	2040
TGATGAGTAG AATGTTGGAA TTGATGTTTA TCGAATGGTT TAAGTGCAAA TTTTTCACGT	2100
ATTTGTTTCT CAACACTTTC AGGTTCTACA TTGCCGACAA CATAAACAGA ACATTGATCA	2160
TTATTAATCA TTGATTGATA TGTATGATAT AGTGTTCAG CAGTAATATG TGGGATTTGT	2220
TCTAGTTGTC CTGTAGATAA GTATTTATAT GCTTCATTTT CAAACATATG GTCGAGTAAT	2280
TTTAAAAACG AATATTGTGC TTATTATCT ACCATTGCTT CTATTTTTTT GGCTAATAAT	2340
GTTTTCTCTT GGTTAACAAA ATTATCATTG AATGCTTTAT TTTCAATTAA TGGATTCCAA	2400
ATGATTTCTT GtAATAAATC TAATCCTTGa TTAAATAATG AwTCACCGkT TCyTAAATAA	2460
CGkkCaTTAA caATTyCTAA tGaAAATGtA ATgACaTGCT GaTCTTtGAA TTTTGAAATT	2520

GTACTATTCA CATACGCACC ATATAAATCG GCTA

2554

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

TnTCGCTATT TThAATTGGT TTTGTATGGT TTAAGTTATA TCAATATACA ACAnACCCTA	60
AAGCTGATAT CCCAGGTATC ATTTTtagTA CGATTGGTTT TGGTGCTTTG TTATATGGTT	120
TCTCAGAAGC TGGCAACAAA GGTGGGGT CAGTAGAGAT AGAAACAATG TTTGCGATTG	180
GTATTATCTT TATTATTCTA TTCGTTATTA GAGAATTAAG AATGAAATCA CCAATGTTGA	240
ATTTAGAAGT ATTGAAATTC CCaACATTTA CATTAAACAA AATTATTAAT ATGGTTGTAA	300
TGTTAAGTTT ATATGGTGGT ATGATTTTAT TACCGATTTA TTTACAAAAT TTACGCGGAT	360
TcTCAGCATT AGATTCCGGA TTGTTATTAT TACCTGGTTC TCTAATTATG GGTCTACTAG	420
GACCATTTCG AGGTAAATTG TTAGATACTA TTGGTTTAAA ACCATTAGCT ATCTTTGGTA	480
TTGCTGTAAT GACTTATGCA ACATGGGAAT TAACTAAATT AAATATGGATACACCATATA	540
TGACAATCAT GGGTATCTAT GTACTTCGTT CATTTGGTAT GGCATTTATA ATGATGCCAA	600
TGGTAACTGC AGCTATTAAT GCGTTACCGG GACGACTTGC CTCTCATGGT AATGCTTTCT	660
TAAATACGAT GCGTCAATTA GCAGGCTCTA TAGGTACAGC AATCTTAGTT ACTGTAATGA	720
CAACACAAAC TACACAACAC TTATCAGCTT TTGGGGAAGA GTTAGATAAA ACGAATCCTG	780
TTGTACAAGA TCATATGCGT GAATTAGCAT CACAATATGG CGGACAAGAA GGCGCAATGA	840
AAGTGTTACT ACAATTTGTA AATAAACTAG CAACGGTTGA AGGTATTAAT GATGCATTTA	900
TAGTTGCAAC GATATTTAGC ATCATCGCCT AATTTTATG TTTATTTTAA CAAAGTAATA	960
AAAAAGCAAA AGCTACAGCT CAAAAGTTAG ATGCAGATAA TAGTATCAAT CATGAATAAA	1020
TAAAATAAAT TAATTGAAGT GTGACTAATC AAAAATTATG TTGTGGGGAC ATGATTTTTA	1080
AAGTATCGGT GCCAAATATG GTTATCGATA CTTTTTTTAT TTGTTGATTT ATAGAAATT	1140
AGAGGAATTA TATTAAAATT TGGCATTGAC GTAGTAGGTC ATTAATAAAG AAAAAGCAGG	1200
AAGTGGGTCA ACGAAATGAA TTTTGTGAAA ATAACATTTT TGTCCCAATC CCTACTATAT	1260
AACATTATTT TAAACGAGGC ATGCGATTAC GGAAGAATAA GCTTATAACA AGTAAACCGA	1320
TGCTACAGCC AAGTAAATG ATGCCGTTAT GAATAGCGTC ACTTgCTGTA ATCACTTGAT	1380
CTGGTGGTAC ATTTAAATAA TATTTTTTGA AAACATCTGC AATT	1424

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

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TCTCCCATGT TCTGCTAAAT GACGCATCAC TTTTACTTCA TGAGGCGTCA ATACACGTCC      60
TTCACCAGCA TTCAAACCGA CAACATTTAA AGGCCATAT TCAATACGAG ACAGTTTCGT      120
CACTTGATGA CCAAAATGTT CGAACATTCT TCTGACTTGG CGATTACGAC CTTCTGTAAT      180
TGTAATTTCA ACCAATGTTG TGTTTTTATC TTTATCTTGT TTCTTAACTT TCACTTCAGC      240
CGGTTGCGTC ATACCATCTT CTAATTCAAT ACCTTTTTCT AGCGCTTTCA CTTCTTCTCT      300
CATTAAATAA CCTTTTAATT TCGCAACATA TTTTTCCTTA ATTTGATATC TTGGATGTGT      360
CATTAAATTA GTAAATTCAC CATCATTTGT GAGTAATAAC AATCCAGAAG TATCATAGTC      420
TAAACGACCA ACAGGATAAA TACGTGCTTC TATATCTTTA AAGTAATCTG TAACCACTGT      480
ACGTCCTCTA TCATCAGATA CACTTGtKAT CACTTGAGTT GGkTTATGGA AkAAAATGkA      540
AAtTTTGTCT TCTAGTTCTA TTTTAATACC TTCAACTTCA ATCGTATCTG ATGGCTTCAC      600
TTTTGTTCCCT AATTCAGTGA CAGTCGTACC ATTCACTTTC ACTTTTCCTT CAGAAATTAA      660
AGTTTCTGCC TTACGT                                     676
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(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

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GAAACGGTTC TACCAAAAAA CAGTAAGGGC TAAACCCAAT CATGGTAAGA CAAAAGTAC      60
AAATAGCCAT GCCCAAGTTG AACTCGCTGT ACGCCTATTT CTTTCTAAAA AGATAATAAT      120
AAAAGCCAAT ACTAAATTAA TGATGAATCC AATGGCTAAA ATAATAGTAA ATAACGTTCC      180
TAAATCGTTT GAAAATGTAA ATCGCATAGT CTTTCTCCT ATAAAGAAAG GCACAAAAAA      240
ACATTTTGCA CCTTTCACGT CATATTATTT ATTCACAGAT AAAGTTAAAA TTGcATTGAA      300
TTCTTCTTCA TTATTGGGA ATGTTCTTTC TTCTATTTCT TTAATAGTAA TATTTACTAA      360
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TTTTAAATTT GTAGCTTCTT CAGAACTTAA AAAAGCATTA ATGTTTTTTT CTAATAACTC 420
 kAAAGTCTCA GCTGtAAAaG TTTTAAGTTT AATT 454

(2) INFORMATION FOR SEQ ID NO: 569:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 894 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

ACGATATTAC CACCCTCTGA AATAACATCA ATCATGTGAT CTGTAAAGTC CCAAGGATGA 60
 CTTGTTGTGA AACGAACTCT TGGAATCGCT ATTTTAGAAA TECTTGTA AAGATCTCCT 120
 AAGTCATATT CTATATCCTG TAAATCTTTA CCATAAGAAT TTACATTTTG ACCTAAAAGC 180
 GTTATTTCTT TGTAACCTTC ACGAGCAAAGT TCACGTA CT CATCTATAAT GTCTTCAGGT 240
 CTACGGCTTC GTTCTTTACC TCTTGTAAT GGAACAATAC AATATGTACA AAAC TTATCA 300
 CAACCATACA TAATATTGAC CCATGCTTTA ATGTTGCCTT CACGGACTTT TGGAAGATTT 360
 TCAATAACGT CTCCTTCTTT AGACCATACT TCAACAACCA TTGCTTTAGA TAAGTATGCT 420
 TCTTCTAAAA TTTCTGGTAA ATGATGAATA TTATGTGTAC CAAATATCAT ATCTACATTT 480
 TGATACGATT TTAAAATTTT ATTACTACT GACTCTTCTT GTGACATACA ACCACAAACA 540
 CCGATTAAAA TATCAGGTCG TTCTTTTTTC AAATrCTTCA AATTACCTAT TTCCTAAAC 600
 ACTTTGTTCT CGGCATTTTC TCTAATCGCA CATGTATTAA TTAAAATAAC ATCTGCAGTG 660
 TTAATATCAG TCGTkGCTTG aTAGCCTAAT GCyTCmAGTA TACCAGCAATGACCTCAGTG 720
 TCATGTGCAT TCATTTGACA TCCATATGTT TTAATTAAAA ATGTACGCTC GTTCCCCATA 780
 CCGCGATATT TTyCATCAAT TtGGgAAATC nCTATTATAA CGAACTTCTk GTtTACCnCC 840
 TTTTTTnCGC TCCTTTAAAA TTAAGGCGGC TGATAAACAG GTCCAAAATA TTAC 894

(2) INFORMATION FOR SEQ ID NO: 570:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

TATCAATCCC ACAGCACATG CTGAACAAGA TCAAACATGG GAGAAGATTA AAGAACGCGG 60
 TGAACCTAGA GTGGGTCTTT CTGCAGATTA TGCACCAATG GAATTTGAGC ATACAGTTAA 120

TGGTAAGACT GAGTATGCAG GTGTAGATAT TGATTTAGCT AAAAAAATTG CGAAAGATAA	180
TAATTTAAAA TTAAAAATCG TCAATATGTC ATTTGATAGT TTGTTAGGAG CTCTTAAAAAC	240
TGGAAAAATT GATATTATTA TTTCCGGAAT GACTTCAACG CCTGAACGTA AGAAGCAAGT	300
TGATTTTTTCA GATTCATATA TGATGACTAA AAATATCATG CTTGTAAAGA AAGATAAAGT	360
TAATGAATAT AAAGATATCm AAGACTTTAA TAATAAAanA GTnGGGGCAC AAAGGACTG	420
AACCAGAAAA AATCGCTCAA C	441

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

TGTTAAAAAT TGTTTTTGTT TACGACTTGT TTCTGCAAAA TCTCCTGGAA ACAGGTGATT	60
AAGTCGTTCA TCTTTTTCTA CAAGGGTGTA AAAATAATCA ATCATATCGT ATAACGCTTC	120
TTTACCAATG ATGTCATATG GTGTTGTTGT CATTTAATCA CCCATTTTCA AAAATTTACT	180
GTTACGAACT TAAGTTAATA TATAACTAAT ATAACATGAT TTTAAACATT TGAAAGAAAT	240
ATGCATATTT GCCAATTTAA TTTATATTGT TTGAAAGTGT TTCTTTTTTC TTGAAAAAAC	300
GTTGAACTTT ATTTAAAGGT tGATGATGTT CGAGGTTTAG TTCGTTtAAT AAAGATtGGA	360
ACTTTTGTAAC ACCTTGATTA TAGTCTTTAA CTTCGAACTC TAACTCATAA TCCGTAGTAT	420
CGAAATACTC ACTTTTATCT AAAACCAGTA AATCACCTTT ATATTTAGTT TCTTGCGGAT	480
ATGTCGTTAA TGCACCAAGT ATTGATAAAG TTGTATCTTT TACACCAAAC TGTTCACTA	540
TAATTTGACG AATGTCATCT GGAAGATTGT CGTTTGAAAT AATCAAGTTC ATCTCTGGTT	600
TAATGTCGAC GATATAGTTG TATTCTAATA GACCAACCTT TGCTGGTGTC TTTAAAGTCA	660
TTTCATATTG ATTGTCTTTA ACTCTTATGC GTAGTGCAGA GCGATGTTCC TTTAATTTGA	720
AATCGGGTGT ATCAATATAG TAATTGACTT GCTTAmAAAG CACACTGTCT TTAAAATATT	780
TCTCTTGCAA TTTATTATAG ATTGAtGCAG TTATCATTTG TtTAAATTCT ATtTCATGAT	840
TTGTTGCCAT GATATGTATA CACCTCGTAT CAAATTCAAT TTATCTTAAC TATATTATGA	900
ATGACAAAGT TGAATTTTAA AAGTAATTTT CTTTATCAT TATCAATGTT AATTTGACCA	960
TTAAAAATAG TGTTGCTAAG TGTTTTGTAT TATTGAtTTG TGTTAAAAATG TTATGGAATA	1020
AGAGGAGGAT TAAGCATGsG TTTwTATATT AATGAAATTA AAATTAAAGA TGACATACTT	1080

TATTGTTATA CAGAAGATTC TATTAAAGGA TTATCTGAAG TAGGACAAAT GCTCGTTGAT	1140
AGTGATAATT ATGCCTTTGC GTATACATTA GATGATGGTA AAGCGTATGC TTATCTCATT	1200
TTCGT	1205

(2) INFORMATION FOR SEQ ID NO: 572:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 570 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

TGAAGAAATA GCAATGATGA AATGCCGTAT GTTATATGAG ACGGGGTCAT TTCTTGAATT	60
AAGAGAAGAA ACAATTGTCT TATTGAAAAC TGGCATACAA CAATATGATG CATTGATGAT	120
TTATTACGTG AAAAGTTTGA TTGGTTTGGG ACAATATTTT GAAGCGGTAG AAGTAATTCA	180
TCAAATTATT GATGAAGTCA AAGATCACAA AACAAGAATG GCATTACATC CTCTTAAAGA	240
ATTTGCTAAG TCAAAATTAA TTGAAGATGA AAAACGATTG ATCAGTCAT TAGCTGATTT	300
TGrTACGTTA TCAATGAGGG AACAGACGCA CTTGATTTTG AAGTTAATAG ACAATGGTCA	360
TTTTCAATTT CAAGAAACGG TATTATATAT ATkAAaAyCT AATaCGTACa GTtATAACCT	420
CATTAGTTTA ATGATTGAGT ATTTAAGGTT CGCAAATTGT ACACAAGAAC TGACAATTGA	480
AAAGTATGGT ATGGATGTAA CTTTTGTACC AGCTAATTTA AAAGGGCTAG AACATACAAC	540
ACTTAAAGAA AAAGTTATAC CTAACGTTAT	570

(2) INFORMATION FOR SEQ ID NO: 573:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GTTGAATGGT TAGCAGCTGC AGTTGTATTA TATTTCTGTG GTGTAATTGT TGACGCTCAT	60
GTATCATTCA TGCCTTTTAT TGCAATATTT ATCATTGCTG CATTATCAGG TTTAGTCAGC	120
TTTATTCCTG GTGGTTTCGG CGCTTTTCGAT TTAGTTGTAT TACTAGGATT TAAAACTTTA	180
GGTGTCCCTG AGGAAAAAGT ATTATTAATG CTACTTCTAT ATCGTTTTGC GTACTATTTT	240
GTACCGGTAA TTATTGCATT AATTTTATCA TCATTTGAAT TTGGACATC AGCTAAGAAG	300
TACATTGAGG GATCTAAATA CTTTATTCCT GCTAAAGATG TTACGTCATT TTTAATGTCT	360

TATCAAAAGG ATATTATTGC TAAAATTCCA TCATTATCAT TAGCAATTTT AGTATTCTTT	420
ACAAGTATGA TCTTTTTTGT AAATAACTTA ACGATTGTkt ACGATGCTTT tATATGATGG	480
AAATCACTTA ACGTATTATA TTCTATtGGC AATTCATACT AGTGCTTGTT TATTACTTTT	540
ACTGAATGTA GTTGGTATTT ATAAGCAAAG TAGACGTGCC ATTATCTTTG CTATGATTTT	600
AATTTTATTA ATCACAGTGG CGACATTCTT CACTTACGCT TCATATATTT TAATAACATG	660
GTTAGCTATT ATTTTTGTTC TGCTTATtGT AGCTTTCCGT AGAGCGAATA GGTGAAACG	720
CCCAGTAAGA ATGAGAAATA TAGTTGCAAT GCTTTTATTC AGTTTATTTA TTTTATATGT	780
TAACCATATA TTTaTTGCTG GAACGTTATA TGCATTAGAT ATTTATACGA TTGAAATGCA	840
TACATCTGTA TTGCGCTATT ACTTCTGGCT TACGATTTTA ATCATCGCTA TtTCATAGG	900
TATGATTGCA TGGTTGTTTG ATTATCAATT TAGCAAAGT	939

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

GAATTAATTA AATATTACAC ACAGCCTCAT TTTTCATTTT CAAATAAATG GCTATATCAA	60
TATGATAATG GAAACATTTA TGTTGAACTT AnGAGATATT CATGGTCAGC ACATATATCT	120
TTATGGGGCG CTGAAaGtyG GGGAAATATT AATCAGTTAA AAGATCGTTA CGTAGATGTG	180
TTTGGACTION AAGACAAAGA TACTGATCAG TTATGGTGGT CTTATAGAGA GACATTTACA	240
GGTGGCGTTA CACCAGCCGC AAAACCTTCT GATAAACTT ATAATCTTTT TGTGCAATAC	300
AAAGATAAAC TACAAACGAT TATTGGTGCG CATAAAATAT ACCAAGGCAA TAAACCAGTA	360
TTAACATTGA AAGAAATCGA TTTCCGTGCA CGAGAAGCGT TAATAAAAAA TAAATATTA	420
TATAACGAAA ATCGTAATAA AGGTAAGCTT AAGATCACCG GTGGCGGTAA TAACTACACT	480
ATTGATTTAA GCAAAAGATT ACATTCAGAT CTAGCAAATG TTTATGTTAA AAATCTAAT	540
AAAATAACTG TTGACGTCCT CTTTGATTAG TATATGAAGG TGACTTATAC TTCATGCACT	600
TTAATTCCAA ATCAGATTAT TTAAATGATA ATTTTTAAAG TGTATGATGT ATATAATAGG	660
TAAAATTTTC TATATATTTA AATGGAATTG GGAGTAGGAA TGTGACAGAA ATAGTATTTT	720
ATAAAATTTA TTCTTGTCAC TCCCCAACTT GCACATTATT GTAAGCTGAC TTTCGCCAG	780
CTTCTATGTT GGGGCCCCGC CAACTTGCAT TGTCTGTAGA aTTTCTTTT GAAATTCTCT	840

ATGTTGGGGC CCCGCCTATA ATTGAAAAAT GCTTGTTACA TGGGCATTTT CATTGGGTCA	900
ACTACTACCA ATATAATATT GtAGaGCCTA AGACAT E AT TTATTATGTC TTAGGCTCTA	960
TTCCTTCATT TAATGATTAA nTTATTATAG CAATACTTTA TTGTCCCATG ATTAGTGTTT	1020
TTTTAATGAG ACATAGTAAC TATAAAGTTT AATAATCGT	1059

(2) INFORMATION FOR SEQ ID NO: 575:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

GTTTGCTTTA GGTCTGTTT CATATTTATA CTTCGAAGGA TTTACCTTTT TGaAGTCT G	60
ATTTTTGtAG AATCTAAACA AATCACCATT AAGCACGtKg TCACTCATTT CGAGATCctT	120
TTCAACTkGC TTTTATTCT TTTCGAAATC AGCTGGTTGA GTAGTTATGA GTTCATTATT	180
TTTATTAGmA TAAATCTTAC CATTAACATA TTTATAATCT TTTGTTATAA AGTCACCATT	240
TCTGAATGGA ACTACTTGAT TATGACCTTT AGAGAATAAA TCAGTACCGA ACATTAAATA	300
GTTCTTCGTA TCTATACCAG CCAAATGTAA AATTGTTGGC ATTACATCGA CTTGACCAGC	360
ATATTCATTA TTGATACCAC CAGATTTACC AGGGATTTTA ATCCAGAAAC CAGTTCTGTT	420
TAAATCTGTA AATTTAGCCG GTGTGATTTT TTCACCTAATAGTTTTTCCA TGGCATTGTT	480
ATGGTTTTTCA GAGATACCAT AGTGGTCACC ATAAATCATA ATCACTGAAT TGTCATATAA	540
TCCTTTTTTTC TTCAAGTCAT TAATATATTC TTCT	574

(2) INFORMATION FOR SEQ ID NO: 576:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

CAATGTTTTA TAGTACAATA TATTTTnAAT AATACTCGTT AAGGAGAATG ATATGATATC	60
AATTCACGCA ATTTGACAG GAAAAATCCA AGATTTCCT TATAGCTCGA AAAGACCGAT	120
GCGCTCTGCT TTAGATAAAA CTAAGATTTT ACAAACAACA TGGTTATCTT CAACTGGTTT	180
CACTGGTGAT GAACAGGCTT ATAAAGATCA TGGTGGACCA CATAAAGCAG TTTGTGGGTT	240
TAGTAAGCAT AATTATGCAC TGTATCAAGA TGATTTACCT AACTACCTA CTCATGCGAT	300

GTTTGGAGAG AATTTAACAT TTGATTATTT AGACGAATCT GATGTTTACT TTGGTAATCA	360
ATATCGTTTA GGTGAAGCGT TAATTGAGGT TTCTGAAATT AGAGAACCAT ACTGGAAAAT	420
TCAAGCAAAA TATAATATTC CTGATTTAGT GAAGCGCATG TCT E ATCTG GTAAAACAGG	480
TTTCTATTTT CGGGTATTAA AACCAAGGCTA TGTATCTCCA AATGATCAGC TTTACTTAAT	540
ACAAGAAGCA CCAATCGAAC ATCGTTTATC TGTACAACAG CTTAATGACC TTTATTATAA	600
TGATAGACAA AATCAAGaTA TGTTACGATA TGCACTAAAC AATCCATTTT TGTCACCAAC	660
AAGACGCGAT AA A CTTCAAA AAATGTATAA CAGAACATTG GAAATAATTA CCTTTCA T n	720
ATAAGTGTTA AATGA A CTTT TCAAAACAnA AAGGAATCAA CTTCACACAT CGTTTGTATG	780
AATAGTCTTA TCTATA	796

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

AGAAATTATG ACAAATATA AAGATGGAAA GTTAGTTTAT GCATCAGTCG AACCAGGATC	60
TTACGTAATA CATAAAGATG ATGCAATTAA ATATGACGAT TATTCTAAGT TAAAAAATT	120
AAGTCAGCTA ACTAACTTG ATCATCCAAA ACCAGTTCCA TATAGCGTaC TCAAATCAAA	180
TCTTTTCGGAG TACCTTTAAC AAGCGTTTCA TTTATGACAC ATGGAT E AA GGATACTAAA	240
GATGAAGTGT TGCCGGCATT GGCTATTTC ACTTTTTCAC CAAAAAATTA TGAAGACAAG	300
TCTAATCCAG ATCCAAAAGT TTTAAATTTA GTACATATGG ATTTCTTAAA TGCATCTAGT	360
GATTTTGGTA ACGCACATTT TGTGTGTTTA AGTAAATATA TTAAAGAGTA TGAATCAAAC	420
TATGAAACAG CGTCAGATGA TTCTTTAAAA TAGTATTTAC TGTGTGAAAA ATAAATAGTG	480
TACTACATTA AATAATCGCA ATAATAATCC CGATAAACAA TCAGCATTAC TGCTTATCAC	540
ATAGAGTTCG TAATAACTAT AACTCTATGA TTCGCAAATA ATAAATGATT GTCATCGGGA	600
TTTATTTTTT TCAATTTATA AAGTGACAT ACCTTGTTCA TCAGCAGGTT TGAAAACAGT	660
AATCACTGCA CTAATAATTG CTAAAATGTG TGGGATACCT GTCCAACAGA ATATTAAGTG	720
TAGAATACCT TGCATATTCT TGCCGGCATA AAATTTATGA ATACCAAAAC TACCTAAGAA	780
CAATGCTAAT AAAATATAAA TAACTTTGTT TACTTGCAAT TCTTTCCCTC CAGTGAATT	840
GCTTATAATG ACATTAGCTT CTCTTTTAT TATACCCACT TTTAGTTCAA ACATTCTAGT	900

TTAAGCATTC CCAATCATCT AAATTTTCAGT TATTCAATCC TTACAATAAA TTTAGGATTA	960
CATTTTCAGTT GCATTGTATT ATTTTACGTG TGAAATATAC GTAATGAATC ACATGACAAy	1020
CTyCAAATTG AAAAATATAC ATTCTATGAT GTAAGGTCGC ATTTTTAATA TATTTACGTn	1080
AAAATAGTTT GGATG	1095

(2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

GACATCCATA CCAAGTTCAT TGATTAATTG TGC GTTCTTT TTAGGTGATA ATGTGATTGC	60
ACTGCCAAAA TAATCATAGC CATGTTCTAC AETGCTTTC GCTACAATAT CCAAACGCAT	120
TTCAAAACAA GCGGTACAAC GTAAGCCGCC TTCTTTTTCA TCAGCTAATT CTTTATCCTT	180
CACCATTTTC ACAAACTTAT GTGGTTCATA AGGTGCTTCA ATATACTTCA CATTGCGACC	240
AGTCTTGCGA TTAAAATCTT CCACAAATTG TTCTTGCACT TTAGCACGTC GTAAGTATC	300
ATTTTTTCGGA TGAATATTTG AATTCGCGAA ATAAATTGCA ATGTCTGCAT ATTGTGTTAA	360
AAACTCTAAT GTATATGTAC TACAAGGTGC ACAACAATA TGCAATAAGa TTTTAGGTCT	420
GATTGCTTCT CTTTCCCACT GsCCGATTAA TnTCTTCAAC ACCTTGTCCTA TAATTAATTT	480
GTnGATTTn	489

(2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

CGTACTGCAT CATTTGTTGA AAAATTTGCA AACTTCTTCA AGATGTTATG GCTTAGACTT	60
AAAGCGATGA AGCACTACAA AGCCTTAAAT AAAGAATCTA AGAAGCAAGA ATTTGAAAAT	120
TCATTCAAAG ATGTTCAAAA AATTATGCGT ATTGGAATC ACAATATTAT TTTACGCTTA	180
AAAGAAGAAC AAAATAGTAC AAATGTACTT GAGGTTAGCT TAGTCATTAA TCATTACTAT	240
GATATGAGTC GCTCATTAAG GTGGCGTGCA CAACGTCGAA AAGAACGTCA AGAAAACAGC	300
AATCAAATCA TACCGCAAGC TATGTTCCAT AACCACAAAT TGGAAGCATT GTACTTACAA	360

CGTCATCTTT TAGATGAATT AATTCGCAAA AATAAAATCA ACAATATCGT TGCAGCTCAA	420
ATTCGAGAAA ATATCAATTa CAACGAAATT GTCTTGTCTT TACAGTCCAA ACATTaAGCA	480
AGaCwTaCaw TmCCCCCGTA CATATGAGAC AAAGTCATTA TCATCTCATA TGTACGGGGT	540
TTTTATATTC AACATCAAAA AATCAGATTG ATGAAAAGTA AATAACCTTT CATCAATCCG	600
ATTTGATTAT AGAATCTATT TTTTAAGTTT AAATGGAATT GTACATACGT TAACATTCTT	660
TTGATAAATT AAATACAATT TCATACGCAA ACTAGTTTGA TTGTGTAATA AATTATGCCA	720
ACGTTTCTTA GTAATAAATT CTGGTATCAC TACTGTAATC AATAGTTTT GATCGTTGGC	780
TTTACGATTA ATCTTATCGA TAAAACGTGA AATTGGTCGT ATAATACTGC GATATTCCGA	840
ATGTAAAATA ACTAATCTTA CATCTGGGAA ATGACGTTTC CATTTCTCTT GGAATGCTTT	900
TTCATCTTCA TCTCCAAATG ATACATGTAC TGCTATGACA TCATTATTCG CAAGCATTTG	960
TGCGTAATAA ATAGACTTAT CAACTGCTGT TGTAATACTT GTTATCGGCA CAATTGCTAA	1020
ATTACGATCT ACCACGTCCA CATTAGAAC ATCAATGTCA GAACGTAATT GTTCTGCGAT	1080
ATCTCGATAA TGkTTGkTAA TTTTCAAGAA GAAAATCACC ACGAACGGCA AGAAAATAAG	1140
TATCGGCCAT ACTTGGCTAA ATTTAGTTAT GAGTAAAATC cATAAnAACA ATAAATGTCA	1200
CGATACCACC AAGTAAGTTC ACAGACAACT TACTTAACCA ATTCTTAGGA CGTTCATGAA	1260
TCCATTTAAT AACCATACCG AATTGTG	1287

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

GCCTCCTTTC CTATATCCAT GGGTGTCTTA GTTGGGAATG GCTTATCCC TATCCCAAAC	60
ATCTGTCAAT TCAAGACTAT CACTGTATAC TAAATCGCCT nTCTATACnT CCATnCATTT	120
CATTTTCCAG TTGGAACAAT TTGTTTAATT ATTTTAAATA TCATTATCAA TCCAGAAGTA	180
TTTACTATTC ACTTTTACAA TAATCAATCA TTTAACTACA CATGGGTTAGT CGGTGGTTTG	240
CTTGGGGTTA GCTTTTAAAC TGGCAATTTA TTGTTATTGC CAAAATTAGG TGCAACATTA	300
ACTGTAATTG CAACAGTTGC GGGTCAAATT ATTATGGGTG TCATTATTGA TACATTTGGA	360
TTATTTGGCG CTACAATTCA TGATTTTAAT TTAATTAAAG CAATTGGAGT ATTGTTACTC	420
ATTGTCGGCA TCGTCATAAT GAATCAATT AACAAGAATA ATTTATTACT AACTGATCAA	480

AAGTATTTAC TGTTTTGGCT TCTATTAGGA TTTATTTTTG GTTCTTTCC ACCTATTCAA	540
ACGACAATTA ATAGTGCTTT AGCTAGTCAT ACTCATTAC CAGCCTTTGC ATCATTAGTA	600
TCATTTACAA TTGGGTCAAT AGCGCTATTG ATTTTAACCG CTATTTTTAA TGTTCTTTA	660
AAACTAAAA CAAGTCATTT AAAATTCGGT AAATTAAAGC CTATCTATTT TACTGGCGGT	720
ATACTTGGCA TGGCTTTTGT AACAGCTAAC ATTATCTTAA TGCCTCATAT GGGTGCAGCA	780
TTAACAACAC TTATTGGGAT GTTTGGCCAG ATTCTAATGG GCATATTGAT AGATCACTTT	840
GGATTATTTG GTTCACCTAA AATAGCAATG ACATCCAGAA AAACATTGG TCTATTATGT	900
ATTTTGACAG GCATTATACT TTTAAGATTA TTTTAAATTA ACTTTTAGCT TATCATTTTA	960
ACTTGTAATT ATTTTTAAAA GTGATAAGCT ATTTTTTTGT GGTCTAAAAA TCTTTAGAAA	1020
AGCGTTGATT TGGGTAGTAT GCTTTGACAC AACAAATTTT AATTTAGCAA ATTCGATAGT	1080
CAACTCATT CTAAGACCTA AATTAATGTT ATnTTTTAAT AATTTACACC AAATTAATAG	1140
CAAAAATTAT GTTATTCGTG CTAATATTTT ATAGTTGGTT ATTCAATTAA TTAATAATAA	1200
GTCAAAATGC ACAACTTTTT ATn	1223

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

CACCTTTTTA TCATGCTTAG TTATCAATAA ATCTATATTT TGCTGTTTTA CAATTTTTTT	60
AACTTTATCA ATCTCATTAT CTTGGACTAA ATAAATATAT GATCTTGCAT CTGTTGCTAG	120
AGCTTGTTCTG TGTTTTTCTG ATAAACATA TGTGATGGAA GCGTGAATAA TAATGCCTAA	180
TGTAACAAAA CTGATAATTA ATATACTGCT TATCAATAAC ATTAAGCGGT GGTGAAACTT	240
CATCATTGTT CTTTAGGTCT TTCCAATTTA TAGCCTAAGC CACGCACAGT TTTAATAAGT	300
TGTGGCTTCT TAGGATTATC TTCTAATTTA TCTCTTAAAT GACTGATATG TACATCAACA	360
ATTCTTGAGT CTCCTGCAAA TTCATAATTC CATACCGAT TTAACATATG CTCTCTCGTA	420
ATGACTCTGC CTTGTCTTTC TATCAAATAA AGCA	454

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

TTTATAAGAT TTTATTTACA AATAATTGGT TTTCATATGT ATAAACACTT TTGACTTTCA	60
AATCTTAACG ATAATTCTAT TACAATACAA TCCCCTATTA GAATGATTTA TGTAATAAAA	120
AAAGCGGAGT TTCCCCCAGC TTTTCTAAAC GACTACATAA AATATAAGAT TGCAATTAAA	180
TGCAATAGTG ATGCTATTAC AATAAAAATA TGCCAAATCA TATGAAAATA TGGTCTATTC	240
TTTTGTGCAT AAAACCATGC ACCAATTGTA TAAGACACAC CACCTAAGAA AATGAATAAT	300
ATGAATATCC ATGATGTGCG AATAAAAATA ATTGGTAACA AGATAATACC TACCCAGCCC	360
ATCACTAAAT AGACAATTAA GCTTAACTTT TGGTAACTT TGACAGCTAT GGATTTATAT	420
AAAATCCCCC AAAGTGTCGT TCCCATAAT AA	452

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

CGCTTTTTGC AATAAGTCAT TAGCCGCTTT TAAGCCTCT TCTTTTCGAT CTACAACAAG	60
TAAAATAAAT GGCTTTAACG CTTCTTCTTT TTTCACTTTCA AGCATATCTG GTTTTTGAAC	120
CATTTCAAAT GGAGATTTCA ATCCATTATT ATCGCTCATT TCAATAATTG CATCATACTG	180
TGCTTGTGAC ATACTTGCAA TAGCCTGTTT TGCATTTTCT TGAAGGAAAT ATAAGTTTTT	240
CAATTTAGGA TGCTTATTTA ATGTACTTAA TGTAATCGGT GTAATGTCTT TCTCATAAGA	300
CACTTCAATC ACTGTACTAT TTGTTCTACC AGGAATTGGT GGTTTTTCAT GAATATGCTT	360
TGATACTTCT CCAATTCCAA CGACAGATTG ATTTTTCGTT CGATTATAAA AAATAATATT	420
GTCGCCTTCT TCTAACTGAG TATAAAAATG ATAACCATTA CGTTTAATAC CGTTGTACGT	480
GTGCGTATAA ATCGTATATT GGTTCACAGG TTCAAATTCT TCAGTTTCAG CTAAAAAGAA	540
ATAACGCGGT ATCTTAATTT CGCCTTTACC AAGACCACTT ATTAAATCAA ACTCTTCTGC	600
AGTGATTTGA TTGAACAATG TCTCTTTCAT ATnACTTATA CGAATTCCA AAGCTTCACT	660
ACGCTTTAAA TAATCTGCTG TTAATGGTTT CAATTGTTCA TTAAAACGAA ACTGTACACG	720
TATTTTATTT TGTGCACCTG TTTCAACACT AATAATTTCA CCACATCCAA GTAGTCCAGT	780
ATCCGTCTGA ACTTGATAAA AGATGACTTG ATCTCCTACT TTAGCCTTTT TAAACGCTCT	840

AAATCCTTGA GATGGGTTAA AATGTGCGCC TGATTCAAAT AAAGCTGTTT GTCCTACTAA	900
CGGTTTCATTA TGATTCCAAC GGTTATATCC ACAATTCAAC CAAAAATAAT TCGTTTCTGC	960
TGTCATCTTA ATACTCCTTA ACCTGAATAA ATTTTAGAAA CACTATGAAT TACATTCTTT	1020
tAGTGTCTTCT TATGCAGTTG GACGCGTATG CGAACAACTG TATACCCTTT GTTCACTGCG	1080
ATTTTAATCG CATTTCCTAT AACATTGTAG CGCCCAGGAC ATTAATTTAC GTCCCAGACC	1140
CTTATCGTTT TCACTTCTAA GTAAGTCGAA CTATTTTGCT TTACAACAAG TGC GACTCTA	1200
AATACAGTTG GACACACATA CGAGCAACTG TATACCTTTT AATCAGTTT TATATTTTA	1260
TTTATTATAT CTGTCTTAAT GATAAAAATT GTTACAAACA GTTTAACATA TTTAGCTACC	1320
TATTTTGCAT ATAAAAACA TGCTTGCATA CACTATGCAA TAAAAATTAC AAATnTATAT	1380
ATGATACCAC TATGCTTGCh TATCTCTATA GCGCCATTGA TACACATTTT TAAATATCTA	1440
TACTGCCGTT AGAATTTTAT CATGTCTnAA TT	1472

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

GGTAGTGAAT GGGGTTCAAG ACAACAGTAT TGGAAGTACG AATGAATCAC AGTTTTTAGG	60
AAATTATATT GTAATTAAGC ACGCAGAAAA TGAGTATAGC TTAATAGCTC ATTTACACCA	120
ATATTCAATC ATTGTGAATG AGGGGCAAAA TGTTAAATAT GGTGATATCA TTGGGAAGGT	180
TGGGAATTCT GGCAATTCTA CTGAACCTCA TATACATTTT CAAGTAATGA ATGATAAGAA	240
TATTGAAGCA TGTACATCTT TAAAAATTCG ATTTATAAAT AATCGAGAAC TTATCAAAGG	300
GGATGTGGTC TGCGGATTAC AAGCTGAATG ATGGCGATAC TTATAAAATC TCGAECTAT	360
AAAAATGGTA TAGTGTGAG ATTTTCTTGC TTATTTAGTT AATTCAAAGT GCACGCCGGA	420
TTCATTAGAA GTCGACGTAT TTTTGTTTGT AATAGAGTAA CCGGTCATTG AAATTTTAGA	480
TTCAATATCT GAAGCGGAAT TTGTAGATTC AGGATTATAG AAGCTACATT CATAAGTGTT	540
ATCATCTTTC TTTTAAAGTA TAAACATACC TTTGGCTTTA ACTTCGACTT TAGTGTTGTT	600
AATGTCAAAA GTTTGAGTGC TATTACTATA ATTAACACCA GCCCAAACCG ATTCATTATC	660
TTTCACAACG GGGAAGTCAT CTTCTTGCTT AACGACGTnA CTTCATCTTT CTCTGTCTTA	720
AAGACATCTT TAGATAAGCC TGGATACAAC ACATATCAT ATTTATTGTC AGAATTAGAA	780
TGCTTTT	787

(2) INFORMATION FOR SEQ ID NO: 585:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

```
ATGCTAAATT AGGGGGAATA TTTACGATAA AGAGACCAGA AAAATAATAA AACACATGCT      60
ATAGCGGTAT ACCGTTTATG AATTGAATCA AAAGTACACA GGTGCTAAAG TATGTGCTT      120
TAAATGAAG ACTATTTTTT ATTACAAGAA AATGTATCTA GTAAACTTAA AGTAGCAAGA      180
CCTAATAAAT TTAATGCATG TTGTGCACCT TTTTACCTT GGCCAGCTTC GAAATGTTTG      240
TAAGCAGCTA CACTTAAAT GCCTATCGTT GATAGTGATG CAAGGCGAGA AATGTTTTTA      300
TTGATAAAGC TAGCTGAGTA TAAAGCAGCA GTAGTTGCTT CTGCAATGCC GACGTATTTT      360
ACAAGTTCTT TTTGCAAGCC AAAAGTATGT TCAAACAGTT CAATCATACC CTTATCTTCT      420
TGCAATTTAG GTTTACTGGC TTGGTATAGC TCTTTCGCAA GTTTTAAATT CGTTGCGTAA      480
CGCAAAATCA TATTTAATTC CTCCCAATAT TTGATTTTTTGTGAAAGATG ATTACTTTAT      540
CATTTTTACC CGTTTCTATA AAAATGAATC AATTATGTAA CGTATGTGTA GTTTAGGAAT      600
GTTTGCTATG GAAATATAAT TCTGTTCACT CAAAATGTAT GAAATTAATG TGTAGTTTTG      660
TCGAGTTGCT CTTTAAATTT GGTTAGATTG TTTTITAGAG AAGCGGTACT ATTTTAAAGT      720
GCATCAACAG ATTTACCTTC GTTTTGAGAC ATTGAGTTTA TTACAGCACG AAGTTCTGTT      780
TCTAGTATGT CaGCGTCGCT TTAGCATTAG AACTTAaTat TTAtAcTCTT      830
```

(2) INFORMATION FOR SEQ ID NO: 586:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

```
TTAGGACGTT TTTACAATCA GTACAATGAG CTCATTGTTA TTAGTCCTTT AACGGCGTCT      60
TTTAATGCTG GCGCTACATT TGGGCGATTT CATCATTTAA TTGATACTGA AACTTTAGCA      120
AAATTAGAAC ATGAAAAAGG ACATTATTAT CAGAAGATGA TATGTGATGA CAATGTAGAA      180
ATGATTTCTA TAAATAACAT ACCGAAATAT CCGAGAAATC ATAATGTATT AACTAATCAT      240
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GACTCATACG AATATTCATT GAATTTAGGA AGTAGTAATA GTTÆTCAAA GTATGAGCTT	300
ACCTTAGATG ATATTTATGT TGGTGCTACC TTTtAACAAA TTATATTTAT ATTCTAGCCm	360
ACtAAATAAAA AGGGkaCtaT TTGaATCaAA CmATaTGtAT TAACCTTTTT TA	412

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

TTCAGTTTGA AATTAATCAT ATAAATTTCT TATGGGAGGG TTGATATCTT AATGATTAAC	60
ATTATTTTCAG CTATAGGATC TATTGGAACA TTTATTATGG CTTTATTTTA TTTTGTATCA	120
GTTTCAGTTC AACTTTATCA AATGAAAATT AGCTTTCTGC CAGCTTTAGG TTTTAACCAA	180
ATTTTATTAG AAAGGGAGGA GGATCAACTT AATATAATGA ATTCGGCAAC AGAAGAGCAT	240
CATCATAAAAG ATTATATTAA ACTATATAAT TTAGGTGGCG GTGCTGCTAA rAAAATTGCA	300
ATAGAGGTTT TATTGGGGAA GGATArAGTC ATTCAGAAAA AATACGTGCA TATTktACCT	360
AGTAAAGAAG GGTACATGTT ACCAATTAAT AAAAATGTGT ACGAAGAATT AGAAAGAACG	420
ATTGAsAACA ATGGTCATGA AGCTGATTTG AATGTACGTA TGACTTÆTA TCATAATGTA	480
AGTCGCAAAAC AACAGGAAGT TATATTAAAA GGTCAAATCG ACCGTTTTAA TACTTATAAT	540
AATAAAGAAA TTTATGATTT GCAGTTTATC TAAAAATTGA TTTAAGAGGG TAGTTGTTTA	600
TTGCGAAAAA TATCATTCAA TTTTAATGAA ATAATGGCGT CATTACTATA AAATATTACT	660
TTATGTTGTA ATGCATTTTT CTATAAGATA GAACTAAAAG GAGGGGCAAA GATGCAAATT	720
AGACAAATAC ATCAACATGA CTTTGCTCAA GTGGACCAGT TAATTAGAAC GGCATTTGAA	780
AATAGTGAAC ATGGTTATGG TAATGAATCA GAGCTAGTAG ACCAAATTCG TCTAAGTGAT	840
ACGTATGACA ATACCTTAGA ATTAGTAGT GTTCTTCAAA ATGAAGTTGT AGGGCACGGT	900
TTACTAAGTG AAGTTTATCT TGATAACGAG GCACAACGGG AAATTGGATT AGTGTTAGCA	960
CCTGTATCTG TTGATATTCA TCATCAAAAT AAAGGTATTG GGAAGCGATT GATTCAAGCA	1020
TTAGAACGAG AAGCAATATT AAAAGGATAT AATTTTATCA GTGTATTAGG ATGCCGACG	1080
TATTATGCCA ATCTAGGATA TCAACGCGCA AGTATGTACG ACATTTATCC ACCATATGAT	1140
GGTATACCAG ACGAAGCGTT TTTAATTAAA GAATTAAAAG TGAACAGTTT AGCGGGAAAA	1200
ACAGGTACCA TAAATTACAC ATCTGCTTTT GAAAAAATAT GATTTCAAGC TAGGATTACA	1260
TTAGGTAGAG TTCATATTAA TAATAAAAAA TGTTTGCAAT CAAATCGTAC GTTGTCGTTT	1320

GTAATTCTTA AAATAGCAAT AAATAAAATG TTTGTTAGTA AAGTATTATT GTGGATAATA	1380
AAATATCGAT ACAAATTAAT TGCTATAATG CAaTTTTAGT GTATAATTCC ATTGACAGAG	1440
ATTAAATATA TCTTTAAAGG GTATATAGTT AATATAAAT GACTTTTTTAA AAAGAGGGAA	1500
TAAAATGAAT ATGAAGAAAA AAGAAAAACA CGCAATTCGG AAAAAATCGA TTGGCGTGGC	1560
TTCAGTGCTT GTAGGTACGT TAATCGGTTT TGGACTACTC AGCAGTAAAG AAGCAGATGC	1620
AAGTGAAAAT AGTGTTACGC AATCTGATAG CGCAAGTAAC GAAAGCAAAA GTAATGATTC	1680
AAGTAGCGTT AGTGCTGCAC CTAAAACAGA CGACACAAAC GTGAGTGATa CTAAAACATC	1740
GTCAAACACT AATAATGGCG AAACGAGTGT GGCACAAAAT CCAGCACAAAC AGGAAACGAC	1800
ACAATCATCA TCAACAAATG CAACTACGGA AGAAACGCCG GTAACTGGTG AAGCTACTAC	1860
TACGACAACG AATCAAGCTA ATACACCGGC AACAACTCAA TCAAGCAATA CAAATGCGGA	1920
GGAATTAGTG AATCAAACAA GTAATGAAAC GACTTCTAAT GATACTAATA CAGTATCATC	1980
TGTAAATTCA CCTCAAATTT CTACAAATGC GGAAAATGTT TCAACAACGC AAGATACTTC	2040
AACTGAAGCA ACACCTTCAA ACAATGAATC AGCTCCACAG AGACAGATG CAAGTAATAA	2100
AGATGTAGTT AATCAAGCGG TTAATACAAG TGCGCCTAGA ATGAGAGCAT TTAGTTTAGC	2160
GGCAGTAGCT GCAGATGCAC CGGTAGCTGG CACAGATATT ACGAATCAGT TGACGAATGT	2220
GACAGTTGGT ATTGACTCTG GTACGACTGT GTATCCGCAC CAAGCAGGTT ATGTCAAAC	2280
GAATTATGGT TTTTCAGTGC CTAATTCTGC TGTAAAGGT GACACATTCA AAATAACTGT	2340
ACCTAAAGAA TTAAACTTAA ATGGTGTAAC TTCAACTGCT AAAGTGCCAC CAATTATGGC	2400
TGGAGATCAA GTATTGGCAA ATGGTGTAAT CGATAGTGAT GGTAATGTTA TTTATACATT	2460
TACAGACTAT GTAAATACTA AAGATGATGT AAAAGCAACT TTGACCATGC CCGCTTATAT	2520
TGACCCTGAA AATGTTAAAA AGACAGGTAA TGTGACATTG GCTACTGGCA TAGGTAGTAC	2580
AACAGCAAAC AAAACAGTAT TAGTAGATTA TGAAAAATAT GGTAAGTTTT ATAACCTATC	2640
TATTAAAGGT ACAATTGACC AAATCGATAA AACAAATAAT ACGTATCGTCAGACAATTTA	2700
TGTCAATCCA AGTGGAGATA ACGTTATTGC GCCGGTTTTA ACAGGTAATT TAAAACCAAA	2760
TACGGATAGT AATGCATTAA TAGATCAGCA AAATACAAGT ATTAAAGTAT ATAAAGTAGA	2820
TAATGCAGCT GATTTATCTG AAAGTTACTT TGTGAATCCA GAAAACCTTG AGGATGTCAC	2880
TAATAGTGTG AATATTACAT TCCCAAATCC AAATCAATAT AAAGTAGAGT TTAATACGCC	2940
TGATGATCAA ATTACAACAC CGTATATAGT AGTTGTTAAT GGTCATATTG ATCCGAATAG	3000
CAAAGGTGAT TTAGCTTTAC GTTCAACTTT ATATGGGTAT AACTCGAATA TAATTTGGCG	3060
CTCTATGTCA TGGGACAACG AAGTAGCATT TATAACGGA TCAGGTTCTG GTGACGGTAT	3120

CGATAAACCA GTTGTTCCTG AACAAACCTGA TGAGCCTGGT GAAATTGAAC CAATTCCAGA	3180
GGATTTCAGAT TCTGACCCAG GTTCAGATTC TGGCAGCGAT TCTAATTCAG ATAGCGGTTC	3240
AGATTCGGGT AGTGATTCTA CATCAGATAG TGGTTCAGAT TCAGCGAGTG ATTCAGATTC	3300
AGCAAGTGAT TCAGACTCAG CGAGTGATTC AGATTTCAGCA AGCGATTCCG ACTCAGCGAG	3360
CGATTCCGAC TCAGACAATG ACTCGGATTC AGATAGCGAT TCTGACTCAG ACAGTGA CTC	3420
AGATTCCGAC AGTGA CTCAG ATTCAGATAG CGATTCTGAC TCAGACAGTG ACTCGGATTC	3480
AGATAGCGAT TCAGATTTCAG ATAGCGATTC AGATTCCGAC AGTGATTCCG ACTCAGACAG	3540
CGATTCTGAC TCCGACAGTG ATTCCGACTC AGACAGCGAT TCAGATTCCG ACAGTGATTC	3600
CGACTCAGAT AGCGATTCCG ACTCAGATAG CGACTCAGAT TCAGACAGCG ATTCAGATTC	3660
AGACAGCGAT TCAGATTTCAG ATAGCGATTC AGATTCCGACAGTGACTCAG ATTCCGACAG	3720
TGACTCGGAT TCAGATAGCG ATTCAGATTC CGACAGTGAC TCAGATTCCG ACAGTGA CTC	3780
AGACTCAGAC AGTGATTTCGG ATTCAGCGAG TGATTTCGGAT TCAGATAGTG ATTCCGACTC	3840
CGACAGTGAC TCGGATTTCAG ATAGCGACTC AGACTCGGAT AGCGACTCGG ATTCAGATAG	3900
CGATTCCGAC TCAGATAGCG ATTCAGAA TC AGACAGCGAT TCAGATTTCAG ACAGCGACTC	3960
AGACAGTGAC TCAGATTTCAG ATAGTGA CTC GGATTTCAGCG AGTGATTTCAG ACTCAGGTAG	4020
TGACTCCGAT TCATCAAGTG ATTCCGACTC AGAAAGTGAT TCAAATAGCG ATTCCGAGTC	4080
AGTTTCTAAC AATAATGTAG TTCGCCTAA TTCACCTAAA AATGGTACTA ATGCTTCTAA	4140
TAAAAATGAG GCTAAAGATA GTAAAGAACC ATTACCAGAT ACAGGTTC TG AAGATGAAGC	4200
AAATACGTCA CTAATTTGGG GATTATTAGC ATCAATAGGT TCATTACTAC TTTTCAGAAG	4260
AAAAAAGAA AATAAAGATA AGAAATAAGT AATAATGATA TTAAATAT CATATGATTC	4320
ATGAAg nAAc rCCTTAAAG GTGGCTTTTT TACTTG GATT TTCCAAATAT ATTGTTTGAA	4380
TATAATTAAT AATTAATTCA TCAACAGTTA ATTATTTTAA AAAGGTAGAT GTTATATAAT	4440
TTGGCTTGGC GAAAAAATAG GGTGTAAGGT AGGTTGT TAA TTAGGGAAAA TTAAGGAGAA	4500
AATACAGTTG AAAAATAAAT TGCTAGTTTT ATCATTGGGA GCATTATGTG TATCACAAT	4560
TTGGGAAAGT AATCGTGCGA GTGCAGTGGT TTCTGGGGAG AAGAATCCAT ATGTATCTAG	4620
TCGTTGAAAC TGACTAATAA TAAAAATAAA TCTAGAACAG TAGAAGAGTA TAAGAAAAGA	4680
TTGGATGATT TCAATATGGT CCnTTCCCA	4709

(2) INFORMATION FOR SEQ ID NO: 588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1554 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

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CTTTTTTAAAt TAwCgGaAtA TTGtCaTgaT tAcAcTTCGt TAGGGTTTAc gTCGtAATTT      60
CATTTTaaTAA gCgCTTCaC ATTAAtGTG gTAmCCTTTA ATTCGCCAGT AGAAACATCA      120
CAGTAACTAA GCGCAATTTc AGGTTGATTC ATAACAAAAC TTAAATATAGTTATTTTGT      180
TTATCATCTA CACCACCTTG CTCCATCACA GTTCCTGGAG TCACAATTCT TACTACCTCA      240
CGTCTAACCA TACCTTTCGT TTGTTTCGGA TCTTCCATCT GTTCACAAAT AGCTACTTTA      300
TATCCATTAT TAACAAGTGT ATCTATATAA CTATCTGCAG AATGATACGG AACACCACAC      360
ATCGGAATTG GATTTTCTTT TTTAGCATCT CTTTtagTTA AAGTAATTTc AAGTAyACGT      420
GATGCCTCCT TGGCATCTTC ATAAACATT TCATAGAAAT CACCTAGTCT AAAAAATAAT      480
AAGCAATCTT GGTATTCTGA TTTTATTTTT AAATATTGCT GCATCATTGG TGTAACATTA      540
GACATATTAT TTCTTCACAA CCCTTGTCtC TTTTAAAAAT TTGTCTTTAC AATATATTCG      600
TTTGTAAGyT TTTAATTAT TAATTATTTA ACTTATACAT TTTAACATAC TTACTTTTAC      660
AAACCTATTC ATACCATATA ATCACGAAGC ATCTTAAATG TATAAGAAAA CGCCTCAAAC      720
CTAATAAAAT GTGTCAATAG CATGTTTAgA ATTAAATTAA AATTCTAACA TTCAAGaAT      780
TTAATTAAGT AAGGGCGTTC AATATTAAAA TGAACAATGA CTCTGTTTGA AATCATATAT      840
CATAAAATTA TTTTATAAAC CTTTGAAGAA TACCACGTTT TTTTAGAGTA ATTAATAAGA      900
AATAACTTAT AATAGATCCG ATAGCACTTG aGACTATGaA CGTAATCATT AACGGTTTAA      960
TGAAGAAGTC TTGAAGCCCA AGGaAATATG CTAATGGtAT aCaAATTAAA cTTCCgATGA      1020
CaCCAGTTCC aAGTACTTCa CCGACCGCGG CCaTAAATAT ATGTTTACGA TATnygTAAA      1080
ACATACTAGC CAATAAAACT CCAATCATAC TACCCGAAAA TGCAAAAGst GTACCAGTAC      1140
CAAAAAGAAC TCTTAAATTT GATGATATAA GCGCTTGAG TAATCCATAC CAAGGACCTA      1200
CTATGACCGC ACTTAATACA TTTACAAAAT GCTGTACTGG TGCTGCCTTA ACTGGTCCTA      1260
GAGGAATGAT GATAATACTG CTTAATACAA CATTTATTGC AATTAAAAGT GCAGTTATAG      1320
CCAGTTTTCT TGATTTcATA TGATTGTTCT CCTTTTTGTT TGTAATTAAT CACTATGCTT      1380
GGCTTTATTA TGGTCATTTA AACGTGTTTC CATtGTTGAT ACAAACATTT TCAATAATTG      1440
ATTCGCTTCA TATTGTGAAG TTTGAACTG TTCAACTATG GGCAATGTAT TTATTTCTGC      1500
TTCTAtACTC TGAATGGtAT GTTCCGACTG nTCCAGCGCA TTTGTTTCCC GnAA      1554
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(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 638 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

TTTTGACGAA AAAAGTTGAT TTACAAATAT ATAAACGTTG TGATTTCAAT GTTTGTATAG	60
GGAATAGACG TATGATATAA TAGGGAAGTT GAAAAAATAA ATTAGTTAAT CATGGAGGTA	120
TATATACATG ACAGCAACTT GGGAAAAAAA GGAAGGTAAC GAAGGTTTAT TAACTGTTAC	180
TGTTCTTGCA GAAAAAGTAA ACAAAGCrCT GAGAGATCCC CTATAATTT CCCCAAAGCG	240
TAACCATGTG TGAATAAATT TTGAGCTAGT AGGGTTGCAG CCACGAGTAA GTCTTCCCTT	300
GTTATTGTGT AGCCAGAATG CCGCAAAACT TCCATGCCTA AGCGAACTGT TGAGAGTACG	360
TTTCGATTTT TGACTGTGTT AGCCTGGAAG TGCTTGTCCC AACCTTGTTT CTGAGCATGA	420
ACGsCCGCAA GCCAACATGT TAGTTGAAGC ATCAGGGCGA TTAGCAGCAT GmTATCAAAA	480
CGCTCTGAGC TGCTCGTTTCG GCTATGGCGT AGGCcTAGTC CGTAGgCAGG ACTTTTCAAG	540
TCTCGGAAGG yTTCTTCAAT CTGCATTTCG TTCGAATAGA TATTAACAAG TTGTTTGGGT	600
GTTcGAATtk CAACArGTaA GTt/GtTGCT AGAnCCCCA	638

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AAAATATTCC CGTACATTTT GATGTCTGTA GGGGCTTTTT TGACTTTAGG ATTTGTCATT	60
TTTTCAATTC ATAAAGGGAG ACGAACGAAA AATGAATCAG CACGTAAAAG TAACATTTGA	120
TTTTACTAAT TATAATTACG GCACATATGA CTTAGCAGTA CCAGtTATT TACCGATAAA	180
AAACTTAATA GCTTTAGTAT TGGATAGTTT GGACATTTCA ATATTTGATG TCAATACACA	240
AATTAAAGTG ATGACGAAAG GTCAATTACT TGTTGAAAAT GATCGACTCA TTGATTATCA	300
AATCGCTGAT GGAGATATTT TGAAGTTACT ATAGGAGGGA AAATAGATGG TAAAAATCA	360
TAACCCTAAA AATGAAATGC aAGATATGTT AACGCCTTTA GATGCTGAAG AAGCAGCTAA	420
AACAAAATTA CGCTTAGATA TGAGAGAGAT TCCTAAGTCT TCAATTAAAC CAGAACATTT	480
TCATTTAATG TACTTATTAG AACAAATTC TCCATATTTT ATAGATGCTG AATTAAGTGA	540
ACTACGTGAC aGTTTCCaAA TACATtATGA CATTAATGAc AATCATAACAC CTTTTGATAA	600

TATTAAATCA TTTACTAAAA ATGAAAAATT ACGTTACTTA CTCAATATCA AAAATTTAGA	660
AGAAgTAAAT CGTACACGCT ACACATTTGT GTTGGCACCA GATGAATTAT TTTTCACAAG	720
AGATGGATTA CCCATTGCTA AAACAAGAGG GTTACAAAAT GTTGTGATC C A TACCTGT	780
GTCAGAAGCT GAATTTTTTAA CAAGATATAA AGCGCTGGTT ATCTGTGCAT TCAATGAGAA	840
ACAATCATTT GATGCTTTAG TTGAAGGAAA CTTAGAACTA CATAAAGGAA CGCCATTTGA	900
AACTAAAGTT ATTGAAGCGG CAACGTTAGA TTTACTAACG GCATTTTTAG ATGAACAGTA	960
TCAGAAACAA GAACAAGATT ATAGTCAAAA TTATGCATAT GTACGCAAAG TAGGACATAC	1020
CGTTTTCAAA TGGGTTGCTA TCGGTATGAC AACGTTAAGT GTTTTATTAA TTGCATTCTT	1080
AGCCTTTTTTA TATTTTTTCAG TAATGAAGCA TAATGAGCGC ATTGAAAAAG GATACCAAGC	1140
ATTTGTAAAG GATGtTATAC GCAAGTACTA AAT E GTATG ATGATTTAGA TGGTaAAAAat	1200
TgaTAAAGAG GCACTTTACA TTTATGCCAA AAGTTATATC CA	1242

(2) INFORMATION FOR SEQ ID NO: 591:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 744 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

TTCCAGATAG AGCCTTAGTT GCTGCCGCTG AATTGTCTGA TCGTTACATC ACTGATCGTT	60
TTTTTACCAG ATAAAGCGAT TGATTTAGTT GACCAAGCAT GTGCAACAAT TCGT A GGAA	120
ATGGGATCAA ATCCAACCTGA ATTGGATCAA GTTAATAGAC GTGTCATGCA ATTAGAAATT	180
GAAGAAAGCG CACTTAAAAA TGAATCTGAC AATGCGAGCA AACAGAGATT ACAAGAACTA	240
CAAGAAGAGC TTGCCAATGA AAAAGAGAAA CAAGCAGCAC TTCAATCTCG TGTAGAATCA	300
GAAAAAGAAA AAATAGCAAA TTTACAAGAA AAACGTGCGC AACTAGATGA AAGTAGACAA	360
GCGTTGGAAG ATGCACAAAC AAATAACAAT TTAGAAAAAG CTGCTGAACT ACAATATGGA	420
ACAATTCCTC AATTGGAAAA AGAACTTAGA GAATTAGAGG ATAATTTCCTA AGATGAGCAA	480
GGTGAAGATA CAGATCGAAT GATTCGTGAA GTTGTAAG A G ACGAAGAAAT TGGCGATATT	540
GTCAGCCAAT GGACAGGCAT ACCAGTTTCA AAATTAGTTG AAACAGAACG TGAAAAATTA	600
CTTCACTTAA GTGACATCTT GCATAAACGT GTTGTAGGTC AAGATAAAGC GGTTGACCTG	660
GTTTCAGATG CAGTAGTTAG AGCAAGAGCA GGTATTAAAG TnCAAACAGA CCTATTGGTA	720
GTTTCTnATT CCTAGGTCCn ACTG	744

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

TTGTTATAGT GTCTGAATCT GTGTAACCTCT TGCCCATGTG TTCTGAGTAA AGCACCCACT	60
GTTTATTTAC TTTTCGTTGT AGTCTAGCTT CGTGTAGTAG TTTGTTTAAAC TTTTGTGCTG	120
ATATACCGTA GTCTCCGCG ATTTGAGTTG TGGCTAATGT GCCAGTTGAT TTTAAGATTT	180
CATCAACATA ATCTGCTTTG GGTTTTAGCT CTCCAATTTC TTGTTGTAAA AGTAAGTTTT	240
GCTCTTTTTT TTTCTTATAC TCAGTCAACA CTGTAATGAT GTAGTCTGGA TCTTTTAATG	300
TTTGTTCAAT TACATTGTCT GTTGCGTATA TACCGTGTTCGCGAATAGCT GGTaGGACAT	360
CTGATGTTAC CCAGCGTTTG AATTTTCTAG CGGTTTCTCT AATTTTTTCG TTTTGTCTTT	420
GTTTAGAAGC ATCGAAGATT AGACTGTATA ATCCTGATTC GTTGATAATG ATCATATTTT	480
TGTTTTGACC TGATGCACTA AATTGGTGCG TCAGTTTGTC CTCGCTATCA ACATGATTTT	540
TAATGGCATT GTCTGATCTT GCATATCCTA AAATCTCAGC AATATCTTTT CCTACAAAAT	600
AAGGTTTCGT TTCAATTTCT ACTGTTCTTA CTGGTAGCTC TTTAAAATTA AATGTTTGTA	660
ATGCTTGCAT TTGAGTATCC TCCTTTTTCC TCAACACCCA CATTGAGCAG ACGGTTATCG	720
CAATGACTAT CGAATGTATT TAAACGCGGC TCATATCATC GCCAGcTCTC GCTCACATCT	780
GCTCAATGTG GATGTTGATA AGCGTGGTTA TATTAAGAAG TGAATGTTAC TGATTCACTT	840
TCCGCCACTC TGTTAAATCA GTAACCTTGT TATCGCTTTC AACACCGTTA AGCTTGTCTA	900
ACGCTTTCAC TACTTTTTGG AACTCTTTGA TAGCACTtCG TAGCTTTTA GTAATTTTCA	960
CTTCTACCAT TTCCAAACCA GCAAATGCGT CTTGTTTATT CATGCTTAGA TGTTTGTTGA	1020
AAAGATCTCG AGTGTATCTT ATTTCTTTAA GTGATTTATC ATAAGCTTCA ATTTGTCCTG	1080
AAAGGTTATG ATATTTTAGT TGTAAGTTTA CTAATTTTAA TGATTGGTCT TGCATTTGTT	1140
ATGTCTCCTT TAAGATGTTT GTTTGCGTTT CGTGTACTTT GTGGGTAAAA AAATATCTCC	1200
AATATTTTCG TCAAAAAAAT CAGCGATAAT AACATCTCA TCATTCTTAA ATTGATGCTT	1260
TCCTAATTCT TTAAACGAT AACCTTCAGT TGATATATTC AAGAGGTTTG CTAAATCTTC	1320
TTGAGTACAC TTTCTTTCTT TTCTCAACTT TATTAAATTC CATTGCATGT TGTCACCTCC	1380
CGCTTTACAA AACCTACTAT ACACGATACG GTACTTGnGT CAACATAAAA GTTTGCTTTT	1440
CGTGTATTT	1449

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

ACCAAAAACA CTTTCTAAAG AAATTGTTTC AGAACCATTT GCTAAAAACCAATTACGTGA	60
AAAAGCTCGT CTAATAACA TTAAAGGTTT AGAGATTCCA AGAGTTTCAT ACACTTTAGA	120
CGATGATGAT TTCATTACAG ACGTAGAAAC AGCAAAAGAA TTAAAAGCAA AAGGTGATAC	180
AGTCAAGTTC ACTACTAATA AATTCAAAGT ATTTGCTGCA ATTTCAGATA CTGTAATTCA	240
TGGATCAGAT GTAGATTTAG TAAACTGGGT TGAAAACGCA CTACAATCAG GATTAGCAGC	300
TAAAGAGCGT AAAGATGCCT TAGCAGTAAG TCCTAAATCT GGATTAGAAC ACATGTCATT	360
TTATAATGGA TCTGTTAAAG AAGTTGARGG AGCAGACATG TATGATGCTA TTATTAACGC	420
TTTAGCAGAT TTACATGAAG ATTATCGTGA TACGCAACA ATTTATATGC GATATGCAGA	480
TTATGTCAA ATTATTAGTG TTCTTTCAA TGGAACAACA AATTTCTTTG ACACACCAGC	540
AGAAAAAGTA TTTGGCAAAC CAGTAGTATT TACAGATGCA GCAGTTAAAC CTATTGTGGG	600
AGATTTCAAT TATTTTGGAA TTAACATGA TGGAACAAC TATGACACTG ATAAAGAT	660
TAAAAAAGGC GAATATTTGT TTGTATTAAC AGCATGGTAT GATCAGCAAC GTACATTAGA	720
CAGTGCATTC AGAATTGCAA AAGCAAAAGA AAATACAGGt CCATTACCCA GCTAAGCCCC	780
AAAAGGTTAA TGTAACAGCT AAGGCTAAAT CAGCTGTAAT ATCAGCCGAA TAGGGGTGAT	840
GAAATGAGTT TAGAGAAAk TAAATTGTGG TTGAGAATTG ACTATAATTT CGAAAATGAT	900
TTAATTGAAG GTCTCATTCA ATCGGCTAAG TCTGAATTAC TATTAAGTGG GGThCCAGAT	960
TATGACAAAG ATGACTTGGA ATACCCGCTT TTTTGTACAG CGATTAAATA TATCATTGCA	1020
AGAGATTATG AAAGTCGTGG ATACTCAAAT GACCAATCTAGAAGCAAGGT GTTTAATGAA	1080
AAAGGATTGC AAAAAATGAn TTTGAAATTA AAAAAGTGGT AGGTGATTTT TAAATGGAAT	1140
TTAATGAATT TAAAGATCGC GCGTATnTTT	1170

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

TGAAGGGTGT TTTGTTTATG GCCAATTGCT GTGTTATTAA AnCGAATGTT TCGAATGGAA	60
CACAATCCAT TATTTGAATA TATTTATCAA CAAAAAGAAG ACATTGATGC ATGTTATTTT	120
ATCATTCCGG AAGAGGACAT GTCTTCAGCT TCTGATTTGA AAGCACAGTT TTATCGCGGT	180
ACTTTGCAGC GCTTTTACCA AtCnTTGCAC GCAGAAAAGC TTACACCTTA TGTTATGTCT	240
TATGACGATA TCATTTTATT TTGTAAAGAA AACAAATATCT CTGAAGTAGT GACTGCGGGT	300
GATATTATGA GTTATCATCT TGAAGAATAT GATATTTTAC ATCAACGTTT TTTATTCAAT	360
GAAGCACGCA TTGCCGTTAC TTTGATACGT GGAATCATT ACTTTAAAGC GAGTAAAACA	420
ATGAATCAAC AAGGGGAGCC ATACAATGTT TTTACTAGTT TCATAAAAA ATGGCGACCT	480
TACTTGAGGC ATAGAGACGT ATATCACTAT GATTTAAAAT CATTTCGAAAA CTTTGTCATT	540
GCATCACCTG ATGATTTAGT GTTTGATGAC ATAGCATTTG GATCCTCACA aATAATTGAA	600
CAGatAAATG GCAACATTTT TTAGATCAAG ATATACAGAA TTACGAAAGC GGAAGAGACT	660
ATTTACCTGA AGTATTAACA AGTCAGCTAA GTGTTGCTTT AGCATATGGA TTATTAGATA	720
TTATTGAAAT TTTAATGAT TTATTGGCGC GTTATGATGA AGATGAGGCA AACTATGAAG	780
CATTTATACG TGAAGTCATT TTTAGAGAAT TTTATTATGT GTTAATGACA CAGTATCCTG	840
AAACCTCATA CCAAGCTTTC AAACCTAAAT ATCGACAGAT AAAATGGTCG CAAAATGAAG	900
CGGATTTTAA TGCATGGTGC GAAGGGCAAA CAGGATTTCC AATCATTGAT GCAGCAATAA	960
TGGAATTGAC ACAAACTGGT TTTATGCATA ATCGAATGAG AATGGTTGTG TCGCAATTTT	1020
TAACCAAAGA TTTATTTATA GATTGGACAT GGGGAGAAAA ATTCTTTAGAAAGCACCTTA	1080
TTGACTATGA TGCAGCATCA AATATTCATG GATGGCAATG GTCTGCTTCT ACAGGTACGG	1140
ATGCAGTGCC GTATTTTAGA ATGTTTAATC CAATAAGACA GAGTGAACGC TTTGATGCTA	1200
AAGCTTTGTA TATCAAAACA TATCTTCCGA TTTTAAATCA AATTGATGCA AAATATTTGC	1260
ATGATACACA ACGCAATGAG TCCAACCTTT TTGAACAGGG GATTGAATTA GGTAGTCATT	1320
ATCCAAGACA AATGGTAGAT CATCAAGAAA AACGTACACA AGTTTTAGCT ACATTTAAAG	1380
CGCTAGACTA ATT	1393

(2) INFORMATION FOR SEQ ID NO: 595

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

TTAACTTGAA AGATTTCCCC GACATCTATA ACTTGTATAA TGTGTATATG TCGTTTTTATAG	60
AGTATAATAA TATAAAAGAC CTTGAATAAA GGAGGGATAA TATGACTACA TTTGATGCTA	120
AAAAATTAAA AAAAGAATAT CTTGATTGGT ATAATCAGAC CTTAGAGTTT TCTAATTTAT	180
CAAACAATGT AGTAAGwATA GATACTCCTT TTAAAGATAA TTCTTTAGAT AATTAAATAA	240
TTTACGCTTT ATACGATCAG TCCAGAGACA TGATTACACT GACAGATGAC GGCTATACTA	300
TATtTGATTT AGAAAATAAT GGTATTTCTT TAAATAAATC AAAAAAACGT AAAAAGATTT	360
TTGAAGAGCA CCTTTCAGCT TACGGTATTA AATATAACGA TAAAACTCAC GAAATTTTTG	420
TTCAAACATA CTTTAAAAAT TTTAATAAAT CGAAACATAA TTTATTACAG TGCCTTATAT	480
TTGTTAATGA TATGTACTTA CTTTcTAATC CTAAGTCACA GAACATATTT ACAGAAGATG	540
TTGCAAAACAA ATTGGATGAA CATAACATTT ATTACGGAAG AGATTTACCT ATTATAGGAA	600
GCAGTGGTGT TGTTCATAAT TTCGACTTTT TTATAGCGC TAAGAAAAAT CAAAAAGAAA	660
AATTTATCAA TGCTATTTCT AACCCTAATA ATTCTATGAT TATTAAGTCG AAAATAACGG	720
ATGCTATGCA AGCAAAAAAA ATAAAAAGAC ACAGGCAAAA TGAGTTTATT TTTATTTTAA	780
ATGACTCAAA AAAAGAAATA AATGAACATA ATAAAAATCT TCTTCATGAA AACTATATTA	840
GTACAATAGA TTATAGCGAA TTAGATGAAA AGATAGGTTT ATTGATTTAA TATATATAGA	900
CGTGATAATA TCAATGTTTA TATTAAATGA AACGAATTTG AAAATTTCTGA AACAGCTTAA	960
GATAGCAAAT TGAATAGCCT TATTGATAAT GCAGAATCGT CTACACTTAG TTGAACAAAT	1020
TCTATGAGAA TAGATATTGT TAAACTATTT GGGTAGGCGA TTTTATTTTG ACAAGAGTCA	1080
GAAGATTATT TAGTTCATAG TTTAAGTTAC AAATGGCTAA ACTTTATGAA AATGGTATGA	1140
CTAGAATCGA AATTATACTC GAATACGATT TAACACTCTC AATCTTCTCG AACTGAATAA	1200
ATACTGGGTC ATTCAATCAT CAAGACAACT TAATAAGTGA BATAAATGT TCATACCATT	1260
TTGCAAATAT AACCAGATAC TCTCAACAAA ATGTAGAGTT CAAAATTAAA AATGTCCCTA	1320
ATTGGCACAT TGCTGTATGA TAATAAATTC AACTTAGATT TCAACAATAT AACTAATGAT	1380
GCTTATATTT ACCGCGATAT CAAACCAAAC AGCCCATCCA CAAACAAATT AGAATATATC	1401
mTGTTAATAA TAGTAAATGA TATATCTTCC AAAGACCGCA AACT	1484

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

TACCCGTTTT	ACCAGCAGTA	GGTACTACTG	TATCTTTAAA	ACTAACATAT	CCaGTACCaT	60
CTTTATCaTT	AAATGCCaTT	TTGaATCCTT	CTTGAATTTG	TTTGATTTCC	TTTTCAGTAT	120
TATTAACCTT	GTTCAAGAcA	GTGCCATTAA	TTTTCTTCTT	GAGTGGACCA	ACCTCATCTT	180
TATTAGTTGA	TTCATGAATC	GTTAATCCAA	TGTGTGGCTG	TATTCTATAA	CCATCATTCTG	240
CTATAGTTGA	AACATATTGT	GaTAATTGTA	ATGGTGTATA	GGTATCATAT	TGACCAATTG	300
ATAAATCTAG	ATAATTACCT	GGATTATTTG	TTAATGGTTC	GATTGACCT	CTTGTTTCAT	360
TTGGTAAATC	TATCCCTGTT	TTCACACCTA	AGCCTACTTG	ATTTAATCCT	CTTCTTAGCT	420
TTTGGGCAGG	TGAAC TTATG	TCTGAAGGTA	AAGCCATACC	AGAATAATAA	GGGTCTCCCG	480
CTAATTTTAA	TGCTGTTTTA	AACATATATA	CGTTTGATGA	ATGCATCAAA	GCTTGCTTAT	540
CATTAATAGT	TACATGCCCC	TTTTTATTGA	AGTATGATCG	TTTTGTCAAA	CCACCTTGGA	600
AATGTAATGG	TTCATCGACC	ATTGTTTCTC	CAACTTTGAT	AGCTTTATTC	TGATAACCGG	660
CTAATAATGT	TCCACCTTTT	ACAGAAGATC	CAACCGCAAA	TTGAGAAGTA	AACGTACCAA	720
TGTCATAATC	AGTCATTTTA	CCACTCTTAT	TAATCTGCTT	TCCGGCAAGC	GCAAGAATGT	780
CTCCATTTTT	AGGATTTTGT	ACAACCATCA	TTGcATTATC	CATATCTTTG	GCACCTTGAC	840
TGCGAsTTCT	TAATTTGTTT	ATCTAATAAT	GCTTCTACTT	CTTTTTGAAG	ATCTATATCG	900
ATCGTTAATT	TCAAATCTTG	ACCGCGAGCG	CCAGGrTTTA	ACACTTCTGA	ATGTAACT	960
TTACCAGATT	TGTCCGTTGT	GTATTTCAAT	TCTTTCTTCT	TACCACGcAA	TACATCTTCA	1020
TATTGATATT	CTAGGTAAGA	TTTTCCAACA	CGATCATTGC	GTGAATATCC	TTTGGATAAG	1080
TAATGTTCTG	TCAATTCITT	TGGaATACCT	TCAGCAGGTG	TCGATACATC	TCCGAATATA	1140
CCTCTTAAAG	TATCGCCATA	TGGATATTTT	CTATCCCAAT	CCATAGACGT	GTTAACACCT	1200
GGTAATTTGG	AAAGTTGCTG	AGAAACTGCT	GCATACTCTT	TTTCACTGAC	ATCTTCATTT	1260
TTTATCATTT	GTGGATCTAA	AACTGTTTCT	GGCATTTCATC	TCTCGAAAAA	TAGCTAAAAC	1320
TTGGTAAATC	TTTAGAAGAC	AATTCATCTA	ATBTGGATT	TTCCGGATTT	CGGATAACAG	1380
TTGGTnTATC	CATAATGGAT	CCTGGTTTTAA	TACCTTCCAn	CnGGCGAACA	TAGCC	1435

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

AGATAGGCGn ATTAGAAAGA CAAAGTCCTC CATTAAACAA GCGTTCAC TA AATTACTACA	60
AGAAAAAGAT TTAGAAAAGA TTACCATT CG CGACATAACA ACACGCGCTG ATAT E ATAG	120
AGGGACATTT TACTTACATT ACGAGGATAA ATATATGT TA CTCGCAGATA TGGAAGATGA	180
GTATATTTCA GAACTAACGA CATATACTCA ATTTGATTTG TTACGCGGTT CTTCArTTGA	240
AGACATTGCG AATACTTTTG TAAATAATAT ACTCAAAAAT ATTTTCCAAC ATATTCATGA	300
TAATTTAGAG TTTTATCATA CTATTTTACA ATTGGAACGC ACGAGTCAAT TAGAATTGAA	360
AATCAACGAA CATATTAAAA ATAATATGCA ACGTTACATT AGTATCAATC ATTCTATCGG	420
AGGCGTTCCA GAGaTGTATT TTTACAGTTA CGTTTCCGGA GCAACAATTT CaATTAnnTA	480
AATACTGGGG TAATGGACAA ACAGCCCAT TTCAGT	516

(2) INFORMATION FOR SEQ ID NO: 598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AGTACTTTAC CATGAGGTAA GACTTTATTC CCTGCTTTTA TAGATTGTGC TTTTATTTGT	60
GTGCCAGAAC CAATAGtAct GGTcTAATGA TTTTGCACTC ACATTATCAA TAGCTTTTTG	120
TTTGTCTTGA CCTTCAACAT CTGGCACTTT ACTATACTCT GCATTAGATG TGTCATCWT	180
TGATTTACCT ACATTTAAAT ATTTCAAAGT ATTTTCCATT ATTGGTTTAA ACGCTTTACT	240
AACACCTAAT TCATAAGCTT CTTGGTCATT TTTTGTGCC AAGCTCATA CAGCGTATAC	300
AATAACTTTA GGATTTTTCT TCGGCGCGTC ACCCATAAAA CTTACAAAAT ATGGGTTTGG	360
ACCTTTAACG TATCACCAC CATTAGGTGC AGCGACTTGT GCTGTACCAG TCTTACCTTC	420
GACCTCATAA CCATCAATAC GATAGTTTGC AGCGTGA CT TTCTTACTAT TCACAACTAA	480
ATCCAATTGC TTTTCAACTT TTTCAGCAGT ATCTTTTGTT ATTGGTTTGC CTGCGATTTG	540
TTTTTGCCCT TTATAAAATT GTCTTTTACT AACAGGATTTTCAACGCTAT TCACAAACCA	600
TGGTTTTAAC ATATTACCAT CATTAAAGAA CGCTGATTGC GCTTGTAACA TTTGAACAGG	660
TGTTACTGTT GTCGATTGAC CAAATGATGA CGTTTTTTGt TGCAACTCAT TACTCCATCC	720
AATTTGaCCA GGTGCTTCTC CATCAAACAT ACCTTTAGTT GaTTTTTCCaA ATCCaAATCG	780
TTCATACCAA GATTTCATTT TGTCTGCACC AACTAAATCT TGTAATGCA TCATCAATGT	840

ATTAGATGAA TAAGTAAATC CGAGTGACAT TGGGATTTCA CCCCACC GA CTCTATTCCA	900
GTCTGAAATA CGTGAACCCA TAATATCTCT ATGTCCAGAT TTATATTTCT TATCAGGATC	960
AAAAGCACCT TCTTGAATAG AGCTGCTAA CCCATATGAT TTAAATGTTG ATCCAGGCTC	1020
GTATGTGTTT TGATAAAGGT CATTTGCCCA CTTTTTACCA AAGTCTTTAC CAGTTTCAGG	1080
ATTAAATGTT GGTCGCTGAC TGTATGCTAA AATTTCTCCA GTTTTGGCAT CCATGACAAC	1140
CGCAAATAAA TCTTTCGGCT GGTATCTTTC AACCATGCCA TCTAAAGTT CTTCAACAAA	1200
TACTTGAATA TTTGAATCGA TTGTTAAATG GACATCATCA CCACGTTTAG GCTGCTTCTC	1260
TTTTTTAGTA TTTGGTGCGA TATATCCCCA AATATCATGA ATATATCTCA ATGATCCTTT	1320
AGATCCACTT AAATAACTAT CAAAAATCTT TTCAACTCCA AGTGCACCTT TAAGTTCACC	1380
AGTATCCGGA TTTTCTGAG CTCTACCAAT TAAGTGTGAT GCAAAATTGC CATTTGGATA	1440
AAAGCGTTCT GTTTCAGGCA ATAAAGAAAT ACCAGGCAAA TTCATTTTCT CTATTTTCAA	1500
TTTGTCTGA TACGTTAAAT TTGTTCCCTT GCGTCCAAAT TCAATTTGGA AAGCTTTCTT	1560
TTGACTAAGT CTCTTTTCAA TTTCTCTCTG CTTCATATTA ATGACTGTAG ATAATTTCTT	1620
TGCAGTCTCT TTTTTATCAA CTACATGCCT AGGTTTTTTA GAATTGGCAC TCGCCTTTTT	1680
ATCTATTACT GCAACAAGTT TATATCTTTC TACATCTTCT GCTAGCACTT TACCATkACG	1740
ATCATATATC TTTCTCGTT CTGGTTGTTG TGCATTCTTA ACTAAATACT TTTATTTGC	1800
CTTCATGACT AAATCTTGAC CATTAGAAATG TCCAGTAATC ATGATATATG AAATTCCTAA	1860
AACCAATATA AAAAAGAGCA GTCCGAATAA ACCAACAAGT AGGACTGCCC CTATTTTATT	1920
TTTTTTAATT TTAATTTTTT TGGTCGCCAT TACTA	1955

(2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

TAGCAAGAGT AGGTGATAAC AGTTCTTTTA ACGTGTTTGC TGCTTGCTCA TTTCTTGGCT	60
CATTGTAGAC TAAAATATAA TAAGCGTTTT CAAATAAGTG CTTTTTAGCA TTTAGTACAC	120
CAGATTTATG ACTACCAGCC ATTGGATGAC CACTGACTAA ATGAATATTA TGCTTTAATA	180
AATTGCATTC GTGTTGCTGT ATCATTGCTT TACTACTACC AGTATCAGAA ACAATAACAC	240
CAGGTTTAGT TGGCATATCT ATAAGCTCGC TAAGATATTT ATTTGTGATA GCAACAGGTG	300
TTGCATAAAT AATTACATCG GCTTTTTTAA TAGCTTCACT ATAATTTAAA CATTTTTTCAT	360

TAATAATGCC GATTGATTTA GCTTTATCTA ACTGAGAAAT ATCTGCATCG TATGCAAAA	420
TATTAGTATT AGGGTTATGG TATTTTATAT TGCTAGCAAG ACTTCCACCA ATTAATCCAA	480
GCCCAACAAA TAAAACTGTT GTCATATAAA TCACCTTATT TCGAAATTTT CAGAATAATA	540
ACATTGTAAA TGAGCTGTTG ACACAGTGCA ATAGTAAATA AAAATCGATA ATAGCATTAA	600
TAGATAAACG GAGATAAATC ATCTACAATA AAGAGTATAG TAACACAATG GCAACGGAGG	660
GGTAAATCAA TGGAACCAAT ATTAGAAATG AttAAAACAT TAAC	704

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

CCTCTAAAGG ATCACGAACC TTTTTCATCG TGAATAAGCC TATAATACCC TTAAAcCTAT	60
TATTATTAAC TTTTACCTCT GTGTATTCCC TATCATTAG GCGACGCCAG TGACGTTTAT	120
CTATATACTT TACTTTCACA GTCACCAACT CCTTGTCATT ATTATATAAA ACTACATAAA	180
TGATGTCATG TCATGATACA GTTTTATAGT TTTTGTTAAT CATATGAAAA TATTTATTAT	240
TATTTTACTA CAACTCGCTT CAATTTACTT AAAATAGACA ATATTAATTA GATAGTACAC	300
ACATTTCTTC ATAAAAGTGA TTTTTCAAAA ATATAAATAA CACACTCTTA TCGTTTTCAA	360
AATCATTTAA TGCTATTTTC ATTAAAAACA GCTGAAGCAT CAAATCTATT CTGATTCAAT	420
CAAGAATACA TATAAAAATG AAGTGACTCA AAGGTTTATT AACAACTTC AAACCACTTC	480
ATTGATCACT TTTATTTTAA AGCATATTTT TCGATTACTG ATTTAAGATG CGGATATTGC	540
GTAATTAATT CAGATTGCTT AAACAATTCA AACTGCTTAA ACTCAAATGC CGGTTGACAC	600
ATACAACCTA CTAAACTAAA AGTATTTGAT ATTTGATTG AAGAAGCAAA AATTGTTCTT	660
TTAGGCACTA CATATTGCAA TACATCTCCA TTTTGGATAT CBTACCCAA TGTTGCAGTC	720
GTATATTCCC CATCCGGATT TATCATATGA ATTGTTAGAG AATCGCCAGC ATGATAGTAC	780
CATACTTCAT CAGCATCAAT TCGATGAAAA TCGGAAATAT TGTCATCTGT AAGTAAAAAA	840
TAAATACTAC TAAACGGCGC TCTGCGTCCA TCTTTCAATA CTTCTCGAAT TGTCTCTCTA	900
TAGAAACCAC CTTCAGGATG TGATTCAAGT TGCAATTcAT CaATCCATTG TTCTGCTGAT	960
TTCATTATTT CAAATCCACA TTATGGAATA CGTTTTGTAC ATCTTCTAAA TCTTCTAATG	1020
CATCGATTAA TTTTTCAAAT GTTACTTGGT CCGCTTCAGA AAGTTCAATA TCTGTTTGAG	1080

GTAACATTTTC AAATTCAGCA ACTTAAATT CTTCAACACC TGCTGCACGA AGCGCATCTT	1140
GAACGACTGC AAATTGAT	1158

(2) INFORMATION FOR SEQ ID NO: 601:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 827 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

TGATACTTAT TTTTCAATAT TATTTGGAAT AAAnTCTTnT AATTGTGGTG TGAAATAAAC	60
ACCGAAATTC TTTTCAGATT CATCTTTTcC ACTACCTGCA TATAAATAC CAATCAGTyC	120
ATGTTTAGAA TTCAATACAG GAGATCCTGA ATTACCTGGT TGTGCATACG CATCAAATTC	180
CATAAACGTT CCACTGATAT GGTTAATCGT TCCTGTCGAT TCAAACATTT TATATTTTGT	240
TTGTGCACCC TTTGGATAAC CAATAACAGA AATTCTATCT TTCACTTTTG CTCCGTCTGC	300
AAATTTTGTA TAACTAACGT TCTTATTAAA ATTCAAACCT TCTGTACTTG TTTCATGAAC	360
ATGAACTATC GCAAGGTCTT CTTTTCCGGG ATATTCTACA ATGTCTTTAA CGTCGTAGTT	420
TCCTCCGCCT TTACCTTTAC TCGAATGATG TGCTGATACT CTATTTTTTAA AAATATCATT	480
ACTTTTAGCG ATATGTTTGT TAGTTACaT TGTATTTTTTA CCAACAATA CACCAGTACC	540
ACCCACAAAT GCTACCACTG aATTGTATGG TTCCTTAGTT GCATCGGTAA TTTCTTTGAC	600
ATTCTTTTCT GCTTTGGCAA TTGAATGArG CTGATTAGAA ATATTTTCAG CAAAACCAAG	660
AGATGTTAAA ATAGTTAAAG CAGTTAAACC TTTAACCATT ACATTTTTTAT TCAATTTTA	720
CCTCCTTCCA AATTTATTTT nATAGTTAAT GTATCTAGAT ACACATTTAC TATATACATT	780
TTAAATAAAA ATATThATTA AATATTAATT AACCACTTAT nAACGTT	827

(2) INFORMATION FOR SEQ ID NO: 602:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

nGGnACGTAA AGTATTTATG TTAAATGGCA nAAATATATG AATGATGAGT TACCTGGATT	60
ACCAATGTTC CAAGGTAAAT CGATAACTAT TGTTAACGAT AAAGTACGAA ACTTAGACAT	120
TGAAATTGGA ACTGATCAAA GTTTATATAA TTAACTAAA GAAGCTTAGT AATGTAACCT	180

CGACGATTTT GTCGAGGTTT ACTTATATGG GGGGATGTTA TGAATAATGT ATTGTTAGAG	240
GTTAAAGATT TAGAAACATC ATTAATAAATA AATAATGAAT GGTTAGCAAC TGTTGAAAAT	300
ATTTCTTTTG AATTATCTAA AGGAGAAGTT TTGGGTATAG TAGGGGAATC TGGTTGCGGT	360
AAGTCCATAT TAAGTAAGTC AATTATTAAA TTATTACCAG AAAAGATATC TAAACTAAGT	420
AATGGAGAAG TTATATTTGA TGGTAAACGA ATCGATACGC TCAATGAGAA GCAATTGTA	480
GATATTGAG GAAATGATAT TGCTATGATT TTTCAAGAAC CTATGACTGC TTTAAATCCT	540
GTATTTACCA TAAAAAATCA ACTTGTGGAA TCTATAAAAT CACATAAAAA AATTTCTAAA	600
AAAGAAGCAA ATAAATTAGC AAAAGATTTA CTAAAAAAG TTGGAATTGC TAGACAAGAT	660
GAAATATTAA ATAGCTATCC TCATCAATTA TCTGGTGGTA TGAGACAAAG AGTAATGATT	720
GCAATGGCCA TTTCATGTTT TCcTAAATTA TTAATTGCTG aTGAACCTAC AACAGCATTG	780
GATGTCACGA TTCAAG	796

(2) INFORMATION FOR SEQ ID NO: 603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

GGATGTGTTT ATCCCAAATT GaAAcAgAaA TTTAGATCA AAtGATGTGG ATTGGTTTTA	60
AaCCATTCAa AATTaCCAAT ATTAmCAAG AATCTGAAGA CATTAAATCA TTTtACAGTT	120
GAAACTGAAG AATATGACTT TAGTGAATTT ACACCAGGCC AATACATCAC AGTTGATGTT	180
TCTAGTGATA AACTTCCATA TAGAGCTAAA CGTCACTATT CTATCGTATC AGGTGAAAAA	240
AACCATTTAA CTTTTGGCGT TAAACGTGAT GTCACAACAG AACATGAAGG CGAAGTTTCA	300
ACAATTTTAC ACGATGAGAT TAAAGAAGGC GATATGATTA ATTTAsTGCG CCTGTAGGTG	360
GATTGCTATT AGAGAATACG ACTGAACCAC AACTTTTCTT AGGTTTCAGGT ATTGGTGTTA	420
CACCTTTAGT AGCTATGTAT GAAGCTGCCT CTGCCAAAGG TTTAGATACA CAGATGGTTC	480
AAGTTGCTGA AAATGAACAA CATTTACCTT TCAAAGACAA CTTCAACAGT ATCGCAAGCC	540
ATCATGACAA CGCTAAATTA TATACACACT TAnAgATAAA CAAGGCTATA TTGGTGCTGA	600
AGAATTACAA GTATTTTTAG CAAATAAACC TGAAATTTAT ACTGTGGTG GTACAAAATT	660
CTTACAaTCT ATGATCGAAG CACTTAAATC TTAAATTAC GATATGGATC GCGTACACTA	720
CGAAACATTT ATTCCAAGAC TAAGCGTTGC AGTATAACTG AGAAAAGAGG TTTAGTGCTC	780

ATATGAAACT TAATCAACGT TACGTAAAAG TATTTGCATT ATATTTTCGTA AGTATTGTTA	804
CTGCAAATAT TATTGTTAAA AATAATAATT TAATTAAAAC AtTGATACAA ACCATAGCCG	900
GGTACACGGT CTTTGCAGTT GGTTTGAAGT ATTTAACTAA ACGTAAAAAT AAATGACATC	960
TATACCAAAA CAGCTATGAC TTTACTTTGT CATGGCTGTT TTTTAATTGG GAGTAGGACA	1020
GAGATGATAT TTTCGCAAAA TTATTTGGT CGTCCCACCA CAACATGCAT TGATGTATGC	1080
TCACTGAATT TCATAAGAAA GGAGTTCACA AGATGACCGT AGATATTGGA CGGATTTATG	1140
ACAATAAAGA TAATACCGAC GCTATTCGTA TCCTAGTCGA TAGAGTCTGG CCGAGAGGTA	1200
TTTCGAAAAAG AACTGCTAAC CTAGATTATT GGTAAAAGA CATTGCCCE TCTACTGAGT	1260
TGCGACAATG GTTCCAACAT GATCCTAAAC TTTTGGAGC TTTTAAAGAA AAATATGAAA	1320
AAGAATTACG TGATCAGGAT GCGCAAAAAG ATGCTTTTGA AAAATTAAAG GATATTGTAA	1380
ATCAGCATAA TCATGTTCTA TTGTTATATG CAGCAAAAGA TACTAAACAT AACCAAGCTG	1440
TAGTACTACA GCAGTTGCTC AATACTTAGT TATATATGTT TATCGTGAAT CACTATAAAT	1500
GTCGCTAACT TCATTTCTAA TATTTATTTT TAAAAAGCAT AATTACTACA ATTAATTGGA	1560
ACTTTAATAA TTAATAAAT TGAACAATA TTTTACTTTA ACAAATAAAA GTTTTAAA	1618

(2) INFORMATION FOR SEQ ID NO: 604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

ATTATAATGC AAATATTGAA GCATTAAAA CAGTCGCTAA AGCAGTAGGC AAAGAGAAAG	60
AAGGCGAGAA GCGTCTGGAA AAGCATGATA AAATATTAGC GGAGATTAGA AAGAAAATTG	120
AACAGAGTAC GTTAAATCT GCATTTGCAT TCGGTATCTC AAGAGCAGGT ATGTTTATTA	180
ATAATGAAGA TACATTTATG GGACAATTCT TAATTAAAAT GGGTATTCAA CTGAAGtca	240
mAAAArAmAA AACTACGCAT GTTGGTGAAC GCAAGGGTGG TCCTTATATA TATTTAAATA	300
ATGAAGAACT TGCCAATATC AATCCAAAAG TTATGATTTT AGCCACTGAC GGAAAAACGG	360
ACAAAAATAG AACGAAATTC ATTGATCCTG CAGTTTGGAA ATCATTAATA GCTGTGAAAG	420
ATAACAAAGT TTATGACGTT GACCGAAATA AGTGGTTGAA ATCAAGGGGG ATTATCGCAA	480
GTGAAAGTAT GGCAGAAGAT TTAGAAAAA TTGCAGAAAA AGCAAAATAA AAATACAGCG	540
CTACTCGTAA ATCATATAAG AGTGGCGCTG TATTTTAAAT TATGTTTATT ATCTGTCGGA	600
TGTGATGATT TACCTGAAAG TTTATTTCTGA ATAAATTTAA TTACATAACC GACAAGGATT	660

GTTTTAACAG TTCTTTTAAT GAATTGGCGC ATCGTTACAT ACCTCATTTT TCTATATCTT	720
ACGAACTATA TACCCATTCA TATATGCTTT TTAAACGTCA TTGTCACAAT TTAATTTTAA	780
GGGAATATAA TATAACCATC TTTATCTGCT TTTTATAGTAA AAATGACAAA AATTGCATG	840
ATTATTG _a GA TGATGGTAGG GATACCTGTC CAGAAAAATA ATAAGTGAAA AAGACCTTGT	900
CCAAATTTAT CAGCATAAAA TTTATG _a ATA CCTAACCTC CAAGAAATAA TGCAAC _m AT _a	960
ACATAAATGG CTTTATTGAC TTTCATTTGT AAtCCTCCTT AACTATAATT CTACTTAAAT	1020
TCGTTGTGAA AACCAATATT TCTAACTTTA GAATTTTCAA ACTTTCTAAA ATTATAAGTA	1080
TATCTTTTTTA AAATAAGCTA GAATTTCTAT ATAATAAATG TTAATAACGT AAAAGGGAAT	1140
GATGACATAG TGATACGTCA AGCACGTCCA GAGGACCGAT TTGATATTGC GAAGTTAGTT	1200
TATATGGTTT GGGATGATAT GGAATTAGAA TTGGTAAAGCATCTACCTAA AGACATGGTA	1260
TTAGATGCAA TTGAAAAAAG CTGTGTTGAT GCAACATATC GAACTTTTTTA TCAGCATATT	1320
TTAGTTTATG AAGTAGAAAA TAAAGTAGCA GGTGTGATTA TTAGCTATAG TGGTGAAAT	1380
GAATTGAAAT ACGAAAAAGC ATGGGAACTA CTTGACTTGC CAGAAAAAAT AAAACAATAT	1440
GGCACGCCAT TACCTGTAAA AGAAGCTAAA GACGATGAGT ATTATATAGA AACAATTGCG	1500
ACATTTGCAG CATATAGAGG TAGAGGCATC GCGACAAAGT TATTAACGTC ATTACTTGAA	1560
TCAAAATACAC ATGTTAAATG GAGTTTGAAT TGCGATATTA ATAATGAAGC AGCATTAAAG	1620
TTATATAAAA AAGTAGGCTT TATATCTGAT GGACAGATTG AATTATACAA GCACATGTAT	1680
CATCATTTAA TTGTTAAATA AAATACTCGA CAGTTCGATG TAAGTCGATT GCCGAGTAGT	1740
ATCATTTTCT ATTAAATGCC TGCAAATAAT GCACTAATAT AAATACCTAA TGCATATAAT	1800
AAACCGAAAA ATGTATTTGT TTTACCAGCA GCAGCCATTG CTGGCAT ET TGTAGGCGGT	1860
GTATCATTCT TCTTGAAACG TCTGATAACT TTAACAGGCA TTGGGAATGA TAACAACGCA	1920
AGTAAGTAAA ATAATGAGCC ACCAGGTTTA ATAATGATCG TAAGTACAAT AAAGGCATAA	1980
GCGATAAAGT ACATGATTGC CATAAATGTT AAAGAAGCAT TTTTACCTAA TAGAATGGGT	2040
AAAGTTTTGC GACCACTTGC TTTATCTTTG ACACGGTCGC GAATATTGTT AGCCATATTA	2100
ATTAAACCGA TAGTG	2115

(2) INFORMATION FOR SEQ ID NO: 605:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1003 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

TATGTCTCAA ACTCAAATTA ATCAAATGTT CCAGCAGAAA AACATGTCTA CTGAATTAAA	60
ACGTCGTTAT GCACAACGTT TATTACAGTT TCCACATGTA CACAATAAAG AATACTTGAA	120
ATCTTATGCT AAAAACCCTA AAGAACTAA AGATAGTTAT ATTTCTGGTT TTAAAGAGAA	180
TCAATTGATT AAAATAGAAG CGATTAAATC ATTGTTTGCA ATGGATAAAT CTCCATTAGA	240
ACATGTTAAA CCTGCTACAA AACCAGACGC TTCTTGGGAT GAGATGAAACAAAAAGCAGT	300
TGAAATTGGT AAAGCTGATA CTACATCGAA TAAATTTGGT ATTAGAGATC AATACTGGAA	360
ATTAATTCAA GAAAGTAAGC GTAAAGTTAG ACGTGACTAC GAATTCAATG TTAATTCTCC	420
AGAATTCCAA GATTTAGAAT TACTTGTAAG AACAATGCGT GCTGCTGGTG CAGATGTTCA	480
ATATGTAAGT ATTCCATCAA ACGGTGTATG GTATGACCAC ATTGGTATCG ATAAAGAACG	540
TCGTCAAGCA GTTTATAAAA AAATCCATTC TACTGTTGTA GATAATGGTG GTAAAATTTA	600
CGATATGACT GATAAAGATT ATGAAAAATA TGTTATCAGT GATGCCGTAC ACATCGGTTG	660
GAAaGGTtGG GTTTATATGG ATGAGCmAAT TCGAAACAT ATGAAAGGTG AACCACAACC	720
TGAAGTAGAT AAACCTAAAA nTTAAAAATAC AAATAGCACA TAACTCAACG ATTTTGATTG	780
AGCGTATGTG CTATTTTTAT ATTTTAAATT TCATAGAATA GAATAGTAAT ATGTGCTTGG	840
ATATGTGGCA ATAATAAAAT AATTAATCAG ATAAaTAGTA TAAAATAACT TTCCCATAG	900
TCCAATTTGA CAGCGAAAAA AGACAGGTAA TAACTGATTA TAAATAATTC AGTATTCCTG	960
TCTTTGTTGT TATTCATAAT ATGTTCTGTT AACTTAATAT CTT	1003

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

GCTnTTATAT TTAAAAAATT TATTnGCGGA TAATTACCTT TATTAAATCC CACCCATTAG	60
GAwTaCGAGT AATAGGACTA ATACTGGAAT CACATAATGT AACATAACGT CCCTCCTTTA	120
ACTTAATTTT AATTGTAATC AAATTTGACA ATAAGTCAAA mCATTAAATAC CTATGATArG	180
TATCATTTAT TAACATATGT ATCATATTTT TAATCTTGCG TAATTTTTAT CGTTAACTAT	240
GTGATTTAAT CAACAGGCCA ATAAGACGTT TGTCAATCGT GCACATAACG GTACGACGCG	300
CTTTTGTCAT TTTAATTATG TTAAGATAAT AGTAGTTATA GAAGTTCAAT CTATAGGAGG	360
CATAGCATGG ATATTCCAAA AATCACGACA TTTTAAATGT TTAATAACCA AGCTGAAGAA	420

GCTGTAAAC TATACACAAG CTTATTTGAA GATAGTGAGA TTATAACAAT GGCTAAGTAT	480
GGTGAAAATG GACCTGGTGA TCCCGGGACT GTACAACACT CAATATTTAC ATTAAATGGA	540
CAAGTATTCA TGGCGATTGA TGCTAATAGT GGCACAGAAT TACCAATGAA TCCTGCGATT	600
TCATTATTTG TTACAGTAAA AGATACTATT GAAATGGAAC GACTATTTAA TGGATTAAAA	660
GATGAAGGTG CCATTTTAAAT GCCAAAAACG AATATGCCAC CATAACAGAGA GTTTGCTTGG	720
GTTCAAGATA AGTTTGGAGT AAGTTTTCAA TTAGCATTAC CTGaGTAAAA GGATTGCGAC	780
AGCtTGgAAT GATAAAGAAA CACTTTTTCT TATGCATGCG TTTTACCTAT GTATTTCTAT	840
TTTAAGTACA CATTAGCATT TTAGTTTCGC TCATTTTTAA AECACAAAG ATAATTTGTA	900
ACTTAAATGA TGATACGTTA TTTAAAAACA CGATACTTCG TTTCAATGAA CGCATTAAAT	960
AATAAATAAA CACCTCACCA TAAGAAAGGA CTACTTTCTT TTGTGAGGTG TTTatTTGTC	1020
GACAACTTGA TTATGATTGT TTCATTTTTT GAATAAGTTC ATAATCAGGT GTAGCATACA	1080
AAGTTTTTTG ATTGTC	1097

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE/ DESCRIPTION: SEQ ID NO: 607:

GAGGTCTAGC ATGTCTCGTT CAAAAAATA CTTTTACTTA TCTAGCTTAA TGATTATTTT	60
AAGCTTTTTTC TTTAATACAA ATAACGTTTT CCTAAGTGGA CTTTTTAATT CTTTTATTAA	120
ATTAATACTT TTCTGCAGTG TTATTAACCT AATTGTACTA ATTTTGTCTA TAATTTTTGC	180
AGATCGTTCA ATTAAATCAC TAAAGCCTGA TGCAGATTGG ATTAGAATTG CGAGTAAAG	240
TTTGCCTTGG aTTATTCTAA TTGTTATTTT AGTACATATC TTTTCAATTG TTCGTACATT	300
CGGTTTTATT TAAAAAGTT AATATGTCAT TGTAGCCTTA ATACAAACA ATACAATGTA	360
TCATGCTATA ATGAGTAAAA CAATTTGATA ACGTTGTTGC GTATAAAAAA TATTAGATTT	420
TCGAAATCAT AACTATGCAT CTAATCGCTA TAGTTATACA ACAAGATATA ACATATAATG	480
AGGTTTGATA ATGCATCGAC AATTTTTGTC GTCGCGTTGC CAAAACCTCT TTTTTAAATT	540
CAAACACTT CTTTTCGAGG TGAACCAAAT GCAATATGTA TATATTTTTA TCGGTGGTGC	600
TTTAGGCGCT TTATTACGTT ACCTCATTTT TTTTCTGAAT ACTGACGGAG GTTTTCCAAT	660
CGGAACACTG ATAGCCAATT TGAATGGTGC CTTTGTAATG GGATTGCTAA CAGCCTTAAC	720

AATTGCATTT TTTTCAAACC ATCCGACCT AAAAAAGCT ATTACGACTG GTTTTCTTGG	780
TGCTTTAACG ACTTTTTCAA CATTTCAATT AGAATTAATA CATATGTTTG ATCATCAACA	840
ATTTATAACT TTACTACTAT ATGCTGTAAC AAGTTATGTC TTTGGTATTT TGTTATGTAA	900
CGTCGGTATA AAAGTAGGTG GTGGTTTATC ATGATATCAA TCATTTTAGT CAGATTGGC	960
GGCGGTTTTG GCGCAATTGC TAGAAGTGCC ATTACTGATT ATTTTAATCA TAAATTTACT	1020
TCAAAGTTAC CTATCGCAAC ATTGATAGTA AATCTAGTTG GTAGTTTTTT AATTGGATTA	1080
ACTATAGGCT TATCAATTTT AATCTCATGG TTCCCTGCGT TCTTTGTTAC CGGTTTTTTA	1140
GGTGGCTTAA CAACTTTCTC AACGTTAGCC AAAGAACTTA CACTAATGAT GACGCCAAAA	1200
TTTAATATTA ACCTTTTTCT CAATTATTCA CTTTTACAAT TCATCATTGG ATTTATAGCT	1260
TGTTATATTG GCTATCATAT TTAAAAATAA AATGCTTCAT TCAGCAAATA GTAAATTAC	1320
GACACCTTCC TGAACGAAGC ATTTTTTAAT TTTATGCAA ATTTTAAAGC ACCATATAAT	1380
GCCTACCAAA TTTCAATAAT CTTTGTGTC GTTTAAATAA TGTGAATGTC AATAAATTCT	1440
CCAACTAGT CGAAAATAAA GGGAGTGGGA CATAAATCCC TAAAAAACA GCAGTAAGAT	1500
AATTTTCAAT TAGAAAATAT CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAa	1560
TGGcTTCGCT TTCCTAGGGT GCCGTCTCAG CCTCGGcTTC GACTGGCACT GCTCCCTCAG	1620
GAGTCTCGCC ATTAATAcTA CGTATTAACA TGTAATTTTA CTTTACATA CTTTAAAAAA	1680
TAAGACACTT TGCCCAACTT AACTACCAA TAGAAACCTC TGTTAGAATT CCTCAAAATG	1740
ATATTTTCGCG ATATGTTAAT GAAATTGTTG AAACGATACC TGATAGCGAA TTCGATGAAT	1800
TCAGACATCA TCGTGGCGCA ACATCCTATC ATCCAAAAAT GATGTTAAAA ATCATCTTAT	1860
ATGCATATAC TCAATCTGTA TTTTCTGGTC GAAGAATAGA GAAATTACTT CATGACAGTA	1920
TTGAATGAT GTGGTTAGCT CAAAATCAAA CACCTTCTTA AAAACTATT AATCGTTTTA	1980
GAGTGAATCC TAATACTGAT GCGTTAATTG AATCTTTATT TATTCAGTTC C	2031

(2) INFORMATION FOR SEQ ID NO: 608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

TCCCCGGGAA TCGAACCCGC GAnCTCCTGC GTGACATGCA GGCGTGTTAA CCGCTACACT	60
ACGAGACCTA TTAnATTAAA AACTATGTAT TGCGGGAGGC GGATTTGAAC CACCGACCTT	120
CGGGTTATGA GCCCGACGAG CTACCGAACT GCTCCATCCC GCGCTAATAT TATTTTGAAT	180

TACCTAATTA ATATACCATA ATCAAAAACC TAAAGTsrrG AACTTTTTGA ATTTAATTTA	240
AATGTTATCT CTAAATAAT TACTTAAATA TCGTAGCAAC ATGTTCTCTG TTGAACACAA	300
ATATTAGTAT ATTCATTTTT GTAGTGACG TCAACGACAT TTTCAAAGTT TTTTGTGTAA	360
AAAAACGCTT CTTATTCCCT TTTATCATAT AAGTGTCTAA TAGTTGTCAT AAATAGTGkT	420
AAAGCATTTA AAAAGGTATA GGAGTTATAA AGTTTACAAC GCCTATACCT TCTGAAAAAG	480
AAATTATAAA AGCTTGTTAC ACCGCATATT CTTTCAGTCA GCGACACCA ATATAACATT	540
GTAGCCCTAA GACATTGCTT GACGCCTCAn TTACAACAAT TTTTCAAAAT CAGCAGCTAC	600
CTACTGACAC AACATAACAC AACCCnTACA CTAnCTATCG TGTCATGTAA TCTTGCATCC	660
GATCTTGCAA CGCTGTAAAT GTTTCGA	687

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

GTGTTGAATA CTTTGACAAA ATGAAATCAT TTGTTCTTTC GTTTCAAATT TAACTGTTTG	60
AATTAAATCA GTTCGTTTTT CGTAGTACTT CGGCGTTGTG TTCATATTCA TTTTTTCTAA	120
AAATAAACTA GTAAACAATG CACCTTTAAG ACTCTGACTG ACAACGTGTG GTGCTAAAAA	180
GAAACCTTGA TACATTTCAA GCATGTCATT TAATGATGCA CCCGCTTCTT TACCAATACC	240
AGGTGCTGTC AATCTATAAC CACATCGTTC AATTAAATCT TTTCTACCAG CAATGTATCC	300
ACCAATCTTA GCTAAACCAC CGCCAGGGTT TTTAATTAAT GATCCTGCTA TTAAATCGGC	360
ACCACATTCT ATAGGTTTAC GTCTTTCAAC AAATTCCCCA TAACAGTTA CCACAAATAT	420
TAAAATATTA GGATGCACGT TTTTCAACCT AGTAATTACC TTTTCAATTT CATCTAGCGG	480
AATTGAAGGT CTTTGATCAT AGCCTTTTCA ACGTTGAATC GCTATTACTT TGGTGCGCTC	540
AGAAACCCCa TCTAACACAC TTTCAATATC GATCTTACCT TCTTTAAGTG CAATATCTTT	600
ATACGATmCG CCATGCTCCA TTAAACTTTC AATACCATTT CCGTTTACGC CAATGACTTC	660
AAGTAAAGTG TCATATGGAC TACCCGTTAT ATAAATTAAT TCATCACCAT GTTTTAATAA	720
ACTTTGTAAT GCAATAGTAA TCGCATGCGT ACCTGAAATA ATTTGCGGAC GAACAATTGC	780
ATCTTCTGCT TTAAATGCCT GCGCATATAT TTCTTAATTG AACGAATTTA GAACTAATCG	840
TAA	843

(2) INFORMATION FOR SEQ ID NO: 610:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 775 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

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GATTATTATA AACCGAATGA AACAAAAAAG TTTTACATA TTTTCAACAA CTTTATTTC      60
ATAAAGCATC AAGTTGATCT AAAGTTTGAT TCATACCTTG TTCAACACCC AGTTTATGA      120
CTTGTTGAGC GGCTTCTTTT GTTGGAATA CCGATGTTGA TGTCACGTGTC GTTTTCGTTG      180
TATTGCTCTT GGAAAATGAC AAAGTAATTT TCATGCTTGG CATTTTTGTA TCTTTTGCAC      240
CTTGAGGTGT CGCAAATGAG TCAATATATT CAATTAAATA TGGACGCTTA ACCGTTTTAT      300
ATTCTGCTAA TGTATAGCTG GTCATTGTAG GTGTTTTAAT CGCATAAAAT GCATCACCGC      360
CTGAAACAGC ATTAAAGCGA AACACTTTGG TACTAGCGTC TTTTGGAtGA AACCATTTTT      420
CAAATAATGC TTTkGTCGTA TAGGCATCAA ACACCTTTTC AATCGGTGCT TCTATCGTTC      480
TTGAAAAAAT AATTTTATTA TCTTCAACTT TAAEGTCAT CTTCCCACTC CCTATCTTTT      540
ATATTTACTC ATCTTAACAT GCATTGAGTA ACATATGTTA CCAAATCATT TGTTATAAAC      600
TATAGTAATA TTAATCATTC CCTCTGTnGA AATTGATAAC TACGAAATAA AAAACACACT      660
CTATTCAGCT ATTAACAGTT GAGTAGAGTG TGCAAACCTG TTGAATTAAT GCGCTAACAT      720
TTCTTCTTTG ATTTGGTCTT nATnTAATTT TGAAGGATAA TATGTTGGCC AGTTA      775
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(2) INFORMATION FOR SEQ ID NO: 611:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 728 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

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ATCAAAATTT GATACTAAAG GGCTCACGCT ATTTTATGTA TTTATTGGAT TGATTATGTT      60
TGCTTTATTA AACCAACAGC TGTTACTTTT AAATTTCTTG AGTTTTATCT TAGCTATCGT      120
TGTGGCAATG TGTTATTTA AAGTAGAAAA ACATGTTTCT TCACCATTTT TACCTGTGGT      180
TGAATTTAAT CGTTCGATTA CTTTAGTTTT TATAACTGAC CTTCTAACAG CTATTTGTTT      240
AATGGGATTC AATTTATATA TTCCAGTCTA CCTTCAAGAA CAACTAGGAT TATCTCCATT      300
GCAAAGTGGA TTGGTTATTT TTCCTTTATC TGTAGCTEG ATTACATTGA ATTTTAATTT      360
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ACaTCGAATT GAAGCAAAAC TATCAAGGAA AGTTATTTAC TTACTATCAT TTACATTGCT	420
ACTAGTAAGT AGTATTATCA TTTCATTTGG TATTAAATTG CCGGTACTTA TAGCATTTGT	480
GTTAATTTTG GCAGGATTAA GTTTTGGATA TATTTATACG AAAGATAGTG TGATTGTCCA	540
AGAGGAAACT AGCCCATTAC AAATGAAGAA AATGATGTCA TTTTATGGAT TAACTAAAAA	600
TCTTGGGGCA TCAATAGGTT CAACAATAAT GGGATATCTT TATGCGATAC AATCAGGAAT	660
CTTTGGTCCA AACTTACACA nTGTGTTAAG TGCTGTTGCT GTAATTAGCA TGGGCTTATn	720
GTTTTATG	728

(2) INFORMATION FOR SEQ ID NO: 612:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 913 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

TATCAGAGCA AATAAGCAAG TTAGATAAAA AGATTTCTGA CTTACAATTA ATTAGACGCT	60
CTGTATGTGA ATTTATTAAA GGACTCTCTC TAATAGATAC CAGCATTTTA AACAAGACAC	120
TACAGTCACA ATATGATAAA GAAGCATCTA TAAAATATGG TATACGAAA GCATATCAnT	180
CATTTATTAG ACGTAAAGAC AGCTTACAAT CGCAGGATAT CAGACATAAA TTGACAACATA	240
TCTTCAATAA ATTTAATCAT ATGTCTTTGA GTCATTATCC AATCCAAGAT TGTAGTGATC	300
TCGTATTTGA GTGGAAGGCA TTTATGAACA CTATCGCTGA TTTTGmTGAT GAAACATTAT	360
GCTGTATTGC TAAAACATAT GAAGATGATA CGCGTTTCAA AGATTACTTT AATTCATATG	420
ATAATCAAAA TTTAGCATCA TACATTTTCA AAGCTGTAA TTATTTTTTG AGCAATGTGA	480
ATAAGAGCGA CAATTTTTAA TCCTCATACA GATGCTACAA CACTGAATAC ACCAACTAAA	540
ATAATTGTTC AAAGTAGAAA ACTAATCATT TATTCTCTAA ATCAATAACT ATATTAAAAG	600
TTATACCTTT GCAAAGCGAA TTAGTATAGG TTACCGAAAG GAGAAAGGAT TAGGTTCCAT	660
TCGATTTATA AAAAAATATA TTTCGAAACA TACAAAAGCG CCAGAAGATA ATCATTTCTT	720
CTCGCGCTTT TATACTGAAT TATATTAATT TCAAACCTCTA AAACCTCTA AATTTCTTTT	780
TCAATGCATA TTCAACTAGC TCAGGTTTAC TCTTTAAGCC AAGCTTTGTC ATAATATGCG	840
TCTTATGTGC TTCTACTGTT TTCACAGATA CAAATAATTT CTCTGCAATT tCTTTATTCC	900
CGTAACCTTT GGC	913

(2) INFORMATION FOR SEQ ID NO: 613:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 654 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

ACAAGTGTG ATGTCATAGT AGCGTCAAwT GTGCTTTATT TCTGGGACAC ATTTAAATTT	60
TTCCACCCCA TTACTTGAG CTTAATCTTT ATTACAATTT TACTATTATT AAACATTTTT	120
TCTGTAAAT CATTGGAGA AACTGAGTTT TGGTTATCAT TGATTAAAGT GTTAACAATT	180
ATCGTATTCG TTATTTTTGG CTTTTTATG ATTTTCGGTA TCTTAGGTGG TCATACATAT	240
GGATTTGAAA ACTATACAAA AGGCCAAGCA CCGTTTGTTG GTGGTATCTC TGGTTTCTTA	300
GGCGTATTAT TAGTCGCCGG ATTTTCGGTT GGTGGTACAG AAGTAGTAGC AGTAACTGCT	360
GGTGAATCAG ATGACCCTAA AAAGTCTATG CCTAAGCAA TTAAACAAGT ATTTGGCGT	420
ATTCTTTTAT TCTATGTCTT ATCAATTGCA GTAATTGGTG CAATTATTCC GTACACAGAT	480
CCATCATTAT TAAGAGCAAG TAGTTCAATA AGTCAAAGCC CATTTACAAT TGTATTCGAT	540
AGAGtAGgCA TAGCCTTTGC AGCATCAGTA ATCAACGCGG TTATTTTAAC TTCATTATTA	600
TCCGCTGCAA ATTCAGGTGT TTATACAACA GGCAGAATGT TGTATTCCTT AAGT	654

(2) INFORMATION FOR SEQ ID NO: 614:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

TCGATCTTTA TTGATAATAA TTAAATTGTC GCCTTTAAAA TGTGATATTA ATCCTGCGGC	60
AGGnTGTACA ACGAGTGATG AACCTAGTAC AACAAGGGTG TCAGCATGTT CAATTTTATT	120
TAATGCCCTT ATGATGGTAG GTTGATCTAA CATTTCACCG TATAATACGA TGTCCGGTCG	180
AATGGCACCA CCACAATTAT CACAATGTTT CAAAGTTCTA TCAATAACAT CTGACTTCGT	240
ATAAGATTTA TGACATACAT TACAATAAAA ACGATTTAAC GTGCCATGTA ATTCATCAAC	300
ATGTTGACTT CCAGCGTCTG AGTGCAAACC ATCGATATTT TCGGTGATGA CACCTAAGA	360
TTGTTGATTA CGTTCTAATT TTGCAATCCA ATCATGAACG ATATTGGGCA TCGTATCGAC	420
AAATAGTAAG CGCTTATGGC AGAAATTGAT AAAACCTTCA GGATCATCTT CTAAATAATC	480
ACGGCTTAAC AAGTATTCTG GCGAAAGCCC ATCTTTTGaA ATTTTCATCAA ATAAGCCACC	540

CATTG _a ACGG AAATCTGGAA CGCCACTTGC GACAGATACA CCAGCACCTG TAAAAAATGT	600
AATACGATTC GAACTATCTA TAATATGTTT TAGTGTCTCT AA	642

(2) INFORMATION FOR SEQ ID NO: 615:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

TTTCCCCnCC CCnCCAAATA TCCAAnGGAA CTTTAATAGT CCAATTGGCA CAGTAA _A ACT	60
ATGGCATT _T TTT ATAAGTATAA TATATCTGTA ATTATGGTC AATTAGTAAA TTGTTTTTTTA	120
TTTGAAACAT ATTTACAT _c AAAATCACAA AGACTTTTAG ATTTTG _t TCT AAAAATCTCT	180
TAATAATTTA TTTAATGAGA AGAGTTGCTT ATATAGTAAA TTGTGAAGCC GTTAA _A ACAA	240
CGTTACAAAA CCTATATCTT TAATACGGAA CCATATGGTA TGAATCAAGG A _A ACTTAA	300
CTAA _A ACTTC TCTATCAGAT TTATTTGTTG CGAAATCAAC AACTTTAATT GCTTGCCCTT	360
CATTTAATGG ATAATTTGCT TGC _G TAATTT TAACTTTTAC AATTTGACCT ATGAGTGATT	420
CGTCACCTTC AAATTGTACT TTCATATAAT TATCTGCATA TCCA _A CTAAT GTACCTTCTG	480
TG _t CACCCTG TTCCTCAGGA ATTACTTCAA GCACATCTTG ATCAAATTTA GACGCATATA	540
ACTTTCCGAG TTGATTGCTT AGCGTAATTA ACTTATGCAC CCGTTCATTT TTAATTTCTT	600
CATCAATTTG GTCATCCATT CTTGCAGCTG GCGTGCCAAT TCTAGGAGAA TAAGG _G AAAA	660
CATGCAGTTC AGAGAACTTA TGCTTTACGA TAA _A ATCATATGTTTCTTG AACTCAGCTT	720
CAGTTTCACC TGGGAAACCA ACAATTACAT CACTCGTAA _y TGCCAAGTCT GGTA _A AGCTT	780
TATGCAATTT TGTTAATCGT TCTGAAAATC TATCCATTGT ATACTTACGT CTCATACGTT	840
TTAATACTGT ATCTGAACCA GATTGTAATG GAATATGCAA ATGACGCACA ACTTTTGTTG	900
AACGTTCTAA AACGTCAATT ACTTCATCTG TAAGTTGACT TGCTTCAATT GAAGAAATTC	960
GAATTCGTTT TAATCCATTA ATCGTTTCAA GATCACGTAA TAATTGGGCC AAGTTATAAT	1020
CTTTTAAATC TTGACCATAT CCACCTGTAT GAATTC _C CGT CAATACAATT TCCTTATATC	1080
CTGAATTCAC TAGTTGCGTC GCTGTTCAA CTACTTTTTC CGGATCTCTT GAACGCATTA	1140
AGCCACGAGC CCATGGAATA ATAcAGAATG TGCAGAAGTT GTTACAACCT TCTTGAATTT	1200
TTAATGACGC	1210

(2) INFORMATION FOR SEQ ID NO: 616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 652 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

TAATAAAATA CAATACTTTT CAATACAGAG AATCCCGCAA TGTGGGATT CTTATTTATG	60
CTGATTTTGT TTTTGTCTAT GATCAGGGAC TTTcAGGGAC TCAATTAATT ATCACATTCA	120
TATTTTCTTA TGACCAAATT GATACATATG ATGCTATTTA ATGAGAAAAT TAGGCATCAC	180
TTGGTTATTG AATTTCTTTC ATTAACTTTT CCAGCTCAAT TTAATAGTTA GTCGACTATT	240
ATTCATTAAA CACTTTTTTAA TCATAAAAAA GTGTTTTTGTa TAATTCACTa CCaAAAACAC	300
CTTCTTACTT ATAATTCTAT TTGTTCCACCA TTTCTAATCT TATCGGCTAA ATCATTTCAGT	360
TTTCTTAATC GGTGATTTAC ACCTGATTTT GAAATTGGAC CAGTTGATAC CATTTCTCCA	420
AGCTCTTTCA ACGAAATTTT TTGATCTTCT ACTCGAATTC TAGCAATCTC TCTCAACCTG	480
TCTGGTAAAT TTTCAATACC AATTTCTTTA TCAATCAATT TAATGCTCTC AACTTGTTTC	540
ATCGCAGCAC TAACTGTTTT ATTTAGATTG GcCGTTTCAC AATTAACGAG TCGGTTAACA	600
GAATTACGCA TATCTCTTAC AATACGTACG TCTTCAAATT TTAATAACGC T	652

(2) INFORMATION FOR SEQ ID NO: 617:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

TnACCACTTT AAAATAGCGC TTAATAAAAtG AAGGGGGCAA GTCTTATGAC GtTTTACaAT	60
TTCATCaTGG GTTTTCAAAA TGrtAACACA CCATTTGGTA TATTGGCCGa ACACGTTAGT	120
GAAGATAAAG CATTCCCTCG ATTAGAAGAA AGACACCAAG TAATTAGAGC ATATGTGATG	180
TCTAATTACA CAGATCATCA ATTAATTGAA ACTACAAATA GAGCTATTAG CTTATATATG	240
GCAAATTAAT TTGAGTAGTA CCAATTATGA TGTATTAGTG CATCCCAAAT ATCTTTTGTT	300
TTAAAGTTTA TTTCATCATT TCTTATCGAA AATGGTGTA TAATGTCTTT ATCTAACCAA	360
GTGTTGATAA GTTCATTTGG TACACCATCT AACAACATTT CACTTTTACT AATTATAAAA	420
CATTCCCAGT CAAGTGAAAC ATTTTGTGGA TTCACATAAT TACATTGATT ATGATTATCC	480
ATAAACACTC ACTCCTTTAA AATTCTGTAC TCTTCATTGC GTTTTACCCC GTCACATTAT	540

CTTTTAAACT AAAATCATCA TTACTTATGA AAAAAATGTA CATCAAAAGC AAAGTTTC	600
GCTACCGAAA AAGTTTAAAT AATGGTttAA TATATttGGT ACTCATTTTA ATAAAAAGAG	660
AATACATTTT GAGCTATCAA TACTTTTTAT TGAAGAGGTG TTATTsYtGG CTAAAACGTT	720
ATATTTAATG CGCCACGGAC AAACTTTGTT TAATTTTAAG GGACTAATTc AGGGATTTGG	780
AGATTCGCCG CTAACAGA	798

(2) INFORMATION FOR SEQ ID NO: 618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ATACGCTCAA TTGATAAAAA TTTAATATCT GCCATTTGTA TACGCATCGC TTCGAATGTT	60
TCCGTTGCAA TATCAAATGA TAATTGTGAC TGGAACCTTA AACATCGAAT CATACGTAAA	120
GCATCTTCTT GGAATCGTTC CTCAGCTATA CTACAGTTC TTATTATTCG ATTATTAATA	180
TCTTGTTGAC CATCAAAATA ATCATACAAT TTGTATGCTG TATCCATTGC TATCGCATTC	240
ATCGTGAAAT CTCGTCGTTG CAAATCTTCG TATAAATCAC GAACAAATGT AACACCACTT	300
GGTCTACGGT GATCGACATA ATCTTCTTCA GCCCGGAATG TTGTCACTTC ATAATTTcA	360
TCATtAAAAa CTACATttAT CGTGCCAtGT yCTTnACCTA CAGGTATCGT ATGACTAAAG	420
ATAGATTCTA TTTCATCCGG CGTTGCACTT GTTGTGATAT CTATATCATG AATATTTCTT	480
CCCATGACAT AATCTCTTAC AGAGCCACCT ACATAATATG CTTCAAAACC ATTGTCTTGA	540
ATTTGTTCTA ATATAGGCCT TGCCTGTTCA AATAATGATT TATCCATATT ATTACTCGCC	600
TTTACTTTTG TTATGCTCAT TTAGCATTTT TTGATAATAA TACTCATATT GATCTGTAAT	660
AAGTTCTGAT CCAAAACGTT CAGCAATATC TGCTAGCATG TTTTCTGAA GTTTGTTGTA	720
TAACACCTTA TCTTCAAGTA ATCGGATAGC ATAGTCACTCGCTGAATCAC AATCACCAC	780
ATCTACGACA AATCCAGTTT CACCATGTTT AATAACCTCT TTAATTCCAC CGGCATTTGA	840
ACCAATTGGA ACGACGCCTG TwTTCATAGC CTCAAGTAAA GTTAGTCCAA AGCTTTCTTT	900
TTCACTTAAT AATAATACTA AGTCAGATAA TTGGTAAAAT TCACTTACGC AATCTTGTTT	960
CCCTAAAAAT AAAACATCCT CTTCTACGTT TAACTCTTTC GTCAATTGAC GCATTGGCAC	1020
TAATTCAGGA CCATCTCCAA GTAAATTAA TTTACTAGGT ATCTTTTTCAC GTACTTTTGC	1080
AAATGTTTCT ATAATAGTAT CTATGCGTTT TACTTGTCTA AAATTCGATA CATGTATTAA	1140

CACTTTTTC	A TCTGGTGCTA	TACCAAATTG	TGATTTTAAT	GCTGTGTTAT	GTTTAGTTGG	1200
AAACTCATT	TTCACGTACAA	AATTATAAAT	CGGTATAATT	TCTTTGTTAG	TTTCAATAAT	1260
TTCATGTGT	TCTTGTGCTA	AAGATTTACT	CACACTTGTC	ACAATATCAC	TTTTTTCAAT	1320
GCCAAATTT	ATTGCACCTT	GGAGTGAATG	ATCATAGCCC	AAAACAGAA	TATCAGTACC	1380
GTGTAGCGT	GTCATAATTT	TTATATCTTT	ACCTGACATC	TCACGAGCTA	AAATCCCACA	1440
AATTGCATG	GGTACAGCAT	AGTGCATATG	CAACAAATCA	AGATCATATT	CTTTAATAAC	1500
TTCAGCGAT	TTAGTACTTA	ACGTAATATC	ATACGGTGGA	TACTGAAATA	CTGCATATTG	1560
ATTCACTTC	ACTTGATGAA	AAATCATATT	CGGTAATGGT	TTTCTTATTC	TAAACGGGAT	1620
ATTTGAAGT	ATAAAATGTA	CTTCGTGACC	TCGCTCTGCT	AATTTAATTC	CTAATTCTGT	1680
GGCAATAAT	CCAGAACCAC	CCATGGACGG	GTAACATGTT	ATACCTATCh	TCATTCGCTT	1740
GCCCATCCT	TCTTTCTATT	TCTChCTAT	ATnCTCGATG	CGTAGA		1786

(2) INFORMATION FOR SEQ ID NO: 619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 844 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ACAGGTATGG	ACTTnGCTCA	AATGACACGA	CATTATTTAT	CAAGACCTAT	TGCTATAATC	60
TTTTGGATCA	TTGCAGAACT	AGCAATTATC	GCTACAGATA	TTGCTGAGGT	TATTGGTAGT	120
GCTATTGCTC	TTAATCTCCT	ATTTAACATA	CCTTTAATCG	TCGGTGCAC	TAATAACTGTA	180
CTTGATGTAT	TTTTACTACT	TTTTATAATG	AAATATGGTT	TTAGAAAAAT	TGAAGCTATT	240
GTTGGTACAT	TAATTTTCAC	AGTGTTATTC	ATCTTTATAT	TTGAAGTCTA	TATTTTCATCA	300
CCACAGTTGA	ATGCTGTGTT	AAATGGATTT	ATACCACATA	GTGAAATCAT	TACAAATAAC	360
GGCATTCTCT	ATATTGCATT	AGGTATTATT	GGCGCTACAA	TTATGCCTCA	TAATTTGTAC	420
TTACATTCAT	CAATTGTACA	ATCTAGAACA	TACTCAAGAC	ATAACAATGA	AGAAAAAGCG	480
CAAGGaTTAA	ATTTGCTACG	ATAGATTTCG	ACATTCAGTT	ATCAATCGCA	TTTGTAGTCA	540
ATTGCTTATT	ATTAGTGtTA	GGAGCATCAC	TATTTtkCAA	CTCAAATGCT	GACGATTTAG	600
GTGGTTTCTA	TGATTTATAT	CACGCCTTAA	AAACTGAACC	TGTACTAGGT	GCAACAATGG	660
GTGCAATCAT	GAGTACATTA	TTTGCAGTTG	CATTATTAGC	GTCAGGTCAA	AATTCAACGA	720
TTACTGGTAC	TTTAGCAGGA	CAAATTGTAA	TGGAAGGATT	TTTAAGATTA	CACATACAA	780
ATTGGTTAAG	ACGTTTAATT	ACACGTTCTC	TTGCTGTCAT	TCCTGTTATC	GTATGCTTAA	840

TCAT

844

(2) INFORMATION FOR SEQ ID NO: 620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 574 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

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TGTATTGCAG TCATGCCATA AATTTTTTTGA ATAATAAACG GAGACGCAGA AATATAAGTA      60
AATAATATTA CAAATGTCAT ACCTTGGAAT GAGCATTGGT AATACAAAAC GTGGCGTCTT      120
CAnTAATATT TTGAAGTTTT TAAACATTGT CTTTAaTCCA CTA CTACTTGACT CACGATTTGT      180
CACTGTTAAT GATTCAAGTA CTTTTAATAA AGAACCTATG ACCATGACGA AGCCAAAGAT      240
AGTCAGAATG ACAAAGACCA TACGCCAGAC AGAATATTT AAAATTATGC CCCCTATTGT      300
TGGCGCAACA ACTGGTGCAA TACCATTAAC AAGCATCAAT AATGCCATAA ACTTAGTTAG      360
TTCATTACCA CTATACATAT CACTTGCTAT AGCTCTTGAA ATA ACTGCTG tGCGCCACCT      420
GTCACCTCCTT GAAGaAATCT TAATGCAACC ATCAGCCAAA TATTATGTAC AAAACAATA      480
CCTAAACTTG CTAATGTAAA AATAATCATA GCTATAATAA GCGGCTTTCT GCGCCAGTT      540
GAATCTGAAA TTGGACnAGC AACCAAATTA CCAA      574
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(2) INFORMATION FOR SEQ ID NO: 621:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 523 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

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AAGCAAGAGA GAGTACAACA TTTATATGAT ATTAAAGACT TACATCGATA CTACTCATCA      60
GAAAGTTTTG AATTCAGTAA TATTAGTGGT AAGGTTGAAA ATTATAACGG TTCTAACGTT      120
GTACGCTTTA ACCAAGAAAA TCAAAATCAC CAATTATTCT TATTAGGTAA AGATAAAGAG      180
AAATATAAAG AAGGCATTGA AGGCAAAGAT GTCTTTGTGG TAAAAGAATT AATTGATCCA      240
AACGGTAGAT TATCTACTGT TGGTGGTGTG ACTAAGAAAATAACAAATC TTCTGAAACT      300
AATACACATT TATTTGTTAA TAAAGTGTAT GCGGGAATT TAGATGCATC AATTGACTCA      360
TTTTCAATTA ATAAAGAAGA AGTTTCACTG AAAGAACTTG aTTTCAAAAT TAGACAACAT      420
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TTAGTTAAAA ATTATGGTTT ATATAAAGGT ACGACTAAAT ACGGTAAGaT CACTATCAAT	480
TTGAAAGATG GAGAAAAGCA AGAAATTGAT TTAGGTGATA AAT	523

(2) INFORMATION FOR SEQ ID NO: 622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AGAAGTGTGA nAAAAATTTA AnAGAGATAT GCACATAGAT GACGCATTGC TATATCCAAG	60
CAATTGAGAA AGCTGCTGAT GCTCCAAATC aCGGAATGAG GGAACCATGG AGAGTTGTGC	120
ATGTTCCGAA AGACAGATTA GGAGATATGA GTAAGGATAT TTCTAAATTT GCATTTTCCTA	180
ATGAATTAGA TAAGCAACAA TGTCATTATG ATGCAGTTAC GAAACTAGGT GGCATGTTAT	240
TGCTTATTTT AAAAACAGAT CCAAGACAAC GTCAAAATGA TGAAACTAC TTTGCATTTG	300
tGCATATGCA CAAAATCTTA TGTTGTTACT TTATGAAGCG GAAATAGGTA CATGTTGGAA	360
aTCGCCATTA TATATCTATG ATCCTAAAGT AAGnAAACAC TTGGTATAAA GnAAGATGAA	420
GTTCTTGCTG GATTCTTATA TTTAACGGAT TTAGAAGnAG ATATGCCTAA AGCACCACGT	480
AAAAATAGAA ACTTAATTAC ATTATATTAA TATGTATAAT TATAGAAACA TTAATAAAAG	540
CTGAGTCATG AATTGATGGA CATCTATCGA GTTAGAGATT TAATCTAACT TACTAGAGTC	600
GGTACAATAA CAGTCTCAGC TTTTATTGT GCAGTATATA CACATTTTTA TTTTAGTATT	660
TATTtAAAAAG TtCTGCTaA AAATGATTCA ACTTGTTTCTAG GTGACTTAGC ATTTGCTGAA	720
TGAAGGTGTG CAATTTTATC GCCGTTTTTA AATACTAGCA AGCTAGGGAT ACCCATAACT	780
TCATTTTCAA CAACTACATC TTCTAATTCA TCACGATTAA CAGTATACCA TTGGTAATCA	840
TTATATTGTT CTACGATTGG GTCAATCCAT AAATCCATAG CACGACAGTC TGGGCACCAT	900
CCTGCCTCAA ATTTAACAAT TACAGGTGTA TCGCTATTAA TTACAGATTTAAATGATTCA	960
TTACTTTTGA TTGATTGCAT TGTAACAACT CCTCTAGATA GTTTAATAAT TTTTATTATA	1020
GCTAAATTTA TATCATAATA AAAAATTTTA GCTTCAAAT GAAAGCCTTT TGCTTTGGAA	1080
AATGATATAT TTATTTTAAA TACATAAAGG AGGTTGCAGT CGTATGATTA AATTTTACCA	1140
ATATAAGAAT TGTACAACCT GTAAAAAGGC AGCAAAGTTT TTAGATGAAT aTGGCGTAAG	1200
TTATGAACCA ATTGATATCG TTCAACATAC ACCTACAATA AATGAATTTA AAACAATAAT	1260
TGCAAATACA GGCGTAGAAA TTAATAAATT GTTTAATACA CACGGCGCGA AATATCGTGA	1320
GCTTGATTTG AAAAATAAAT TACAAACTTT ACAGATGAT GAAAAGTTAG AGTTGTTATC	1380

ATCTGATGGT ATGTTAGTAA AGCGTCCTCT AGCAGTAATG GGCGATAAGA TAACATTAGG	1440
ATTTAAAGAA GATCAATATA AAGAGACTTG GTTAGCGTAA GTGaAATGTA AGCGTTTACT	1500
AAATATCTCG ATATTTAGAT TCATTACATG TAAAATGAAA TAAGCTATAC AATTG TA T	1560
TTTTATAAAT ATAGTTGAAT AGCATCTAGC CTTATGGCAT CATTAATGAT GTAAAGATTA	1620
ATTAGGAGGG GATTCTCTTG GCAGTACCAA ATGAAYTGAA ATATTCAAAA GAGCATGAAT	1680
GGGTAAAGT TGAAGGTAAT GTAGCAATAA TTGGAATCAC AGAATACGCA CAAAGCGAGT	1740
TAGGTGATAT TGTTTTCGTT GAATTACCAG AACAGATGA TGAAATTAAT GAAGGGGATA	1800
CGTTTGGTAG CGTAGAATCA GTTAAACTG TATCAGAATT ATATGCACCA ATCTCTGGTA	1860
AAGTAGTTnA A	1871

(2) INFORMATION FOR SEQ ID NO: 623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

TTGCTGTAGA AGATAAAGAG TCCCATCAAT GGAT AG GCTT TATAGGTTTG AATTATATTC	60
CAGAAACAAG CGATTATCCA TTAAAGAAT TACCGCTTTA TGAAATAGGT TGGCGCTTGT	120
TGCCAGAATT TTGGGGAAAA GGATTAGCAA CTGAAGGCGC AAAGGCAACA TTGAAGTTAG	180
CAGAAGAACA TCAAATATAC GATGTCTATA GTTTTACAGC AGAAGCAAAT AAAGCTTCAC	240
AACGTGTAAT GGAAAAAATT GGCATGACAG TGTATGATCA TTTCGAATTA CCCAATCTAA	300
GTAAGTATCA TTTATTaAAA AGGcAAGTGC GCTATTACAT TAATCTTCcG AAAGTGGA	360
AaTTTATACA TAAGCGtAAC aAACACCCc TAACATTGgT TtaGCTGgAT GgATAACmAT	420
ATTAgGGGGT GtTTnGtKn ATTTTTTTAA n	451

(2) INFORMATION FOR SEQ ID NO: 624:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

CGATAGTTAT CTAAAGCCAT TTTnGATTGT GTTATGAAAT CTAATGATGC GTGATAATTT	60
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AATGCrACAT AACGrTaATA TAAAATATCA ATAGTGAACA TTTGAGCAAA TAATGAAGTT	120
GTTGCTCCCA TATGCATCTC ATTTTCATCA GTTTTCCC AAGTTAAAAC AATATTTGAT	180
GCCTGTGCTA CGGGATTATC CCTTGTAATA GTAATTGTAA TTATAGGTAT ATGGTAGTCA	240
TCAATAACTT TAACCATTGA TTGCATTTCA CTTTGCGTAC CATTGTTAGT AATAAGAATA	300
aCACTGTCGT TCGAATTGTG AGTTGCTAAT AATGTAGCAA AAATATGTGT TTCTTGAACA	360
AGTTGAATAT TAAGACCTAT TCTTGATAAC TTTTGGTATA AGTCGGTAGC AACTACAAAA	420
GATGCGCCAA AACCATATAT AAAAATCGTC TCAGAACGTT TTAAACAATG ACATATTTGA	480
TCAATAGTTT TATCATTTAA TTCGTTATTT GCATGATTAA GTGCGCGTGT AGTACGTGTA	540
TGGAGTTTAG TTCTTAAAGA TTCTGTGCTT TCGTTATTCA TTAATTCAAC ATTGTAAATT	600
GATGATGCTT TAGGAACATA TTTAGATATA TTTATTTTCA AGTCGTGAAA ACCGCCATCA	660
GTAAT	665

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

GATGCCAATT AACCGTGCAT ATAATGTTGA GAAGTTAATC AAGCAATTC AATATTATCA	60
AGAAAAAACA AATCGTCGTG TTAATTTTGA ATATGGTCTG TTTGGTGGTG TGAATGACCA	120
ACTAGAACAAT GCAAGAGAAT TAGCACATTT AwTAAAAGGC TTAAACTGCC ATGTAACTT	180
AATTCCtGTC AACCATGTTT CAGAAAGAAA TTATGTGAAA ACGGCTAAAA ATGATATCTT	240
TAAATTTGAA AAAGAATTAA AGAGACTAGG AATTAATGCC ACAATACGTC GTGAACAAGG	300
TTCGGATATT GACGCAGCTT GTGGTCAATT AAGAGCAAAG GAACGACAAG TAGAAACGAG	360
GTAAAGACAA ATGCTAGAGG CACAATTTTT TACTGATACT GGACAACATA GAGATAAGAA	420
TGAAGATGCG GGTGGTATTT TTATAATCA AACTAATCAA CAACTTTTAG TTCTGTGTGA	480
TGGTATGGGT GGCCATAAAG CAGGAGAAGT TGCAAGTAAA TTTGTTACAG ATGAGTTGAA	540
ATCyCGTTTT GAAGCGGAAA ATCTTATAGA ACAACATCAA GCTGAAAATT GGTGCGTAA	600
TAATATAAAA GATATAAATT TTCAGTTATA TCACTATGCA CAAGAAAAE CAGAATATAA	660
AGGTATGGGT ACAACATGTG TTTGTGCACT TGTTTTTGAA AAATCAGTTG TGATAGCAAA	720
TGTCGGTGAT TCTAGAGCCT ATGTTATTAA TAGTCGACAA ATTGAACAAA TTACTAGTGA	780
TCACTCATTT GTTAATCATC TTGTTTTAAC GGGTCAAATT ACGCCGGAAG AAGCATTTAC	840

ACATCCACAA CGTAATATTA TTACGAAGGT GATGGGCACA GATAAACGTG TGAGTCCAGA	900
TTTGTTTTATT AAGCGATTAA ATTTTTATGA TTATTTATTA TTAAATTCAG ATGGATTAAAC	960
TGATTATGTT AAAGACAATG AAATTAAGCG TTTGTTAGTA AAAGAAGGTA CAATAGAAGA	1020
TCATGGTGAT CAATTAATGC AATTGGCATT AGATAACCAT TCGAAAGATA ACGTTACTTT	1080
CATACTCGCG GCTATTGAAG GTGATAAAGT ATGATAGGTA AAATAATAAA TGAACGATAT	1140
AAAATTGTAG ATAAGCTTGG CGGCGGTGGC ATGAGTACCG TTTATCTTGC TGAAGATACG	1200
ATACTTAACA TTAAAGTTGC AATTAAGGCG ATTTTTATAC CACCTAGAGA AAAAGAGAA	1260
ACATTAAAAC GTTTTGAACG AGAAGTACAT AACTCATCAC AGCTATCACA TCAAAATATA	1320
GTAAGTATGA TCGATGTTGA TGAAGAAGAT GACTGTTACT ACTTAGTAAT GGAATATATC	1380
GAAGGTCCGA CTTTGTCTGA GTATATTGAA AGTCATGGGC CATTAAAGTG TGACACAGCG	1440
ATTAATTTTA CGAATCAAAT ATTGGATGGC ATTAAACATG CGCATGATAT GCGTATTGTA	1500
CATAGAGATA TTAAGCCACA AAATATATTA ATTGACAGCA ATAAAACGTT GAAAATATTT	1560
GATTTTGGAA TTGCTAAAGC TTTAAGTGAG ACGTCTTTAA CTCAGACTAA TCATGTGTTA	1620
GGTACTGTGC AGTACTTTTC GCCAGAACAA GCAAAAGTG AGGCAACGGA TGAATGTACA	1680
GATATTTATT CTATAGGTAT kGTGTTATAT GAAaTGCTTG TTGGTGAACC ACCCTTTAAT	1740
GGAGAAACTG CAGTTAGCAT TGCGATTAAA CATATTCAGG ATTCTGTGCC AAATGTGACA	1800
ACAGATGTAC GTAAGGATAT TCCGCAATCT TTAAGTAATG TCATTTTACG CGCTACAGAA	1860
AAAGACnAAG CGAATCGTTA CAAAACAATT CAAGAAATGA AAGATGATTT GAGTAGTGTT	1920
TTACATGAAA ATCGAGCGAA TGAAGATGTC TATGAACTCG ATAAAATGAA AACGATAGCG	1980
GTACCTTTGA AAAAGAAGA TCTAGCAAAG CATATTAGTG AACATAAGTC GAATCAACCT	2040
AAACGTGAAA CrwCGcAAtA CCTATTGTAA ATGGGcCTGC TCATCATCAG CAwTTCCmrA	2100
AGCCAGAAGG TACGGTGTAC GAACCAAAAC CTAAAAGAA ATCAACACGA AAGATTGTGC	2160
TCTTATCACT AATCTTTTCG TTGTTAATGA TTGCACTTGT TTCTTTTGTG GCAATGGCAA	2220
TGTTTGGTAA TAAATACGAA GAGaCACCTG ATGTAATCGG GAAATGTGA AAAGAAGCAG	2280
AGCAAATATT CAATAAAAC AACCTGAAAT TGGGTAAAAT TTCTAGAAGT TATAGTGATA	2340
AATATCCTGA AAATGAAATT ATTAAGACAA CTCCTAATAC TGGTGAACGT GTTGAACGTG	2400
GTGACAGTGT TGATGTTGTT ATATCAAAGG GCCCTGAAAA GGTTAAAATG CCAAATGTCA	2460
TTGGTTTACC TAAGGAGGAA GCCTTGCAGA AATTAAAATC GTTAGGTCTT AAAGATGTTA	2520
CGATTGAAAA AGTATATAAT AATCAAGCG	2549

(2) INFORMATION FOR SEQ ID NO: 626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

TGCTTACTTC GCCTTCAATA CGTACTAATT CATGTCCACA ACTTGGACAA TGGGTTGGCA	60
TATGATATGT GACAGCATCC TQAGGTCTAC GTTCTGGAAT ACTACGTACA ACTTCAGGTA	120
TGATGTCACC TGCTTTTTTTC ACTACAACAC TATCACCAAT TCGAATATCT CTGTCATGAA	180
TTAAATCCTC ATTGTGCAAA GATGCTCTTG aTACAGTTGT ACCAGCTACT TTTACTGGTT	240
CTAAAATAGC AGTAGGTGTG ACTACACCTG TTCGTCCAAT ACTTAATCA ATATCTAATA	300
ATTTAGTTAC TACTTCCTCA GCTGGAAATT TATAAGCAAT GGCCCATCTA GGAGATTTTT	360
GTGTGAATCC CATCTCATCC TGTTGATCTA AATCATTAAC CTTAATAACA ATCCCATCAA	420
TATCATAAGG TAATGACTCT CTTTGGCTTG TCCATTTTTTC AATATACTCT AAAACACCAT	480
CGATATTATT TACACGCGCT CTATTTTTTAT TCGTTGTAAA ACCTAATTTA TCTAACTCAT	540
CTAATGCTTC ACTTTGCGAA CGCGCATTGA AATCAGTGAA ATCATTGACA CTATATATAA	600
ATACGCTTAG CTTTCGTTTT GCCGTTAATT TAGAATCTAA CTGTCTTAAT GATCCCGCAG	660
CAGCGTTTCT TGGATTnGCA AATAACTGCT CATCATTTTT TTCTTTTTCT TCATTTAATC	720
GTAAAAATGA ACGTCTCGGC ATATATGCTT CACCACGAAC TTCTACATTT AATGGtTCTT	780
TCATTTTCAA AGGTATCGCA TGAATTGTTT TTaAATTTTC GGTAATATCT TCACCTGTTG	840
TTCCATCACC ACGTGTTAAA CCTTGaACGA AGTATCCATC AACATATTTT AATGtACTG	900
CTAAGCCATC AATTTTTTAAT TCGCACATAT ATTCAACGTT GCCAATTGTG TCACGTATGC	960
GTTGGTCGAA TTTTCTCAA TCATCCTCAT TAAATGCATT CCCTAAACTT AACATTGGCG	1020
TGTCATGGTT GACTTTATTG AAAGAGGCTT GGGCTTCACC GCCAACTCTA ACTGTTGGAG	1080
AATCTACAGT CTTATACTCA GGATGCTCCT CTTCTATTTT AATCAGTTCA TGAAGTAATT	1140
TGTCATATTC ACTATCTGGT ACAGATGGAT TATCCTCTAC ATAGTATTCA TAACTGTATT	1200
GATTTAATAA ATCATGTAAC TCGTTCACAC GAGACGATAA ATCAGCCATC CCTTAATCCT	1260
CCTTTTTTtC AATTGGTGCA AATTGCGCTA ACAAACtTT TGGCCCTTGT GATTTAAAGA	1320
TAATATCTAG TTCGATTGAG CCATTTTTCT CGTTTACATT ACTCACCATG CCTTCTCCCC	1380
AGGCTTTATG CATCACTTTG TCACCTACAT TCCAATCAGA TGACAATACT TGTTTTTTCG	1440
TTGACGTTGT TCGTTGACTA AATCCGCGTT TAGCAAAAGG TTTTGCCTTA GGTTGTATCG	1500
TTTGTCGTTT GCCACTTGAA TGATTTTCTA ATAGTGATTG TGGAATTTCC TTTAAAAATC	1560

TGGATGGCAT ATTTGACTGA GGGCGACCAA ATAACATTCT TGATGTCGCA TGAGTGATAT	1620
ATAACACCTC TTCAGCCCTT GTAATTGCTA CATAACAAAT ACGACGTTCT TCTTGCAATTT	1680
CATGATCATC TTCACTCTTA ATCGCTCTAA TATGTGGGAA TAAAGATTCT TCCATCCCCA	1740
TTATAAAGAC AATTGGAAAT TCAAGGCCCT TAGCCGAGTG CATCGTCATT AGTGTTACGC	1800
CATTTTCAGT ATCTGCCTCA TCAATATCAG CTACTAACGA TAAATCCGTT AAAAAGTTAA	1860
TTAATGACTG TTCTTCTAAT GGGGTATTTT CCTCATAGTC TTTTGGTACT GACATAAATT	1920
CATCGATGTT TTCTAATCTA CTTTCGAGATT CTAATGTATT TTCACGTTCA AGCATTCTCT	1980
GATAGCCAGA CTTTTGTAAT ACTTCATCAA CTATTTTCATG AATTTCTAAA AATTCTTGTT	2040
CTTTTATCAA GCTTTGGATT AACTCGTAAA AATTAAGACA CTCTTGTGTC ACCTTTTTTG	2100
aCAATCCGAT AAAATCAGCT TCTCCAAGTG CATCAAACAT ACTGATATTG TTTTGAAGTG	2160
CATAGTTTTG AACTTTTTCA ACAGATGAAG GACCTACACC TCTTTTTTGA ACATTaATAA	2220
TACGTTGCAA ACTAATGTCA TCATTACTAT TGGCAATTAT ACGCAAATAA CTTAATAAAT	2280
CTTTGA	2286

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

GAAGAATATT GAAGTAGGTG ACCAAATTGA AGTCAAAGTC ACAGACCCTG GATTCCCTAG	60
TGACATTAAA AGTTGGGTGA AnAAACAAGG CATACTTTAG TTAAGCTTGA TGAAAATAAC	120
AATGGAATTA ATGCGATTAT TCAAAAAGAA AAAGCAAAAG ATTTAGAAAT AAATTATTCT	180
GCTAAAGGTA CTACCAATTG TATTATTTAG TGGAGAATTA GACAAGCTGT AGCAGCGTTG	240
ATTATTGCCA ATGGTGCTAG AGCTGCTGGA AAAGATGTAA CTACCTCCTT ACTTTTTGGG	300
GGCTTATGCC nTTAAAAAAG TGCCACCGTT AATGTTAAAA GCAGTTGCCA AAATGTTTGA	360
TTnATGTTGC CCCAAAAGAT TTACGATGCC CCTTCCCAA	400

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

AATAATTTGG GCGCTnTTTG CGTCGGGATA TTATACCGCT TCCTTAATTG TTCAACATTG	60
TAATCACTGT TTTTCAATTG ATATTTTGCA GAGTAAATTG GTACTTCTGG GTTATATGAC	120
ACTTCGTCCT CTTTATAGTT TTCCAATTCT TTGAAATTCC CGTATTGTAC AAAGAAGTTA	180
AATTCTTCGA TTTCTTTTTT TACTTTTTTCG TCATCGATTG GTTTTAATGG AATCATTTTA	240
TTAkTTTCCA TTTTCACAGG ATATCTTTTT GTATGATTGT GTGTCATTCC ATCGCTATCT	300
TCAACAACTT CTCTAACAAT ATAATGCCCT TTAGCCGTTT TAGTATTTCT ETA ATTTCT	360
AAAAGTCTC CTCTrGATT CAGATTTTCT CCTTTTAATT GGATTTTCAT TTCAGATCTA	420
ATTAGcCAAG TACCTTTATC ATCTtTTTTA AAT	453

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

TCATATGCAT TTGCAAAATA AACGCCAGAA GCAAGGTTTA GAATTGGGCC GTCCGTTTTG	60
CTCAaTTCAC TTGcATTCAA TAATTCATGC TGATCATGAT CAATTTGCTT ATCTAATTCT	120
GCaATTTTCT TCATTTGCTT ATCTGATTTG TTTTCTTTTCG CCATCATTTG ATCACGACGA	180
TTTTCTTTGT CATTCAATTC CTGTTGCAAC TTTAACACAT ATTCATCAAG GTCAATATAT	240
GCTAATGGTA CTAATACTTT ATCTCCATr GTGTCAATAA AGTTATAAAA ATAATCATCT	300
GTTTTTGATA CAAATCCAGC ACGCTCTTCA GTTTCACGAT ATAAATCTAA GAAAAGATTG	360
AACTCATCAC GTTCAAGGAA TCTGACTTTA ACACCATAGT TTATCGCTTT ATTAATATTA	420
CGTTTACGTT GACTATCAAA TGTCTTTTTT AATGTTTCGG GTGTTTTACC TTCAGGTTT	480
AATACGCCCA TCCATCGTAC TTGGCTCGAT GTATCATACT CAGTTGTAAA GCCATGATGC	540
TCGTAACCAT GTGATTTAAA CAAGTTTACT AGGGCATCAT TTTTCTCGCG ACCTTCAAAT	600
GGCACGATAT CTTTATCATA TAGATGATAT AACCAATACG GATCTAATTT AACATATAAA	660
CATTGATGTT GCTGTAAATA TTTATCTAAC TCTTTTAAAT AATAATCAAC TAATCCTAAA	720
TCTGAAAAAT CCATTACTGG ACCACGATTC GAATAGTAAA CATAACTTCC CATAGTAGGA	780
ATTTTAGAGA AAAGGCTTGC TGCAATTACT TTGTTATTGT CGTCTTTAAT ACCTAATAAA	840
ACTACTTCAA AGCCATCATT CTCACGGGTA ACTATrTTT CTTTACTTG GAAATAATGA	900

CTTTCCAATG ATGGATTTTG TACAAAGTTG TCAAATTCGG TAACAGTTAA CTCTGTAAAT	960
TTCATGTTTT GATAATTCCT TCCTAAAAAA TTCTGTCTTT AACTTTTTTTA AGTGCGGTAT	1020
ATGCTGCGTA AACAGGTTTA TTAATTGGTT TAATAAAGTC ACCAACATAT TCmATAATTT	1080
CAGCATTGTA ACCTTTTTTG AATTAACTA CACCAGCATC TTCAGCATCT TCTGTAAATT	1140
TrCCACTAAC ACCATAGAAA TTATAACGGT CAATGCATGA TTTAATGCAT AATTAATCAT	1200
TTCCCATTGC ACTGCATAAC T	1221

(2) INFORMATION FOR SEQ ID NO: 630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

TGGCCCAAnT AACACAAGTA ATTGCTGCTA ATGGTAACAT CACAAAAAAT GAAATCGTAA	60
CTACAAATGT TAAACCTTGG AATACACCAA CCATTTCTGG TAATCGTTTA CTATAGTATC	120
TATTGTGAAT CCAAGTAATA ATAGCTGAAA TAATAATACC ACCTAGAATA TTCGTATCCA	180
ATGTGGCAAT ACCTGCAATT GATTTTAAAC CAGGTACAT TTCAACGCCT TTTTCTAAAT	240
TAGCGCCAAA CGTATGTGGC CATTGTGTTA AAATGGCATT TATAAATGTA TTAAACATTA	300
AGTAACCCAT CAATGCTGCA AGTGCTGCAT GACCTGGTGC TTTTITAGCT AAAGAAAGTG	360
GTAGACCTAC AACAAATACA ACTTCCATAT GCGTAAAAAT AACCCAGCCA CCAGATTCTA	420
TTACTGACCA AAATTTAAAC CAAAACGTAT GTTGATCTGC TAAACTCCCC ATGATTGTAG	480
GATTTTTTAAA TAATGTCGCA AAGCCAAGCA CTATCCCAA GAAAGCGAAC ATTAATACCG	540
GTACAATCAT TGCCTACCG AAACGCTTTA TCGCATTCAT CTTCTATTCC CTCCATATCA	600
TCTTTCCTAA CAATACATCT AATTAGATTC ATTTATAAAT AGATGTCTTA CTATTTAAAT	660
ATAATATATA GTAAACGCTT ACACACCTAC AACGACATTG ACGTATTTTG AAAGTATTTT	720
GTATAATCAG ATTATCTTTT CATATAGTGA AAATTTTTTC ACGACCTTAT ATATGACATC	780
GTTGTATTTG TAATACATTC GTTTTAAACG CATAATCAA CCTATCAA TACACAAATA	840
TATATAATGA CATAAAGAT TTTAATGTAA TAACGATCTA TTACACATTT ATTTTCAAGG	900
AGGTTGAATA TGTTTTTAGA TGAACACATT AATCGAACT TTGATAAACT TAATGATAAT	960
GATTTACATA TCGCTCACTT TATCAATACA CATATAGATG AATGTAAAAA TATGAAAATA	1020
CAAGATTTAG CGCAATTCAC ACATGCCTCG AATGCAACCA TTCACAGATT TACACGCAA	1080

TnAGGTTTTG ACGGTnATAG TGGATTTAAA TCGTACCTTA A

1121

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4005 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

AACCTTCCAT TTTACTTGAT CGATAACATC AGTTCTGCTT TACAAATCTC TTCATTAATA	60
TGCGTCTTAA AACCATGAAA TTACATGT TCCGATAAAT GATAATCTTC TACAAGTTGT	120
CGATATTCTG ACAAACCATT TCCATGTCCA TAAATATTCA ATTGAATATT GGGATGTTTT	180
GTTACTAATT GCTTGATTAC TTCAATTTGA TGTTTAATTT GTTTATTTTC AACGAGGCGA	240
GCAATTGATA TGATATGATT TTTCTCCTTT TGATTGATGT CAAATTGAA CTTTAAATTT	300
GCCACGTAGC CAACCGGAAT ATTGATAACT GGTATTTTAT TTTCAATATA TTGTGAAATA	360
TCTTGGCATT GCTTTTCTGT TGATACAACA ATCGCTTTAT AACGTGTTAA ATTATTAAAC	420
ACTGTTTTAT AAAAATTTT TATACCATTA CCGGCACCGG ATAAATGTGT ACTATGGAGC	480
ACAACAATAA CTGGAATACT TTGATTTAAT CCCGCTATAA CATTTCTTAA TTCATGAGGA	540
CGATCTAATA TGATTTGATC ATTATTTTTA CATAATTGAT GGAGAAAATA TTGAACTAAT	600
TCATCTTCTG TATCAAAAAA TTGTTGATGC TGGTCTTCAT TTAAGATAAC CTTTGTGAGC	660
GTGTTTTTCC CTTTTATATC GTCAAAATAT TTTTGGATGA CGATTTCCTT ATTAGGTGTA	720
TAGTAATTTT CGAGTACAAT CCGTTGTCCT TCACCTAAAA TTCGAGAACA ACTTAAAAAG	780
CCTCTTCCAT CATACAATTC GCGTTTTACT TTTCTTCTTT TATGATCAAA ATAATTCACA	840
TAATTTAATT GATGATACTG TTTATCTAAA AAATGAGCAT ACATTACAAA TTGCTTCTCA	900
TCATATATTC TGACATCATT TGAATTTTCC ACAAATTTCA ATGTGTACCT ACATGACTTT	960
TCCCAATACT GTATCCAGTT AACTTGCTTT GTCTTTTTAT AATTGATTGC TTTTGGAAAA	1020
TAGTCATACA TTGTAAATAC ATCATTTTCA ATCTGATGTT GCTTCGCATA TGTGTATGAA	1080
TAAGGATTCC ATTTAACATA TACACATTTT GAAGATATGC CGTGTTGTTT GAACAACCTC	1140
AATCTATTTA TTTGCGCTTT TTCTACACCT GTAATTTTAC TTTCTAAAAT TGTTCTTAAA	1200
ATGTAATTCA TATTATCGCC TCATATAAGT TTTATTCCGT ATCTTTATTG TTTATTTTAT	1260
ATGAAAAATA CATCTATTGC ATGTGTAATT ATAAAAAAC CAGGCCACAA GGACCTGGGT	1320
CATATTGTAT TATTTGTTTT GTTTTTTGCG ACGACCGAAT AACAAATATG AACCTAATGC	1380
TGCAAATAAT CCACCAAATA ACGTTGCGTT ATTTGAGCCG TTATTTTCAC TACCTGTTTC	1440

TGGTAATGCT	TTTGCTTTAT	TGTGATGGTC	TTTAGTAGTA	CTCATTGGTT	TAACAGGTGT	1500
ATGTTTTTCCT	GCATCCGAGT	CTGAATCGCT	GTCTGAATCA	CTGTCTGAGT	CTGAGTCGCT	1560
ATCAGAGTCT	GAGTCGCTGT	CCGAATCTGA	GTCGCTATCT	GAGTCTGAGT	CGCTGTCTGA	1620
ATCTGAATCA	CTGTCTGAGT	CTGAGTCGCT	ATCTGAGTCT	GAATCGCTGT	CTGAATCTGA	1680
GTCGCTATCT	GAGTCTGAAT	CGCTGTCTGA	ATCTGAGTCG	CTATCTGAGT	CCGAATCGCT	1740
ATCTGAATCT	GAGTCGCTGT	CTGAGTCTGA	GTCGCTATCT	GAGTCTGAAT	CGCTGTCTGA	1800
GTCCGAATCG	CTATCTGAAT	CTGAGTCGCT	GTCTGAGTCT	GAATCGCTAT	CTGAATCTGA	1860
GTCGCTATCT	GAGTCTGAAT	CGCTGTCCGA	ATCTGAGTCG	CTATCTGAAT	CTGAGTCGCT	1920
GTCTGAATCT	GAATCACTGT	CTGAGTCTGA	GTCGCTGTCT	GAGTCTGAGT	CGCTGTCTGA	1980
GTCACATCT	GAGTCTGAAT	CGCTGTCTGA	TGTATCTTCT	TCGAAGTATC	CGTTATCAAG	2040
TGTGAAATCA	TCATGATCCG	TAATTGTTAC	GTCAACTTCG	CCACCATCTG	CATCTTTATC	2100
ATCTTCAGTT	GTATTTGTAA	CTGTTTGTGT	TAAGCCAGCA	GGCTTTTCAA	AAATAACTTT	2160
GTATTTACCG	CTATCTAAAT	TATCAAAGCA	GTATTTACCA	TTTTCATCTG	TTTTAGTTGT	2220
TCCAATTACT	TCGCCTTTTT	CATTTAATAA	AGTAACTTTA	ACATCTTTGA	TACCTTTTTTC	2280
AGTTGAATCT	TGTTTGCCGT	CTTTATTAAT	GTCGTACCAA	ACATAATCAC	CTAAACTATA	2340
TTTTGGTGTT	TTATAGAAAC	CACTGTCTAA	TGTCATGTTA	TCTGCATCTT	TAATGACACC	2400
TGTTGTTGTT	AAACCATTAG	AATCTTTTTTC	AGTATCATTT	CCAGAAGTTA	CTGAAGTTGG	2460
TGTATAACCT	GATGGTGTCT	CGAATTCAAC	TTTATAAGTT	CCATTGTTTA	AACAGTGAA	2520
TTGATATTTA	CCATTTTCAT	CTGTTGTAAC	TGTTTTTAAA	ACTTTGTCGT	TTTCATCTTT	2580
TAACGTAACT	GTTACACCTG	AAATGCCCTT	TTCATCTTTA	TCTTGAACAC	CGTTTTTATT	2640
TGTATCTTCC	CATACATAGT	CACCTAAGTT	GTAAGTCGGT	TTGTAGAAAC	CAGAGTCAAT	2700
AGTATCGTTA	TCTTTATCTT	TAATGACACC	TGTTGTTGAT	GTACCATTTG	AATCTATACC	2760
TTCATCAGTT	CCTGAACCTA	CTTGTGTTGG	TGTGTAACCT	GATGGTGTTT	CGAATTCAAC	2820
TTTATAAGTT	CCATTTTCTA	ATCCAGTAAA	TTGATATTTA	CCATCTTTAT	CTGTTTTAGT	2880
TGTTTGTAATA	ACTTCACCGT	TTTCATTTTT	CAATGTAAC	GTTACGCCTG	AAATACCTTT	2940
TTCAAGTTGAA	TCCTGCTTAC	CATCTTTATT	TGTATCTTCC	CATACATAAT	TACCTAAATT	3000
ATATTTTGGT	GTTTTGTAGA	ATCCACTATC	TAATGTCATG	TTATCAGCAC	CATTAATAAC	3060
ACCTGTTGTT	GTAAACCAT	TAGAGTCTTT	TTCAATGTCG	CTACCAGATG	TACTGTAGT	3120
CGGTGTATAG	CCTTCTGGTG	TAGTAAATTC	AACTTTATAA	TTACCATTAT	CTAAATCAGT	3180
AAATTTATAT	TTGCCATCAG	CGTCTGTTGT	AACTGTTTTT	AaCAgTTACC	GTTTTCATCT	3240

TTTAATGTTA CCGTTACGCC AGATATACCT TTTTCATCTT GGTCTTGGAT ACCATTTTTTA	3300
TTTGTATCTT CCCAGACATA GTCACCTAAG TTGTATTTAG GTTTGTAAAT ACCTAAGTCT	3360
GCAGATAAGT TATCTTTGCC ATTAAGTGA ATAAGTGAAG ATAAGCCGTT TGAATCTAAT	3420
TCTTCGTTAT TACCTTGTTT TGAAGGGGTT ACTTCATAAC CTTTTGGTAA GTTTGAAAAT	3480
TCTACACGGT AATCTCCATT AGGTAAGTTT GGAATCAAGT AGACCCATC TTCTTTAGTA	3540
ACTGCTTCTC CTACTTTTGT ATTTGTATTA TTATCAAATA CAGTTACAGT TACATTGCCA	3600
ACGCCTTTTT CTCCTAATTC TTGAACACCG TTTTATTAG TATCTTCCCA TACGTAGTTA	3660
CCAATTTTAT ATACTTCTTG ACCAGctCCG CCACTTTGGT TATTAGTAAA TCCTAAAGCA	3720
TTGCCAGTAG AAACGGATTT ATTACCTGTT GAAGATAAAG TAGCCATTTG AACAAGTGTT	3780
GGGCTTTTCGC TATTTGTATA TTGGAATTTT GTATTAACCA TTACAACATA AGCAGAATCT	3840
GCATTTCCAA AATCAATAAC AGCGCTATTG TtGTCGCCAT ATGTAATTTT CTGCAAGTAT	3900
TGATTTGTTA CATCTGTAAG CTCTTTAGTA TTCACATCGT ATCCTTTATT TAATGTATAA	3960
CCTTTAGGAA CTTGATATAT TTTTATATCT GTTACATCTT TATTT	4005

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

TATTAGGTTA CTCTAGTTTC CAAAGCGGGA ATTTTAATGT TATTAACAGC AAGGACAGCA	60
AAAGCAATAT CGGCGCATTG ATTGAAAATC CAGGAATATA TCCTTTATG TCTGGATATG	120
AAAACTTGAA GTTATTGAAT GAATCAAAAA AACTCAAGA TATCGATAAA ATTGTCTCAC	180
AACTTCATAT GGATGAATAC ATTCATAAAA AAGCTAAAAC GTATTCTCTT GGTATGAAAC	240
AAAAATTAGG AATTGCTATA GCATTTTTTAA ATAAACCTCA ATTCATTATC TTAGATGAAC	300
CAATGAATGG CTTAGATCCA AAAGCTGTGC GAGATGTACG TGAATTGATT GTCCAAAAG	360
CGCAAGAAGG TGTTACTTTC TTAATTTTCGA GTCATATTTT AAGTGAATTA GTTAAAATCA	420
CAAACCTCTAT CCTTATTATT AACAAAGGTA AAATTGTTAC AGAAACATCG GAAGAAGAAC	480
TTAAACAATT TAAAGATAAT GATTTAGAAA ATGTATTACT AGAAATCATA GAAAGGGAGG	540
ACCAAGCATA AAATGGGAAC TTTAATTAAA CAAGAATGTT TCAAATTATT TAAAAAGAAA	600
TCAACTTTTA TCGCACCTAT TGTCTTTATT CTAATAATGG TTGCTCAAGG TTATATTGCT	660
ACAAAATACA ATGAAATTTT TACGCCACAG GAATCTTTC CATCTGCTTA AATGGTTTT	720

TCATGGTTTG CATTTTTATT AATTATTCAA GCAAGTACAA TCATTTCAT GGAATTCAT	780
TACGGTACGA TTAAAAATTT ACTCTATCGT GAATATTCAA GAACAACTAT GATTGTTAGC	840
AAAATCATCA CATTATTTAT TATTTCTTTA ATTTATTTTG TTATTACAAT TATTGCTTCA	900
ATTGTTATTG GGTCTTTATT CTTTAATGAT TTAAATATAT TTGAAAGTAG CGGTAATCAA	960
TTATCTTTAT TGAATCAATT ATTATTAGTT AGTTTAGGCA CATTTGTTGG CGTTTGTTA	1020
GTTTTAAGCT TAACGTTGCT ATTATCATCT GCAACAAATT CAACGGGAGT AGCCATTGCT	1080
GTAGGTATTG TTTTTTATTT TGCAAGTTCT ATTTAGCAG TTATTCAAAC GGCACTTTTA	1140
GAAAAAATAG ACTGGCTAAA GTGGAATCCT ATTAATATGA TGAATATTAT GCTTCAAACA	1200
GTTGAAAAAG GCTTTAGTAA GTCGACAAAA TTAGAACTTC ATGAATTGTT TATTGGTAAT	1260
ATTGCTTATA TTTCTATTTT CTTAATACTT GTAGTATTTA TTTTCAAGAA GAAAAATAT	1320
TAGTAACTTA AAGTATTAAA TGTCTAAATA CACACATATT CCATCGTAAT TCAAAATCAT	1380
TTTCAAATCC CTTACCCAA ATAATGGTGC GGGGATTTTT TCATCCAAAT TTTGGAAATT	1440

(2) INFORMATION FOR SEQ ID NO: 633:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

GCTGACATAA TTGCATCAAA TTTCACATCC CCATAAAAAT CGCTACCACA TAACCTACGA	60
TAATACCTAC AAGAACTGGA ATTAAAGATA GGAATCCTTT AAAAAATCCT TGAACGACTA	120
TTGTTACAAG CAAGGTTATC ATTGCAACAA TTAAGAACT GATATTGTAA CCTTTCATAT	180
CTCCAGGATT TTCATACATT GCCATATTGA CTGCAGTAGG CGCTAAGCTT AAACCAATTA	240
CCATGATGAC TGGTCCAACA ACAACTGGTG GTAATATTT CATTAACCAT GCTGTCCCAC	300
TTAATTTGAT TAGAATCCCG ATGATGACGT ACATAACACC ACTCATGAAT AATGCTACAA	360
GCATGTCTCC TAAGCTATGC GTACTTAATC CCGTGATAAT TGGCGTGATA AATGCAAAGC	420
TAGATCCCAA GTATGCTGGT ATTTGCGCCT TCGTTATTAA GATATAAAGT AATGTACCGA	480
TTCCCGAAGC TAGTAACGCT GCTGATATTG GTAGTCCTGT TAAGAATGGT ACTAGTACTG	540
TTGCGCCAAA CATCGCAAAT AAATGTTGTA AGCTTAAAA TGCCCATTCG GCTGGTTGTG	600
GTTCATTCATT TACATCTAGT ACGGGTTTTA CTGTTTCGTT AAACATTTCA TCATTTTGCA	660
TAATATTCAT TTCCTCCGAT AATAAAAAA TCTCTTTACA TCAGTATATG TAAAGAGACA	720

AAAAGTGTGA CAAGTTGCTA CAAGTCATTT TCGTCCATAG AAATTGACTT ATAGTTGTCTG	780
AACATGAGGG TATTATTAGA TAAACAAGCA TATGAAACT TATTTATCAT TCAACTCCCC	840
CACCTTTTTT AGTCTCTCGT ACTGAATTAA AAGGGGtATT ATTAATTAT AACTGCATTT	900
CTTTGATCcA TttCTTCyAA ATAGACACTT ACCGTTTCCT CTTTAGAAGT AGGTAWATTT	960
TTACCAACAA AATCTGCTCG AATTGGTAAC TCACGATGTC CTCGATCAAC CAAAGCAGCT	1020
AAACCAATTT TAATAGGTCT AGCATTTAGC AAAATAGCAT CAAGTGAAGC ACGAACC GTT	1080
CGACCAGTAT ACAGCACATC GTCAATAATG ATGACTACTT TATCTGTAAT ATCTGTGTCTG	1140
ATGTCTATTG CGTCTTTTGT CGTAAGTGAT GACATGTGcT CTATATCATC TCTAAAGTAT	1200
GTAATATCAA TTGTTCCAGT AGGTATACGT TGTGCTCAA TTTGATGAAT TttATCTTGT	1260
ATACGATTCTG CTAAATATTC ACCTtTGTh TTGATACCTA AAAGATTAAA TTATCAGTAC	1320
CTT	1323

(2) INFORMATION FOR SEQ ID NO: 634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 761 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

ACCCATCTCA TCGTATTTTG AATTTAATAG ACGAGATCGA TGTATATCTG AATTCATCCC	60
AACTATGGAT TAATGTTGGT ACATCATtAA cGCATAACCA ACATTTEAG CAGTTGTTTT	120
ATAAGTAACG TGATTTTTAT CTAATTGCCC TCTTAATGCG TCCTCTGTAA ATTCAACACT	180
ATCAGAACCA TTAGAGGTCG CTTCAATATAA GTTATTAGAT GCAATATGTG CTAAATCGCT	240
ATTGATTTTC AATGGTTTTA ATCCTTTTAA TTTTCTCATT TCATTTCGTTA CTTCATAAAG	300
AGAAATTAAT TGATTTGGAT TTTGCTCAAC TGGACGCTTA TTATGCTCTT CTGACGTAGA	360
ATTAGAATTT AATTGATAAG GTTCAATATC TGCTAACATT TCTTTTGTTA AAAATCGTAC	420
ACTTAGCACC TTTTTCGATT GTTGATCAGA ATACACTTGT GCATATATGT CGCCATATTT	480
AATCaGTGTT TGTGTTTTTA AATCTTCAT TGAAAGTTCA AATTCATATT TTTTACCATC	540
AACTTTAAAG GACGGTTCCTG GATTAATACT TGTATGATTA AAAATTTCTG CAGAATGTTG	600
TCCTATTTTT AACGGACTAA CATTGACTTT CTCACCTGTA GCATACACTG AAACGATTTT	660
TTCACGTTTA GTTGAAACAA TGTAATAACT GTTTTTGTCT TAAACACAT AATTTTGTA	720
rCCATCTCTA AAAGGGTAGA CrCGATCTGC TTGTCCAAAT T	761

(2) INFORMATION FOR SEQ ID NO: 635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

nTAAATATAT	TTATATATTA	TAGAATAGAA	AGACCTGAAG	ATTGAATATC	TTTCGCAAAG	60
CCTTTAACTG	TATCTACTGA	TAATTCGTTA	ATATCGCGAC	CTAAGTTTGT	ATTCACCTTT	120
TTCACAACAT	CTGCTGGGCA	TGTAATAATA	TCTGCACCAA	TTTCATCAGC	TTGAATCACA	180
TTGAATAATT	CGCGGCAACT	TGCCCATAA	AATTTAACGC	CGTCTTTACT	ATGCGTAACT	240
TTnACAGCCT	CTkTCATTAA	TGGTaATGGA	TCTACGCCTG	TAtCTGCAAT	ACGTCCTGCA	300
AATACTGAAA	CATATGTTGG	CACACCTTCA	GtACTGCTT	CAGTTATTTT	TTTAACTTGT	360
TCAATTGTGT	AAACAGCCGT	AACGTTTAAT	CTCACATTGT	CAGCTGAAAG	TTTTTTAATT	420
AAAGGAATCG	TTGATTCACC	TTTTGTATTT	ACAATAGGAA	TTTTAACAAA	TACATTTTCG	480
CCATATTGTT	TTAAAATTGC	TGCTTCTTTk	TCCATAGTTT	CTAAATCGTC	TGCAAATAT	540
TCAAATGARa	TTGAAGCATC	TGGAATTTCT	TTCACAGCTT	CTTCAGCAAA	AGCTTTGTAA	600
TCTGTTACGC	CCGCTTTAGC	CATTAAACTA	GGATTTGTTG	TAAAACCATC	CACTTGTTTG	660
TTTTTATAAG	CTGCTTTCAT	TnCTTCAATA	TCTGCACCGk	CCGCAAATAC	TTCTACATTT	720
AGTTTAGCCA	TATAAyATAG	CCTCCTTGAT	TCTTATTAAA	ATTTTAACAA	CATCTGCATG	780
kCTTTTTCTT	ACAACCATTT	GTAAAAAATG	ATTTTTATTT	CTTtGTT		827

(2) INFORMATION FOR SEQ ID NO: 636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

TTAGTCGGTA	TAACCATCGG	CTAGGTGGTT	TTTGTATTAA	AAAAGTGGAT	aCCAAAATTT	60
ATTAATAATT	ATTTTAATGT	TAGAAAAAAA	CTAAATAAAA	ACTCGCTAAT	GATATCCAAT	120
AATATGTATA	CAAAACGAGA	CATATATTGC	ATATGATTAA	CGAGATACTG	AAAATATTTT	180
ATCACCCCTA	AAATGATTAT	TCATTTTCAG	CGGTAATTCT	ACCTAAAGTC	AAACTTACAA	240
TAAAACCGAT	GATAAATACT	ACTAATGAAA	CGAACCACAT	CACGATATTA	GTTGGTAAAC	300

CTGGAAATAC TGCAAAGAGG GAGCCAACAA CAAAACCAAT GATTAATGCA AAAGTCATTA	360
GTTTATGATG TGTTAGGAAA TACTGGATAA TTTTGCTTGA AATAATGAAT CCAGCAAGCA	420
CGCCAAATCC GACTGCAAGT AATATAGGAA GACCTGCAAA GTTAAGTTTA ACAACTTCAG	480
ATATTGCTAG CATGACGTA CCATAGACGC CAAATACTAA TAACATAAAT GACCCTGAAA	540
TACCTGGGAG TAACATAGCA CTAGATGCAC ACATACCTGC AATAAAATAT TTAATAATAA	600
GACTAGTTGA TAGAGTAAGT GTTTCTCCAG CATGTTTATC ACCATTATTC ATTAATGTAA	660
TAACAATTAA GATAGCGATA CCAGCTATAA CCATCATGTA A AT TyTAGTT GTAAATGACG	720
TTTTATAGTT AGAAATTTTC AATAAATATG GAACGATACC AATGATTAAT CCACCAAAGA	780
AAAACATAGT TGGAATATGG TGTTGGCTTA ATAAATAATT AAAAAGATTA CTTAGTGATC	840
CCATTGCCAG TAACATTCCA ATTATAATGG GGATTAAAAA TGTAAACTT GGCCAAAAAC	900
GTCGTGAGAA TATGCCGCTA ATTGAAGCGA TAAATTGATT GTAAATACCT ACAATAATG	960
CGATAGTCCC ACCGCTAACA CCAGGTACCA AGTCACTCGT TCCCATAGCA AAACCTTTTA	1020
GAATATTAAT CCATTTAAAT TGTTGCATGA ATAACCTCCTT TCAAACGATT GGAATAAAAT	1080
CATAAATAGC ATCATACCAT ATTCAAATG TCCTAGTGAA ATGATAACAT ATTTTAAATT	1140
CATAAAATCC ATTGAGAAAT TATGTGCACT TATTATCATT TATATTTTAA AAGAGAGCGG	1200
ATTAGAGTTG TACTTTAGAG TTATTAAAAA TAATAAAAAG GGTTTAAGTT GTTTATATTA	1260
AGGTATAAGT AAGTTATAAT TAACTGAACG CATTATTACA AAGTCTTTTGTACTACAAAT	1320
TAAAATTATT ATAACTAGT TAAGAAAAC TATATTTTAA CGGAGGGAAT ATAAAATGGC	1380
ATCAACATTA GAAATyAAAG ACCTACATGT GTCTATTGAG GATAAAGAAA TCTTAAAAGG	1440
TGTTAACTTG ACAATTAACA CTGATGAAAT ACATGCGA	1478

(2) INFORMATION FOR SEQ ID NO: 637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

ATTACAGCAT CTTCTCTAGG TAGATTATTA AAAGATAGAG GTCTAAATGT AACAATTCAA	60
AAATTCGATC CATACTTAAA TGTTGACCCA GGTACAATGA GTCCTTATCA ACATGGTGAA	120
GTATTCGTAA nGGATGATGG TGCAGAAACT GACCTAGACT TAGGACATTA CGAAAGATTT	180
ATTGATATTA ATTTAAACAA GTTTTC AA T GTGACAGCCG GTAAAGTGTA TTCACACGTA	240
TTGAAAAAAG AACGTCGTGG TGATTACTTA GCGGGAACAG TTCAAGTTAT TCCGCATATT	300

ACAAATGAAA TTAAAGAACG TTTATTACTT GCAGGGGAAA GTACGAATGC AGACGTTGTT	360
ATCACTGAAA TTGGCGGTAC AACAGGTGAT ATTGAGTCAT TACCGTTTAT TA AGCGATT	420
CGTCAAATTC GTAGCGATTT AGGTAGAGAA AATGTTATGT ATGTTCACTG TACATTACTG	480
CCTTATATTA AAGCTGCTGG AGAAATGAAA ACGAAGCCAA CACAACATAG TGTTAAAGAA	540
TTACGAGGCT TAGGTATTCA ACCAGACTTA ATCGTTGTAA GAACTGAATA TGAAATGACA	600
CAAGATTTAA AAGATAAAAT TGCATTATTC TGTGACATTA ATAAAGAAAG TGTTATTGAA	660
TGTCGTGATG CAGACTCTTT ATACGAAATT CCATTACAAT TAAGCCAACA AAATATGGAT	720
GATATCGTTA TTAAACGTTT ACAATTAAAC GCGAAATATG AAACACAGCT TGATGAATGG	780
AAACAGTTGT TAGATATCGT TAATAATTTA GAT G TAAAA TTACAATTGG TTTAGTAGGT	840
AAATATGTTA GCTTACAAGA TGCATATTTA TCAGTTGTTG AATCATTGAA ACATGCTGGA	900
TATCCTTTTG CCAAAGATAT TGACATTAGA TGGATTGATT CAAGTGAAGT AACAGATGAA	960
AATGCAGCCG AATACCTTGC AGATGTCGAC GGTATTTTATG TACCAGGTGG ATTTGGTTTC	1020
CGTGCAAGTG AAGGTAAAT TAGTGCAATT AAGTATGCTA GAGAAAACAA TGTACCATTG	1080
TTTGGTATTT GTTTAGGAAT GCAACTTGCA ACAGTTGAAT TTTCAAGAAA CGTATTAGGC	1140
CTTGAAGGCG CACATTCAGC TGAATTAGAC CCAGCAACAC CATACCCAAT TATAGATTTA	1200
TTACCAGAAC AAAAAGATAT CGAAGATTTA GGTGGTACAT TACGCTTAGG CTTATATTCA	1260
TGTTCAATTA AAGAAGGCAC ATTGGCACAA GATGTTTATG GTAAAGCGGA AATTGAAGAA	1320
AGACATCGTC ATCGTTATGA ATTTAATAAT GACTATAGAG AACAATTAGA AGCAAATGGT	1380
ATGGTGATTT CTGGTACAAG tCCAGATGGA CGTTTAGTAG AATGGTAGA GATTCCGACA	1440
AATGtTTCTT TATTGCTTGT CAATTCCACC CAGAATTCTT ATCTAGACCA AATCGTCCGC	1500
ACCCGATTTT TAAATCATTT ATTGAAGCTT CATTAAATA TCAACAAAAT AAATAAATTT	1560
GCTAATAAAA CCGGTACTTT CATTGTTAAA CATTGAAAGT ACCGGTTTnT CGTATAATTT	1620
TAATATTATG TTAGTGACAA GGTATGAAAT AACAATAGTG ACTTTTATAA TTCTAAGTCT	1680
CTTGTCATTT CAATCATTTG TGTATAAATG TCATAGTATA CATAATTCAA TGCCATCGCA	1740
TGTGGTyGGA CAATCTTATC GTAATCTTCA GTGTAGACTA TAGGTcTTGG TGTAGATAAA	1800
TCGATAAAAT GTACGAGATG ATcAGGGAAA TCATCTGTTT TAGGTTTGTG GCTTATTAAG	1860
ACCACATCGA TATCTAAGTC GATAAGTTTT TGAATATCTA ATGCAACTTG ATyATTATAA	1920
AATGGTGCGA ATAATAATAC ACGATCAGTT GAGTCAATTT CTTTAAwkTC TTTAATAGCG	1980
TaAGTTTnCG GCTAG	1995

(2) INFORMATION FOR SEQ ID NO: 638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

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ATTAGTGATG AAAGTCAGAT TGAAGCTTTA TTAACAGCTG AAAAATATTC AGAAATGATT      60
GGTGAATAAT CACCGTGTA  CTCCTTAATC TAAGATTGAG GAGTTTATTT TTAGTCTGAG      120
AAAATAAATG ATATGAAAGA AAAATTATTA GGTACTATTA TTTGGAGTAT TGCTACATTT      180
TATTATTCAA GAATGATGGA AATAATGAAT TTAGCTATTT TAAAAATAAA AATTGGGGGA      240
AGTTAATATG CTAAACATTC AAGACGTTAn CATnCTTTCT AAAAAGGAGC AAAAAGCATA      300
TAACCGTTTC GTAGAATCTG TAGAAAACGG TAATTTACCA GTACTACCAT GTATTGAAAT      360
GGATCTAAAA GAGATGCAAG AAGAAACATT AAACCAGAGT AAGATTGGTG GAATGCCATT      420
TTTAAATCT TTTAAAGATA TACCATTAGA TGAAATAAT GTACCAATGG TATTGCTAGC      480
ACAGATTAAT TTGGATGATC TTCCAGAACA ACAAGAATTA TTTCTGTAA AAGAAGGGAT      540
ATTGCAGTTT TGGATTAGTT CAGAAGATCA AATGTATGGA ATGTCTGAAA TTTAAAGGG      600
AAACAATATA AACTCAAGGC TTGTTTATAT AAAAGAGCCA ATTACAGATT TATCACTCGA      660
AAATATTCAA GCGCATTGGA AGTCATTAGA TGCTGATAAT GAGGATATCC CGTTCAGTGG      720
AGCATTTTCT ATAGAATTTA GATTGTGCGAA ACAAATATT ACATGTACTG ATTATAAGTA      780
CGATGAGGAC GTGCTTGCAT TGTGGAATAA AGTCAATCCA TCCTTCGCGC TAAATCAAT      840
GTTTGGTGGT TATGATGAAT TGATGGAACC TGTGTGTAmC AywTTTACTG CTAAGgAACC      900
ATTTAATCAA CTGGTGGTT ATCCATATTT TGACCAATA GATCCAAGAA CGAACGATcA      960
AGAACTGAAA ATGTATGATA GAGTCTTACT GCMAATTGaT TCTACAAGAG ATGGTAATTC      1020
TTCGATTATa TGGGGTGaTT TAGGTATTGc CAATATCtTA GTGaAATCTA CTGrACCTTG      1080
aGGcTAtGaa GTTTTGAATG ATTACCT      1107
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(2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

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ATTCATATTA TTATAAATTA TTTCTACACC ATCCAATTG AGTTGTTTTT CATAATTAA      60
```

ATGTAATTCC ACTAACTCCC TACCAATTTT AACAAATCCA TATACATCCT TTAATATCGG	120
TATTCGCGGA AAACCTTTAC TCAAATCACT TGAATATTTG TTCACATAAT ATTTATGATG	180
CAAAATTGCA TATATATAAT ATACTATCTC TTCTGAATTA AGATTTATTT TCTTTTTTAA	240
AGAATTAGgA AATATTATCT ACArGCCTCA AACTATCTTT ACCTTTGtAT GTAGCAAAGC	300
CTTkGCCATT ACCAATAAAt TGGAAATTAG GTAATATGTC CGTGATCATA GCCGAGAATT	360
CTTTATTCAT TCCCTGTCCT TGTATATAAA TCACCTGTCC AGTATTCTCC ATTATATTAT	420
AATATCTACT TGGCATTTC ATAATATTTT TGTCGTÆAC TATCCATTTT TTTGTAAATG	480
GTCTATGCAT AAATTTAACA ATTCTCTCTG GATTAATTGA AATATTTTTT CCTTTAGAAA	540
ATTTTTGGGT AAGTCCTCGT GTCCAACtaA TaAATGTTTC ATCTTTGTTC ACTAAATTTA	600
TACGTTCTCT TGAATCTAAG ATATCAATTA ATCTATCTAT TTCAGAATTA TAGTTATCTA	660
CAAGTAATTT TGcATTTACT AATGCTTTTTT CATTCGAAAA ATTTGTTACC CAATTATCTC	720
TTGCTGaATT TACTCCATTA AATkGAKCTA AATATATAGA ATTTTCAATA TCCTTGGAAT	780
CATACATTGG TAAATAATTC CCCATAGTTT ATGTCTCGGT GATTAATCCA ATCATTGGGG	840
TTTAAnCGGG GAAAACCATT CCAACTTTCC AAATTCACCA ATTGAATGGA nGGTTCCATT	900
AAAG	904

(2) INFORMATION FOR SEQ ID NO: 640:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

CGATGTCTTT ACTATTAGAC TTAGCCATTG GTTTCACCTC TCCAAAAATT GTAAATGTGT	60
ATCATCAATA TGAAAGTTAC ATAAAACTGA CATATTTCTTTAAATATCA ACGCCATTGA	120
TAACTTCCTG TTTTAATTGA TACGCTGTAA CAAAATACTA TAGTTAGTGC TTACATGTAT	180
ATGTTAAAGC AAGCAGTGGT AAATGTAAAT TATAATTATT CATTAACCTT GCAATATATT	240
AAATCTTTTA TTCATAGAAG ATAAATATCA AATCAATCAT AATTATTTGA CAACAAATAG	300
CTAACGATTG TTTTAATCTA CATTTGGCTT ATAGCATTTT AAACCTATAC TCTATTTTGA	360
TACAATATAA GTGTAAAATC AATCATAAAA AGGATATTCA ATATCTGCAT CCAAGAAAAA	420
CATTACAATT ACCTTT	436

(2) INFORMATION FOR SEQ ID NO: 641:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

GTTATTAAAT TCAGAGTGGT AGCAAATTAA AGTTAnTCAA GAGTTAAGAT GAATTTAATT	60
CATGAACACG TCTATTATTT TTATAATTGT AGCAAATAAA GCTTTACATC AAGGAGGTAA	120
TTAAATATGT TCAAAAAATA TGA CTCAAAA AATTCAATCG TATTAAAATC TATTCTATCG	180
CTAGGTATCA TCTATGGGGG AACATTTGGA ATATATCCAA AAGAGACGC GTCAACACAA	240
AATTCCTCAA GTGTACAAGA TAAACAATTA CAAAAGTTG AAGAAGTACC AAATAATTCA	300
GAAAAAGCTT TGGTTAAAAA ACTTTACGAT AGATACAGCA AGGATACAAT AAATGGAAAA	360
TCTAATAAAT CTAGGAATTG GGT TTATTCA GAGAGACCTT TAAATGAAAA CCAAGTTCGT	420
ATACATTTAG AAGGAACATA CA	442

(2) INFORMATION FOR SEQ ID NO: 642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

CCAATTTTGG TATGAATTAT ACAGATAATT CnGCGCCCGG AGGATCATTT GCTTATTTAA	60
ATCAATTCGG TGTGGATAAA TGGATGAATG AAGGGTATAT GGCATAAGGA GAACATTTTA	120
ACTACTGCCA ATAACGGAAG ATATATTTAT CAAGCTGGAA CTTCATTAGC CACACCTAAA	180
GTTTCGGGAG CACTAGCTTT AATCATTGAT AAATATCATC TTGAAAAACA TCCAGATAAA	240
GCGATTGAAT TGTTATATCA GCATGGGACA TCTAAGAATA ATAAACCATT TAGTAGATAT	300
GGGCATGGTG AGCTTGATGT GTATAAAGCA TTAAATGTAG CAAATCAA AGCAAGTTAA	360
TAAATCAAAG GAGTTTTTGA TTATGGCAAA ATTAGTTACT GAAAACATTT CGAAGCGGTT	420
TAAAAATCAA GATGTATTAA AGCATATTAA TATCACTTTA GAAAATAACG AAGTTTATGG	480
ATTACTTGGT ATTAATGGAG CCGGTAAAAC GACACTTATG AAAATTATAT GTGGCATACT	540
TCAACAAGAT TCAGGGGAAA TTAAATTAGA TAATAGACCA ATGACACGAA ATGATTTGCA	600
CAAAGTTGGT TCGCTTATTG AAACACCTGC GACATATAAT CATTTAAGTG CACAAGATAA	660
TTTGAAAATT GTGTGTTTAA ATGAAAGCGT TGATTTCaGC GAAATTAATA GTGTTTTAAG	720

CTTAGTCAAT TTAAATGTCG ATAAAAAG A AAAGGTTAAG GACTTTTCTT TAGGTATGAA	780
ACAAAGACTT GGAATTGCAA TGGCaTTAAT TAAAAaGCCA GAAATTTTAG TATTAGACGA	840
ACCATCTAAT GGTTTAGACC CATATGGAAT CCAAGAACTT AGAGAACTTC TAAAATTATT	900
AACAGAACAA GGTACTAGTA TTATTATTTT AAGTCACATT TTATCTGAAA TCC A AGTTTT	960
AGCAGATCAT ATCGGTATTA TTCATGAGGG TGAGCTAAAA TATCAGCAAA GAAATAACAA	1020
AGATGAAAAC TTAGAAGAGA TATTCTTCAA AATAACGAAA GGTGATTACA AATGATACAT	1080
TTAAAGATaG AAGGTATCAA ATTTAAAAAt TCTTTCAGTA TGTATGTTTT ATTAATAAGT	1140
CcGcTGGTAT TTCTTTGTTT TGCTATTTTC ACAGTCTTAT TCGCCAAAAG TAATACGGGA	1200
ACAGCGAATA GTGTGTCACC ATATATAACT TTACTATTTA ATATTTGGCC AATTGCTTTC	1260
ATCCCGATTG TATTATGTAT GGCTTGTAAT TCGTTATTTA AAATTGAAAT GAGAAATAAA	1320
TCATTTAATT ATTACTTAAG TAATAATTGG TCGAT A CAA AAGAAATAAG AGCAAAGATT	1380
TTCATTTTAT CAATAGCATT TTTGGTACAT TGCTTTTTTAG TATTTATTAT TGCTTATATA	1440
GGTGACCTAA TTATTAATCC ACATCCGGTT AATGCTATGT TGTTATTGGT GACAATATTG	1500
TTGATGTATG TAGTATCTCT ACCATTGATA CCGCTCAACT TTTTATTAAC TCGATACTTT	1560
GGTGTGTTTCG TATCAATATT AATAAACTTA GTATTATCAG TCATTTGTGT CTTGTTTTTA	1620
ACATTGAAGA GTTTATTTTG GGTGTTGCCG TGGGGGATAA TGCAGAGAAT CCCGCTTATT	1680
ACGCTTGGTA TACTACCTAA TGGtTTAGTT GTAAACCATA ATTCAAAATA CTTTAATGAT	1740
CTCAATGCCT TATATATTC GATTATTGTT AGCATCATT TTTTCGCGAT AGTAACATTT	1800
TTAAATAATA AGAAAAGTTG GCGATTAAAA TGATAATTAA CGAATTAAAG TCATGTAAGT	1860
TGAAATTTTC TAAGCAAGCG CTCACATTTG TACCCATTAT TGTAACCATA TTGTTTATAT	1920
TATTTATAAA TTGGTATTTA AACGTAAATT TATGGAATGG TC C CAAATm AGTTTGTTTA	1980
CAGCGAGTTT TAATGCAATT ACATCGCTAT TAATTTCTAT AAACGTCTAT CAAGTTATCA	2040
ATTTTGAAGA AAATATTGGT CACTTTAATC ATATTTTAGG AAAAGCTAAT AGGCTAAATT	2100
GGTTAAATGC ATCAATGATT TTTACTTATA CTATTACAGC CATATGTATT CTATTAGCAT	2160
CAATTAATTT ATTGTGGCAT TCACATGATA TG A AAATAAC ACTTATGTTT ATAGGcGTaT	2220
CATTGTTTTT CAATGTaATT ATATTACTGC TACTTTTTAT TTTTAGTATT TTCATTAAAG	2280
ATGTAATGGC TATTGTTGTC GGAGTTTTAA TGTTTATTTT TAACGTTTAT TTTGGATTAG	2340
AAGTGCTTGG AGATCATTCG TGGT T TATT TACCAATCAC ATATGCTACA CGTTACGTTT	2400
ATATGTTTAn CGAAGGGGAG TATACCAGTT ACATTAACAT TGGGCAATCT ATATnATTAT	2460
CACGnTGCCG AT	2472

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

```
ATAATATAGG AATTATTTTCG ATnACAGATT TTACGAATCG TGCTACCTG CAAAATGAAn      60
ATAAAGATCC ATATGGCGAA AAGTTAGCTT ATGGAATTGC TTTTAATGGC AGTGTGGATA      120
TGCAAGGGGA TAAACAAGTC ACAATTCCAA AATATAGTGT AGTTACAATT ACTGGCGAAA      180
ATAGTAAAAA TTATCGTGTT ACCGCCGATA ATAAGACTTA CTATGTTAGT AAAGATAAAT      240
TAGAATATTT TAACCCGGCA GGTTTATATC AAACGCATAG TTTTAAAAAA TTAGCACCAT      300
ATATGAAATC AAATTATAGT AATTACTATG CATACTTTAA TAGTCAATTA CATAAAAAGC      360
ATAGTTCAGT TATAAAAACT TTAGTTCCTG ATGATGATAA CCGTTTCGTT GCATCCGTTA      420
CACAAACAACC GATACAATTA CTTTTCAATE ATAATAATCA GTTATACGGT TTTGTTTATC      480
CAATTGTAGA TAAAAAAGAA TTAAAAGATA AGTTTAATAT TAACAATAAC ATTTGGATTA      540
CTAAAGTTGG GAATGGATAT TGTATTGCCA ATTTGAAAGA AGACAAATGG ATTTATATTG      600
AATTGTAGGT GTAAAGATGC TAGATAATAT TATTTTATAT TTTAAA                      646
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(2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

```
TAATATCGGA ATTTGATAAT GAAGATATCT AATTTTTTTAA TATTCGTAGC TTTTATTTTT      60
CTACTTATTT TATGTTTATT TTTAATCTTA CAAATGACAA ACCATTAAAA GTAGCATCCC      120
AACATCAAAC AAAAAAACAA TTCATCAAAT AAAAATCGCT ACAAACCAA GTCATTAAAC      180
ACGCAATAAT TAAAATTTTC CACTCATTAT AATTCTGAAT TCAAATGTC GAATTCGGAA      240
AACCAAACTC CAAATTCCAA AAACGCAACT CCAAATTAA AAGCATTTCC CTACCATTCC      300
GGAAATGCTT TTTACATACT GgATTACTCT GTCATTAATG ATTTTACAAC GGgAAACCAT      360
GTCGtCATGT ATGACCaAAG TAGCGTCGCT ACaTaAgGt GGTTCCGGATC TTTATTGGAT      420
AATnAT                                           426
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(2) INFORMATION FOR SEQ ID NO: 645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

nTTATTTACC CACAACATGT TCGACATTA GGTAAATGGG TACCTTATTT ACTTGGTATT	60
GTTATGTTAG GTATGGGATT AACAATTACA CCTAATGATT TCAAAATGGT CTTAAAGCA	120
CCTAGAGCAG TAATTATTGG TGTCTGTCTA CAATTCAGTA TTATGCCCAC ATTAGCATTT	180
ATAATTGCAA AGTCTTTTCA TTTACCACCT GATATTGCTG TTGGCGTAAT ATTAGTTGGA	240
TGTTGTCCGG GTGGGACATC AAGTAATGTA ATGAGTTATT TAGCCAAAGC TAACGTAGCA	300
CTTTCTGTTT CTATTACGAC GGTCTCTACG TTGCTAGCGC CATTTCGTTAC ACCTGCGTTA	360
ATATATCTAT TTGCAAATGA ATGGTTGGAA GTATCTTTTCG TGAGTATGTT GTGGTCAGTT	420
GTTCAAGTTG TATTAATTCC AATTGCTTTA GGTATTGTTT TGCAAATTAT TAATCGTAAA	480
ATTGCTGAAA AAGCTTCTAC AGCTTTGCCA ATTAATCAG TTGTTGCTAT TTCATTAATT	540
TTAGCAATAG TTGTAGGTGG CAGTAAGCAC CAAATCTTAA CTACAGGATT ATTAATATTT	600
TTAGTAGTTA TTTTACATAA CGTATTAGGG TATACGATTG GATATTGGTT AGCTCGTCTT	660
TTAAAATTAG ATCGACAAGA TCAAAAAGCA GTCAGTATTG AAGTTGGAAT GCAGAACTCT	720
GGTTTAGCTG TGTCATTAGC aGCATTGCAT TTTAATCCAA TTGCAGCAGT ACCAGGCGCA	780
GTGTTTAGTT TCATTCATAA TATAACAGGG CCTATTTTAG CAAAGTATTG GTCAAAAAG	840
TTATAATTGC ACTAATAGAA TGAAGTGGTC ATCGGACTAT GTTAAGCTTT GATAAAGAGA	900
AAAAATAGAG GAGTAAATAT ATGTATAGAG CAGTTATATT TGATTTTCGAT GGAACAATAA	960
TAGATACGGA ACAACATTTA TTTAATGTTA TTAATAAACA TTTAGAGATG CATAATGCCG	1020
ATCCTATAAG CATTGATTTT TATCGTTCTT CTATTGGAGG AGCAGCTACA GATTTGCATG	1080
ACCATTTAAT TAAAGCGATT GGTTCGAAA ATAAAGATAA AATTATGAA GAACATCATC	1140
TTACTAGTAC AACATTACCG ATGATTGATA CGATTAnATC ATTGATGGCA TTTTAAAGC	1200
AACGTCACAT TCCTATGGCA ATTGCCACAA GTAGTGTGAA AGCGGAAATA ATGCCACCT	1260
TTAAAGCATT AGGTCTAGAC GATTATATAG AGGTAGTTGT TGGTAGAGAm GATGTTGAAC	1320
AAGTTAAACC TGACCCTGAA TTATATTTAT CTGCAGTACA ACAATTAAAT TATATGCCGA	1380
CACAATGTTT GGCTATTGAA GATTCTGTAA ATGGTGCAAC AGCCGCGATT GCAGCTGGAT	1440

TAGATGTTAT	TGTTAATACG	AATAAAATGA	CAAGCGCACA	GGACTTTTCT	AATGTAGATT	1500
ATGTAGCAAA	AGATATTGAT	TACGATCAAA	TTGTAGCGCG	TTTCTTTACG	AAATAGGAGG	1560
CGTATCATGA	TGGGTTACAT	TATATTGTTT	TTTCTAGCTG	GTCCAGTAAT	TTTAGGCGTT	1620
GGAAATTTGG	TGATTGGTCC	TATATTTAAC	AAACAGACAC	CATTTGCGGT	GCAAGTAAGA	1680
TCTTTTGTTG	kTGGkTCmAT	GrTTTACTTA	ATACTCGCAA	CAATTGGCTATTTTTTACTA		1740
TTACAAGGTA	AACTTTAACG	AGAAAACCAC	CTTACCTCAT	TAAATGGACG	ACCATATGTA	1800
TGTGAAATGG	TAGAACGTTT	ATGTTTATGT	ATGAGATAGG	GTGGTTTAAA	TAGTTACATA	1860
TATTTTAATA	ATAACGTCAC	GATGATAAGT	ACAATTAAGA	TAATATCTAT	GCCTACCATA	1920
ATTGTAGCTC	TTGTTGCATT	ACTTCCTTGT	TCTTTTGCTG	ATTTTCATAGC	ACGGTAGTTT	1980
GGCACAAAGC	TAATAATTAG	TAAGATTAAT	ACAATTACAC	CAATTAATGC	TGTTGTCATG	2040
ATGAACGACC	TCCTTTATTT	TTTTCAATCA	ATTCCCAAAT	AAACGTAGCA	ATCACACCGA	2100
TGATTAACCC	AGTGATGACA	CCGATTTGTA	CGTTAmAAA	tATGGCGCCG	AAAATGATAC	2160
CAATAATTAA	TGCAATCGGT	AAAGTCGTAC	CGAGTTTAAT	CTTGCGCTCT	GGAGAATTAA	2220
TAATAGTAAA	TACTGTAAGA	CAAATGAGTA	TGAAAGCAAG	TGTTGCAATA	ATAGTTCTTC	2280
CAACTAAATA	TAGGATGTCA	GGTTTTTCCA	TACCGATATA	ATTTATGATG	AAAAATGTA	2340
CAGCAAAGAG	TACCGATATT	TTTGTAGCAC	GTAGCAGTAT	TTGTTTTAAC	ATTGATATAC	2400
TCCTTTTTTAA	TATTATTAAA	ATTATATCAT	AATTACCAAG	AATAGCTGAA	GTTGTATGTG	2460
ACTCAACGGT	ACTTGAGCAA	CTTTTTTAAT	TTTTTAGAAA	AATCACAAAA	TAATTGTTTG	2520
CAAAGTTGCA	AAAGCCTGCT	ATAGTAGTTC	TGTAAACGAT	TGCATGGTAT	GCAAATATTA	2580
ATGTACCAAA	ATCGATAATT	TATAGTATAA	TTACGGCAAT	AAGTTTTTTT	ATGGATTTAT	2640
TTAGTATCAA	TCAGAGATGG	GGTAAGAAGT	TATGGAGAAC	AATGAACTAC	AAAGGGGATT	2700
GAGTGCCCGT	CAAATTCAAA	TGATTGCACT	TGGTGGTAG	ATTGGCGTGG	GGCTTTTCAT	2760
GGGTGCGACA	AGTACAATTA	AATGGACAGG	CCCATCAGTT	ATCCTTGCAT	ATTTAATTGC	2820
GGGTATCTTT	TTATTTTTTAA	TCATGAGAGC	AATGGGGGAA	ATGATTTATT	TAAACCCTAC	2880
AACAGGATCA	TTTGCAACAT	TTGCAAGTGA	TTATATACAT	CCTGCAGCAG	GTTATATGAC	2940
AGCATGGAGT	AATATATTCC	AATGGATTGT	AGTTGGTATG	AGTGAGGTCA	TCGCAGTAGG	3000
AGAATATATG	AAGTTTTGGT	TCCCGGAATT	GCCAACTTGG	ATTCCTGGTG	TTATTGCTAT	3060
TTTATTATTA	ATGGCAGCGA	ATTTATTCTC	GGTAAAAGCG	TTTGGAGAAT	TTGAATTTTG	3120
GTTTGCTTTA	ATTAAAGTTG	TAACAATTAT	TTTAATGATT	ATTGCTGGTT	TTGGTCTTAT	3180
nnTCTnTGGT	TTTGGAATG	GTGGCCATGC	GGTAGGTATT	TCTAATCTAT	GGACAAATGG	3240
C						3241

(2) INFORMATION FOR SEQ ID NO: 646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

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AGGCGTCAAC TCAGATGGTT TAATAATTGC CGTATTACCT GTGCAATAG CACCGATTAA      60
AGGTtCGAaC ACTAGTtGAA AAGGATAGTT AAATGGTGCA ATGATCAAAA CTGTTCCATA      120
AGGTTCTTTT TTGATATAGC TTTTtGTTGG AAATAAATAT AAAGGTGTGT CTACATTkTT      180
TGTTTTAGTC CAGTTTTTAA GTTCcTTACG GGCAATTTTG AACTTytCA AAGTTATGCC      240
AATTTTCAGTA GCATAAGCTT CGACTTTATT TTTTCTAAA TCTGTATATA GTGCTTCTAA      300
AATATCGCTC TCGTATGATT TAATAGCTTT GCTTAACTTC TTTAATTGCT CTTTTCTAAA      360
ACTAATATCT TTAGTTTGTT GTGTATTGAA AAAAGCTTTA CTGTCATAAA ATTTTTGCTC      420
AATGATATTC ATAATGAAAA GAACCTCCTT ATATGATTAT TTTGGAAAAA GCGATTAATT      480
GATTTGAATG TTGTGGCCGT TAATTTTAAA TGGTCTTTTCG AATTATATAT GTTGAAAGTT      540
GAAAATAGAG CGATGAATCG TGTACATAAT AATATTTATA ACTTTAATCA TAACGAAAAA      600
GGTAGGAAGA AAACAAAAAT TTATACTCAA CATCGCAAAT ATTTTAAGA AATGTAAAGA      660
CAAAAGGGGA ATTGTATAGA AATCACTAAT CTGTGGGTTA GGGTAGCTAA AGGAATAAAA      720
ACTACTATTG AAAAAGGGTT GTAAATTAGT CAAACGTAAA TAAAAAACAG TTCATTGAAA      780
GTGAAATAAA TTCTACTTTA ATGAACTGTT AGTTAAATAC AACATGTCTA TAATTAGACA      840
GTAATATAGT ATTATTTTGT TAATGCTTCA GTGATTTGAG GTACGATTTG TTTTTTTCGA      900
GAAACGACAC CAGATAAGAA GGCCATGTCA TCTTCTAATT GAACATTGAA TGtTCGCCAA      960
CTTTATCTTT TTCAGCACCT ACAACTAAAA TTTTAGAATC ACTATTAATG ATGTCAGTAA     1020
CAACAAGTAC AAATAAGTCA TATTTTTCTT GTGCACTTAC AGCTAACATT TCTTTTTCTA     1080
rATCTTCTTT ACGATTtAAC ACTTCGTCAA GGTCAACAGC ATTAAGTTGT GCAATACGAG     1140
TCACATAGTC ACCCATAGTA AATGATTTAG CATCCATGTT TAATAAGAAT TCAACTGATT     1200
TATCAGTTGT TGAAGCACCT GCTTTtAACA TATCTAAGCC GTACTTTTGA ATATCACTT     1260
TAGCAATATC TTTnAATTCT tCAGCTGCTT TAACATCTTG TTGTGTACAT G              1311
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(2) INFORMATION FOR SEQ ID NO: 647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

CATATACTTT TTCATTTCTT TACGAGATAC TTTACCAGAG GATTTAGACT TCATACGCTG	60
ATCCATATGT GCTTGCGTTT CAGaATGTCC ACAAACACAA CGATATACCG CTTCTTTCCC	120
TTTACCAAAC AACGTTAATT TCTTTTTTACA GTTTGGACAT CTTGCATTTG TTTTGGCGTG	180
TACATTCTTT TTCGTCTTAC AAGATGGATC TTGGCACACA AGCATCTGAC CATTTTTAGT	240
TTTAACTTTA ATCATGAATT TACCACACGT TGGGCATTCT GTGGTTGTTA AATTATCGTG	300
TTTATATTTA CGATCACTAT TTTTAATCCC ATTACAACA TCTTTCGTAA AATCTTTCAT	360
TTCATTAATA AATGTTTTTCG CCTGATATTT ACCACGTTCA ATTAAAAGTA ATTTTTCTTC	420
CCATTGTGcA GTTAAAAGTG GCGACGTTAA TTCTTCTGGT GCTAATTCTA ATATTTGTTT	480
ACCTTTTGAC GTTACTTTAA TTTTACCGTC TCTTGATTCA ATGGCATTCA TATTAAATa	540
TTTATCGATA ATGTCGGCCC TTGTTGCAAC TGTGCCGATA CCACCTGTTT GTTTTAAAGT	600
TTGCGCATAT TTTTATCCT TCAATTGAAT AAAGTTCTGA GGGTTCTCCA TCGCTTTTAA	660
TAACGAACCT TCATTAAAT ATTCTGGAGG TGTGTTTCA TGTTCTCTAA TATTTGTTTT	720
TGAAATCTTC ACTTCATCGC CTTCTGAAAA AGGCTGTTGC ATCTCTGTAA TAGATTCACC	780
TTGTCTAATA GATTTAAAC CTAAAACAGT TGTTACATTC TCTTTCAAAA CAAATGTGTG	840
CCCTGCAACC TCTAAAGTTA CAGTTATCGC GTCATACTCG TGCGGAGGCA TTAAAGCTTC	900
TAAAAACGC TCGACAATCA TATCGTATAA CTTTAATTCTCTATTACTTA AGTCTGACAT	960
GACAGGTCTC ACTTCTGTAG GAATAATTGC ATGGTGATCA GATACTTTTT GATTATTAA	1020
TATCGACATT TTTGATGAAA ATGTTTTAGA CATTAAATGGG CGTGCTTGGT CTTTATATGT	1080
TGTTGCCATC GTCACCTGAA TACGTTCTTT CATAGTATCT ACCATATCAG TTGTTAAATA	1140
GTTTGAATCT GTTCTTGGAT AGGTTACGAC TTTATGTCTC TCATATAAGC TTTGAAGTGT	1200
ATTCAATGTT TCTTTAGGTC CAATTTTATA ACGTCTATAC ATATCTTGTT GTAAATCTGT	1260
TAAATTGTAC AGTGATTGCG GATACGACTT CTTATGTTTA GTAGCAACAG ATTTAATCTT	1320
ACCATCGACA TTTTCAAAT TATTAACCAT CTGTTCTAAA GTTTCTTTAw TGGtATATCG	1380
CTGATTTGaw TCTAGCTGAA AATCAAACCC TTTTACCGTT AATGATAATG TAAAGTATTG	1440
TTGTGGnTTG AACTGATTAA TCTCTTGTTG GTCGTGTAAT TTAATAAATT GAAACGGn	1498

(2) INFORMATION FOR SEQ ID NO: 648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1044 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

TAAAACAATT CGTTTTATTA ATACAGTTTG TAAAAGTATT CTCTAGTAC TAATAGCTAA	60
TGTAATGATA GAAAATACTA GTGTTATTAA AGATTTGAAT AAAATAAAAG AAAGTGAAG	120
ATATTGGAAT GTATTAGATG ATTATTACAC GATTGAATTT GCACCTTATC ACGAAACAAA	180
ACAAAGTTTG ATTGATAATA TGGTGCGATC AGAACAATTA GTAAAGGCTA GTGAAGCAGA	240
AAATAATGCG ATTTTATTCA AACCAAAGGG TGAATCCGTT GACAATGACA ACTTTTCGCC	300
TGATGAGGGG AATGTAATAT TAGTAAATAA TCAGTTCTGG TCGATTATT ACAAGCAGTT	360
TCAACCTGAT ATCCGATAA AAAATCAAAA AAATAATGTC GAAGTAATTA TTCCACAAAA	420
GTTTCATGCA ATGCGTAATG AAATCAATCA AGCATATCAT TCATGGTTTG AATTGTACA	480
AAATAAAAAAT AATAAAGAGA ATAAGTTATC TATACAGTTT ATCAACAAAA ATGATTGTCG	540
AATTTTTTCA TTTGATGCAC GAGATAGTCG CCATTTGTCA TTTATAGAGG CGCCAATCAT	600
TGTGAATGTT CAGGCATCAG ATTTATCGaA TGATTTtAT TATGCCATGaTCaGTCaAGG	660
CGGGTATTTa TTCaAAAATT ATGaCGCGCT AGTAAAAAAT ATTGGAAAAG TATCCATCTT	720
GATGGGGAAA TCCAGTGGA TAACCAATTA TAAAGATAGC GTGATGGAAA TGTATCATGA	780
AAACAATTTG AAATTAACAG TACTCAACTT TTCACAAATC ATTATCGCAA TCATTTTAAT	840
AATTATTATT TTATTTGATG TGAAATATTA TTTTGAACAG CATCGAAAAT TACTCGTAAT	900
CAAAAAGCTA TATGGTTATT CAACATTAAG AGCCAATTAC CAATACTTAT TAATAAATAA	960
TATAGTTGTT ATTTTATTG GAATATTGAC GAATGTAATT TTACATTCTC ACTATATAAT	1020
GATGTTATTT GCAACGATTC TTGT	1044

(2) INFORMATION FOR SEQ ID NO: 649:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

GAACATATTG GGTTATGCAA GGnGGTCACT CTTCACTT ATAAACAACA TTTAATAAT	60
GTAAAGTTTA ACCAGCTAAC ACTTTTGTTA GCTGGTTTTT ATTTTCCTTC AATTTTAA	120

TGGTTAAGTC CCCTTCTATA TCTTATAAGA CAATCATTAT AATCAATTCA ATTATACAT	180
TAACAACCAC AACTAATAAA TATAGTAACT TCAAAATCCA TATTTATGTC TAAAGATAAT	240
CTCAATGTTG TTCACGTCAA TAAAATTATC CCTAGGTTTT TAAAAATTGT ACATGTTTAA	300
ACAATCAAAA GTGTACATTA TTAAATTATC ATTTCCAGTT AGATTTAGAA AACATTCACA	360
CCACGCATGG ACCAACGTAT TCGTCTTcAT TcATTTTAG	399

(2) INFORMATION FOR SEQ ID NO: 650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

GTACTAGGTT CTAnGATTCC CTACTGTAGT CATAGATATT TTCCAAACAG AGCCTGACAA	60
CTTTTCATTT TTAATAGTGA TCACTATATT AATCGCTATT GCAATTTATG CATGTCGATT	120
TGTTTGGGTT TATTTCTGGT ACAAAGATTT TATTTCCCG AAAAATATAC AATCTTATCT	180
AGACGAGGAA CATGATTCAC ATGAAACACC ACCTTCTCGA GTGCGTTACG CATTTATTAT	240
GACCATGTGT GGTATTCACG GTACAATTC ACTTTCAATG GCACTTACAT TACCATTTAT	300
CATTACAAAA GGACAAGCAT TCGAATACCG TAATGATTTA TTGTTTATTG CATCTTTAT	360
GGTATTAATT AGTTTAATCT TAGCGCAAAT TGTTTTACCT TTAATTACAC CATCTGCCGA	420
AGATACTACT TTAAAGGTA TGA CTCTGCCAAA ATTTTCATTG TTCAAAAAGT	480
GATCCAGCAT TTTAAAACG AAAGTAAAAA AGACAAAAC GATACAAATT ATCGCCCAGT	540
ATTAAACCAA TACTATGGAG AATTGTTATT TTTATTAAAT TCAGAACCTG ATAATCAAAA	600
TACrAAAGAA CTCAAACGTT TAGAAGATAT TGCaAAAGTA ATCGAAACAT CTACACTTGA	660
GCGTTTAATT GATAAAGGTA AGGCAACATA TCAGGATATT AATAATTACC GCAATATTGT	720
CGAATTAACA GAGACACACC GTACTGC	747

(2) INFORMATION FOR SEQ ID NO: 651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

ATACAATACT CTTTATTAT TCAATAAGCC ACTTCCTATA GCAAATGTTT AACTTTAAAT	60
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ATTTTTCGAT GCTAACAAAA AATCACACTA TCATCTTTTA AAATGAAAGT GTGATTACAA	120
GCAAAATCTGT AAAATTTTATA AAGCAGAAAC AATTCAACTT TATCATTATG ACATTTCAAT	180
TAAACCTTCT ACATTATAGT TCCAAGCATC TTACACATGA ATGCAAGTAT TTAACGATTT	240
AATTGTGACA TAGCCTGTTG ATATTGTGTT TCATTGATAT AATTTTGTTG CTTCAATTTT	300
TCTAAGTTCG TGCTTACACG TTGCGTAAAA TTCTCTGACA TATTATTGAT ATTATATACG	360
CTAGGTGCAT TGACTTTACT AGCTAAAATA GCGCTTTGTA AAAGTGTAT GTGAGACATT	420
GTTGTACTAT TTTTATTCAC GGTGTTCCA AAGTAATGGT TTGCTGCGCC CTCAAGCGTA	480
TATTGATTAT CCCCAAAGTA AATATTATTT AAATAAAAGC TTAAAATTTT GTTCTTATTA	540
TATwGTwTTT CAACTCGATG AGCTACAAAT AATTCTTTTA CTTTCTAGT AAATGAACGA	600
TCATTATCAT AAAAATAATT TTTGACAACT TGTGTGTAA TGGTACTACC ACCTTGACA	660
TCTCTGTCGC TAATCGTTGA AAATAAAGCT CTAGTTGTAC CTTTCAAATC GAATCCATGA	720
TGATTGTAGA ATCGTTCATC TTCCATTGAA ATAAAGGCAC CTTTAACATA CTCTGGCATG	780
TTATCAGCTG ACACAAAAC ACTTTTATTT TCAATTTTTC TTAGTTCATC CACATTATCG	840
CGTGTAGATA AAAAATACAT GATACCAATA AACAATGCGA TAATGATTAG AATGGTTAAT	900
AATATTTTTTA ATAGTATTCG TTTACTTTTT TTCTTTTTTCG GCGGTTTGCC AACTGGTTGA	960
TAATACGTAT TATAGTGAGG TTCGTTTTC ATATGCTCAA AATGTTTCATT TGAGTTTGAG	1020
TACCTATCGC TTCTTTTCAT GCGTTTGCTC CTTCTTTTAA AACTCACTTA GtATATACCT	1080
TGaGTTTACC AGTACTATCA CAAATAGGCT AACTTTTTTG GGAAAATCAG TCCAAGGGCT	1140
TACAATCGTA TACGCCATCA TACTTACTTT TTTGTTTTTT GAAAAAATTATAGATAAATC	1200
ATTGCAATTT TAAATATTAA TCATGTCAAA TATTGTTATA TTTTATAAAA ATAAAAGACC	1260
ATCCCTATTA AATGCCAATA GAGACGACCT TTTATTTGTT ATTCATTTAT TAAAACATAA	1320
ATCCATATTT CATTTCAAAC GAAAATATAT AAATTTTAAC AATCGrTAAC CAC	1373

(2) INFORMATION FOR SEQ ID NO: 652:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 859 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

GGCAGATAAT TTAGTCATTG TTGAATCGCC TGCAAAAGCA AnAACCATTG AAAAGTATTT	60
AGGTAAGAAA TATAAAGTTA TAGCTTCAAT GGGACACGTC AGAGACTTAC CAAGAAGTCA	120

AATGGGTGTC GACACTGAAG ATAATTACGA ACCAAAATAT ATAACAATAC GCGGAAAAGG	180
TCCTGTTGTA AAAGAATTGA AAAAACAT TC AAAAAAGCG AAAAACGTCT TTCTCGCAAG	240
TGACCCCGAC CGTGAAGGTG AAGCAATTGC TTGGCATTTA TCAAAAATTT TAGAGCTTGA	300
AGATTCTAAA GAAAATCGCG TTGTTTTCAA CGAAATAACT AAAGACGCTG TTAAAGAAAG	360
TTTTAAAAAT CCTAGAGAAA TTGAAATGAA CTTAGTCGAT GCACAACAAG CGGTCTGAAT	420
ATTAGATAGA TTAGTTGGCT ATAACATCTC GCCAGTTCTT TGGAAAAAAG TAAAAAAGG	480
GTTGTCAGCG GGTCGAGTTC AATCTGTTaG CmTTCGTTTA GTCATTGACC GTGAAAATGA	540
nATTCGAAAC TTAAACCAG AnGAATATTG GACTATTGAA GGAGAATTTA GATACAAAAA	600
ATCAAAATTC AATGCTAAAT TCCTTCATTA TAAAAATAAA CCTTTTAAAC TAAAAACGAA	660
aAAAGATGTT GAGAAAATTA CAGCTGCATT AGATGGAGAT CAATTCGAAA TTACAAACGT	720
GAATAAAAAA GAAAAACGC GTAATCCAGC AAACCCATTT ACAACTTCTA CATTACAACA	780
AGAGGCGGcA CGTAAATTAA AcTTTmAAGC AAGA AA ACA ATGATGGTCG CACAACAATT	840
ATATGAAGGT ATAGATTTG	859

(2) INFORMATION FOR SEQ ID NO: 653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

TTCAACTTCG TTTGGAAATC ATGTTCCCTCA ATTGTTGGAC TTAAACGAAT TTCTTTAACA	60
TTGATAAATTT TTTGTTTCTT TTTCATTTCT TTTTCTTTTT TCTGTTGTTT GAATTT CA T	120
TTACCGTAAT CCATAATTCT TGCAACTGGT GGTTCGCAT TCGGTGCAAC GACCACTAAG	180
TCTAAATCTA CACGTTCAGC CATTTCTAAA GCTTCACGCT TTGATTTAAC ACCAATTTGT	240
TCACCATCTT GACCGATTAA ACGTAATTCT TTTGCACGAA TTTTGTCAAT GATTTGAGTT	300
TGATCTTTTG CTATGGTTGA CACCTCCAAA ATTTTACGA AATTTGCACC AAGCAAAAAG	360
GAAGAGCAGG TATAAAATAC CCGCTCTTCC TTATACACAG TTATGTGTAA TGTGATTAAC	420
CTGCCAACTG CTTTATGCGT CGCTACAGGT GAGAAGCGGG TGCTTCTACT TGGTTCGTTT	480
CGTATTCAAC GTTATTAATC ATATCAACAA TTCACATTa AGTCAACACT ATAAGTGTAA	540
TTATTTTTTAT TTAAACCTTT TATTTTCATCC ATTGACACGT CTTGACGTAA ATCTACTTGT	600
TCTAATGGAA TTTTTTTCGT TTTATATCGA AGCTTATGAT AAATAAAGAA TGCTAAAAAT	660
ACTGGAATTC CCATATACGT AATTAAGAAG CGACTAAAAT TAAAATCTCC TG Tn TTAATA	720

AAGTCAACAT CTTGCCCAAn AAnTACT

747

(2) INFORMATION FOR SEQ ID NO: 654:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

TTTCAATGCC ACTGCTTtTG GTTCTTCATT TGATACAGCT GCACCTTTTAT CTGTTTCTGC	60
TTGTGCTTCT TTTTtagCTT CTTGAACCTC TTGTGCCTCT TGTGATGTAT CACTyAAATT	120
ATTTGCACTT GCTTCTTCTT TTATCGCTGC TTGTTGTGCT TTCAATGCCA CTGCTTTTGr	180
TTCTTyATTT GATACAGCCA CACTTTTATC CGCTTCTGCT TGTGCTTCTC TTTTAGCTTC	240
TTGAATCTCT TGTGCTTCTT GTGATGTATC ACTTAAATTA TTTGCACTTG CTTCTTCTTT	300
TATCGCTGCT TGTTGTGCCT TTAATGCCGC TTGCTCATTT TAgATTTGT TTAAAAATCC	360
TTCAACACGT TCTTTTGTAT AGGCAACCGT TTCTTCAAGT TGCGTTTTTC TTTCTTCAAA	420
CTTTTGCGAC AGTTCTTGtn CTTTGACTTT nAAATCATCT GCTTTTTGAT AAACCTTATT	480
TTAAAATACC AACCTAAAGC C	501

(2) INFORMATION FOR SEQ ID NO: 655:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

CACCTTGTCa TAATTAATTT TTTGATTTTT CATTTTACTG ATAATAGGTT CAGCATTAAAT	60
CATGATTTAA CCTCCACAT TTAATCATTa ACTTCTATTA TATATGATTC ATATTAAATG	120
TCAGTCAAAA AAGTTAGAAA TTCATTTTAA TGCATTTATA TTTCGAAAAT CCCTTATGTA	180
TCTAAAAGCA TTTTTTAAAC TTGAATTTTA AAACACTAAA CAACACATAC GTCTCTGTGT	240
CATTTTCATT TTTTGTATGT CATATATATG TTTACTTCAT TTAAATCAAT TTCATCTTAT	300
AATTTATCGT GTATTTTACA AAAGATTGAC TTCAATTCAT CGTAAAAGTT ATACTTTTGC	360
CATTTTTTAA TGTAACATGG TGTTAGTAAT AAAAATAATA CATTGAGTG TTTTACATGA	420
CAGCATTATT CCCTTATATC GCTTTTGAAA ATTCAAAGA AGCCCTTGCA TATTACGAAG	480

AAGTATTTGG TGCAACTGAC GTTAAACGTT TAGAAGTTGG CGAAGAACAA GCGTCACATT 540
 TTGGTATGAC TAAGGAAGAA GCGCAAGAAG CAACTATGCA TGCTGAATTT GAAGTGCTTG 600
 GCGTAAAAGT GTTATGTTCT GATTCTTTTG GTCGCGCTGA CAAAATTaAT AATGGCATAT 660
 CATTATTAAT TGATTATGAT GTTAACAATA AGGAAGATGC TGATAAAGTT GAAGCATTCT 720
 ATGAGCAAAT TAAAGATCAT TCTTCAATTG AAATAGAATT ACCGTTTGCT GACCAATTCT 780
 GGGGTGGCAA AATGGGCGTC TTTACCGTA AATACGGTGT TCGTTGGATG 830

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

GTATCCATGG GCCCGTTnCG CACAACATTT GGnACAATTA GGTACACGnG TTGTCaTCGG 60
 TCGTTTCGGT ATAATTTTAT CGAATGaAGG CGGTGCGTTA CAAACAATGA AACTACCATA 120
 CGAATATTAC ATTGGTGGTA AATTAGGTTC TGGTCAACAA TGGTATTCATGGATTCATAT 180
 CAATGATTTA ATTCAAGCTA TTTTATTTTT AATAAATAAC GAGTCAGCTA GTGGTCCGTT 240
 TAATTTAACT GCACCTATAC CTGAACGTCA AAATTTATTT GGCTACACTT TAGCAAGAGC 300
 TATGCATAAG CCTCATGAAA CTTGGGCACC AAGTCTTGCA ATGCGTCTCA TACTTGGTCA 360
 AATGTCAACA GTAGTATTGG ATACTCAAAA AGTATTACCT aATAAAATTC AAGCATTGGG 420
 aTTCCAATTT AAATATAGTA ATTTAAAAAT GGnACTTGAA GATTTAATTA AAGAATAATC 480
 AATACCATTA ATGAGCATTA GAAACAACAT ATGTACTAAA TGTAATGTCT AGAGCGACT 539

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

ATCAAGTTGA ATATCATCCA TATTTAACC AACATAAATT GArATTATAT TTGGCAGCAC 60
 AACGTATCGT gATGGaATCT TGGTCACCAT TGATGAATGC ACAAATTTTA AATGATGAGA 120
 CAATTAAAGA CATTGCTCAA GAATTAGGAA AGTCACCTGC CCAAGTTGTT TTAAGATGGA 180
 ATGTGCAGCA TGCTGTGGTT ACAATCCCTA AATCGGTGAC ACCAAACAGA ATTCTGAAA 240

ATTTCCAAAT ATTTGATTTT GAATTATCAG ATGAACAAAT GACGCGAATT GATGGTTTAA	300
ATCAAGATAA GAGAATTGGA CCTGATCCAA AAAAATTTGA AGGCTAGATT AAAATCGCTC	360
AACTGATGAA AAGGTTAGAT GAATTGTCAG GGCTTGGGAC ATTAAGTTCT TAGGCAATGT	420
AAAAAAGCTG ATTTCTATTA ATTATTTGAT AGAAATCAGC TTTTTTGATA TGTATTTTAT	480
AATGTACAGC TCGTTGAGCT GCTATTTTCC TTATATTAAG TGCCATTAAT ACAAACCTA	540
GCTCTCGTTT AACTTTATTT AtTCCTCGAA CTGACGTTTC AGTTAAACCC AAAATAGCCT	600
TCATAAATCC AAAACAGGC TCTACATCAA TTTTCTTTG ACTATAGATT TTTTTCGTTT	660
CTGGTTCAGA AAGCTTTTGA TTAATTTGGA CTTTAAAGTA TTCCCAATTA TAATTCCTCA	720
TGATTtTCTT ATTGGATTTT GAATTTGGTT TCATGCATTG TTGCCTCAAA GAACATGCTG	780
AACAGTCATC GCATTCATAT AGTTTGAAGT CTCGTTTAAA ACCATATCTA TCATTACGGT	840
ATGCATATCT TTTAAAACCT ATTCTTTTGT TATTAGGACA TATAAATTCA TCATTAAGTT	900
CGTCATATTT CCAATTTTGA GTGTCGAAAA TGTCACTTTT AAACCTTCTA GTTTTATCtT	960
TAATAAACAT GCCATACGTA ATAAGTGGCG TTTTATTAAA ATCATCTATA ATGGCCATAT	1020
AGTTTTGGCT CACTACCAT AACCTGGCAT CAGCTACCAA ATGAACCGAA GGGATTTTTG	1080
GAATCCATTG GTTGAAAAAA TGGGAA	1106

(2) INFORMATION FOR SEQ ID NO: 658:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

TTTTAACTTT ACTCTTTGAT TTAAAGAGTG ATAAATGTTT ACAGTTTAAT TAAAACTGCA	60
TAAGAACTTC TAGCTTTTCT CTTTCGTTCA AAGAGAAGA GCTGTTTCGCA GTTTAATCAA	120
AACCACATAA AGCTTTTAAAC TTTACTCTTT GATTTAAAGA GTGATAAATG TTTACAGTTT	180
AATTAAAACT GCATAAGAAC TTCTAGCTTT TCTCTTTCGT TCAAAGAGAA GCAGCTGTTC	240
GCAGTTTAAT CAAAACCACA TAAAGCTTTT AACTTTACTC TTTGATTTAA AGAGTGACAA	300
ATGTTTACAG TTTAATTAAA ACTGCATAAG AACTTCTAGC TTTTCTCTTT CGTTCAAAGA	360
GAAGTTCTAA TACCACCATA TCGTGCGATC GGGAACGGTA	400

(2) INFORMATION FOR SEQ ID NO: 659:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1899 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

ATAATTACAA TGGCTACTGC AATTATTGTT GGAATTATAT ATTTTCAGTTT AGTCATCATT	60
TATGCTCCCT TGATTTCAAA TTCATATCAT TAGTTTACCA TATTGAAGAT GATATAATAA	120
CTTATAAGGA GTGAGAACTT TTATGAACAT AAATAAAAAA GTAACATTAC AACGAATTCA	180
AACTTTAACT GAGCTTCATG GGGCACCAGG TTTTGAAGAA GAAGTAAAAA ATTATATGAC	240
TCAGCAAATG GCGCCGTACG TAGATGAATT TATTGAAAATCGTATGGGTG GATTTTTTGG	300
TGTGAAAAAA TCTAAAAATC CAAATGCAAA ACGTGTAATG ATTGCAGCAC ATATGGAaTGA	360
AATCGGATTT ATGATTACAA ATATCACTAA AAATGGAATG ATTCAATTCA CAAATTTAGG	420
TGGTGTGCA AATGATATTT GGCAAGGACA ACGCTTAGTA ATTAATAATA GAAATGGCGA	480
TAAAATTATC GGTGTTGTTT CTAATATACC TAAACATTTT CGTACTGGTA GTGAAGGTGC	540
ACCGGAAATT AAAGATTTAA CATTAGATAT AGGTGCTCAA AATGAAGATG AGGTGCGTGA	600
gCGCGGAATA GATATAGGAG ATACAATTGT ACCTCACACG CCATTCACAC AGTTATCTGA	660
ACATCGATAT AGTGCTAAAG CATGGGATAA TCGTTATGGT TGTGTCTTGG CAATTGAAAT	720
ACTAGAATTA TTAAGAGATA TAGAATTAGA TGTAGACTTG TATGTTGGCG CAAATGTTCA	780
AGAAGAGGTT GGATTACGAG GTGCGAAAGC ATCTGCAGAG ATGATAGACC CAGACGTTGC	840
ATTTGTAGTT GATTGTTTAC CTGCCAATGA CGTTAAAGGA AACCAACET TATCTGGTGA	900
ACTTGGTAAA GGGACGTAA TTCGCATAAA AGACGGTACA ATGATTTTAA AGCCTGTATT	960
TAGAGACTAT TTATTAAAGT TAGTAGAAGC ACATGACATT GAACATCAAT ACTATATGTC	1020
ACCAGGTGGA ACAGATGGTG GAGAAATTCA TAAAGCTAAT ATTGGTATTC GACTGCAGT	1080
TATTGGTGTA TGTGCACGAT ATATTCATAG TACAGACTCA GTATTTGATA TAAGAGACTA	1140
TTTTGCAGCT AGATCTTTAC TTTCAGAAGC CATTTGTAAT TTAGATAATA ATCAAATAGA	1200
AACATTACAA TATAAATAAT CGGGTAATAA CAACTATTAT CTCTAAATAG TTATATATAA	1260
TCATTAATTA AGGAGACATA AAAATGAAAC AACTTGAATC AGAACAACAA TTTGAATCTT	1320
TAAAACAAGG TGCTACAGTA TTTGAATTCA CTGCAGGCTG GTGTCCAGAT TGTAGAGTGA	1380
TAGAACCAGA TTTACCGGAA TTAGAAGCGA GATATCCTAT GTTTGACTTC GTATCAGTAG	1440
ACCGTGATAA ATTTATGGAT ATTTGTATTG AAAATGGTAT TATGGGTATT CCAATTTTC	1500
TAGTATATAA AAATGGAGAA CTGCTTGGA GTTATATTGG AAAAGAACGA AAATCAATTG	1560
AACAGATAGA TGCATTTTTA GCTCAATACG TGTAATTTAG ACTAGAGAAA AACGGGGTAA	1620

TACTCGTTTT TCTCTGTTAC TATGTGTTGA TTTATTGTAA ACTATTATAA GGTGCGAAAT	1680
TAGGAGTGTT ACATATGAAT ACCTTTCAAA TGAGAGATAA ATTAAAGGAA CGTTTAAGCC	1740
ATTTAGACGT TGATTTTAAA TTTAATCGTG AAGAAGAAAC TTTGCGTATT TATCGAACAG	1800
ATAATAACAA AGGTATCACG ATTAAACTTA ACGCTATAGT CGCAAAATAT GAAGATAAAA	1860
AAGAAAAAAT TGTAGATGAA ATTGTTTATT ACGTTGAG	1899

(2) INFORMATION FOR SEQ ID NO: 660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660:

GTATAATATC CTTTCAATCT GTTTTCATAT TTTATATATT TTTTAAATAT AAGTGCTAAA	60
TGTTTTAACT AAAGCATAGA TTGACAAGAT GTTATACAGA ATTTCAAATT CTATCCAATA	120
TTGTTCGAAG TGTAGTATCA CTGGATTGGT ATTAAACAAT GTAAAGGAGA GATTGCAAT	180
GCCGTATAAT TACAAGAAAC AAAATGGAGA GTTAATGTCT GTAATGAGCC AAGGTGAAAA	240
GTTTATTTCAT CAATCACCCG TTAATGATGA ACTTAGTGCA TTGATTAAGT TATTAATTTT	300
TAAATTAAC GGTGTGCATT ATTGTGTTGA TATCCATAAA AAAGAATTAA AGGAATTGGG	360
TGTAAcACAA ATGAAAATTG ATGAAGTCTT GAGTTTTAGA CATTTAGATT TATTTACTGA	420
TCAAGAAAAA GTGACGCTTG AATTTGCAGA AATGTTAAAT TCAATCAAAG ACTTTAAGAA	480
GTTTGAAATT ATTGACCGGC TAAAATCATT TTATGATGAA GAACAAATTA TTGATCTTGT	540
CTTTGTTGTA AACCAAATTA ACGGTTGGAA CAGATTAAATATTATTAGTG ATAGACTATA	600
ATTGTTTCATA TAAATGCAGA GTTTCATCTC GAACGCTATA TCATAACAAA TCATGCCACT	660
ATACAGGTCA AATCTTGAT AGTGGCATTT TAATTTATCC CTTTGAATAC TGTTATTTAA	720
CGAATATCGG TCCACCTGGT CCAACAGGGA TACCTAATAG GAACCAAATG ATGACAAATA	780
CTGTCCATAC AATACTTAGC GCGATTGAAT ACGGCATTAA ACTAGAAAGT AAGGCTCCGA	840
GTTTCATGCG TTTATCGTAT TTTTGTGCAT AAGTTAATAA TAAAGGTAAG TACGGCATCA	900
TCGGTGTAAT TGGATTGGTA ATTGAATCGC CTACACGGTA AATGACTTGT GTGAATGCGG	960
GATGAAAGCC GATAAGGATT ACATTGGTA CGAATATCGG TCCTAAAATA CCCCATTTAG	1020
CCGATGCGCT TCCGATTAAC ATGTTGACCA TTGCACTCAG TACAATAATA CCTAGTATCA	1080
ATACAATACC GTTTTGATGT TCTAATAATT TGGCACCTTT AACAGCAGCG ATAATTCCTA	1140

AATTACTCCA	CTTTAAATAC	GCAAGTAGCT	GTGCTGCAAA	AAACACATA	ACGATAAATG	1200
TTCCCATTTGA	TCCTACAGCA	TCGCCGAACA	TTTTACCTAA	GTCTTTTGTA	TTTTTAATTT	1260
CTTTGCTTAA	AATCCCATAA	ACTAATCCAG	GTACTAAAAA	TACGACAAGA	ATAATTAATC	1320
CGACACCGTT	AATTAATGGC	GCATCGTCTA	GTAAGCTGCC	TGTTTTAGCA	TTTCTTAAAA	1380
AGCTATGTTC	AGGAATGGCT	GTAATAATTA	ATAAAATAAT	TGTGACTATG	AAACTGATAT	1440
TTGCCCATTT	TAAAGCATGT	GCTTCTTTGT	CAGTAATATG	TGAAGATGTT	TCTTCATGGT	1500
CATCATGCAT	TAAACTGTCA	TCATATTTTC	CTAATCTAGG	AATAATGAGC	TTAGTTGTAA	1560
CTAGCAATAT	CGTAGGAAGT	AATACAACGA	CACTCGCTGC	GATAAAGTAC	CAGTTCATAG	1620
CAACGTTTGT	TTTAATAGAA	TCTGAAACGA	TACGTGTTGC	CGGTTCTGTA	AATGAATAGA	1680
CCAAAGCATC	TTGCATACCA	ACAACTATAT	TTGCTGCAAA	TCCTCCAACA	GCGGAAGCAT	1740
ATGCCATCGT	TAGTCCAGCG	ATAGGGTGAT	AGCCAATTTT	AATAAAAAGC	ATTGTGCAA	1800
GCGGCGGCAA	GATAATTGTC	GCAGCATCGC	CGGCTGTACT	ACCTAAAATA	CCAATTAATA	1860
TAATAGTCGG	TAAAATTAAG	AAACGTGGTG	CGCGATTAC	AACAGAAATC	ATTAACCTTAT	1920
CGAAGTATCC	TGTTTTCTCT	GCAACACCAA	TACCAATCAT	CACTGCTAGT	ACTAAGCCTA	1980
ATGCTGGGAA	CTCTGAGAAA	TTTTTAATCG	TATCATTCAT	TATCATCGTA	AATCCATCAT	2040
GGCTAATTAT	ATTTTTAATA	TAAATGGTTT	GATGCGTACC	TGGATGCTTA	ACAGATACAT	2100
TAAATAATGA	GATAACCCAT	GTCATAATGG	CTAAGCCCAC	ACACATTAAA	AAGAATAAGA	2160
CGCTAGGATC	TGGCAATTTA	TTTCCGATTT	TTTCAAACT	ATTCAAGAAA	CGATTGACGA	2220
TAGACCCCTT	TTGTTGATGT	TTTGATGTCA	TCAATTATTC	CCCCCTTTGT	TAAATATTTA	2280
AAGTGTAACA	AAAAATACTC	TCAAAAGTAA	CAATTTTCAG	GAAATAAAAA	AACTAATATT	2340
GTAAATATT	TTGAGTTATT	CAATAGAAAAG	TGTATAGCAG	AGTAGTTAAG	ACTGCCTGAA	2400
GACTTATCTA	TTAGGTTTAT	GAAGCATCGA	ACAGTGGAAG	ATAAGGACTG	TAAGTTTAAG	2460
ATATGTTGTA	TAGGAGTGAC	TGAATGAAAC	GTTTGGAAG	TAAAGTAGCA	GTCGTAACAG	2520
GAGCAAGTAC	AGGTATCGGT	CAAGCTTCTG	CAATCGCTTT	AGCTCAATAA	GGTGCGTATG	2580
TATTGGCGGT	AGACATAGCT	GAAGCGGTAT	CGGAGACTGT	CGATAAAATT	AAAAGTAATG	2640
GTGACAATGC	GAAGGCGTAT	AATGTGGATA	ATGCAAGCGA	ACAACAAGTG	GTAGACTTTG	2700
TGTCTGACAT	AAAGGAACAG	TTTGGAAGAA	TCGATGTGTT	GTTTAATAAT	GCCGGTGTGG	2760
ATAATGCGGC	TGATAGAATT	CATGAGTATC	CAATAGATGT	GTAGACAAG	ATTATGAATG	2820
TAGATATGCG	TGGGACATTT	TTAATGACGA	AAATGATGTT	ACCTTTAATG	ATGAATCAAG	2880
GTGGCTCTAT	TGTTAATACG	TCTTCATTTT	CCGGACAAGC	AGCAGACTTG	TATCGCTCTG	2940
GATATAATGC	TGCGAAAGGT	GCAGTGATTA	ATTTTACAAA	ATCAATCGCA	ATTGAGTATG	3000

GCCGTGATAG CATTTCGAGCC AATGCGATTG CACCAGGTAC AATTGAAACC CCGTTAGTAG	3060
ATAAACTGAC AGGTACGAGT GAGGATGATG CAGGTAAAAC ATTTAGAGAA AATCAAAAAT	3120
GGATGACTCC GCTGGGACGT TTAGGTAAAC CAGAAGAAGT TGCTAAATTA GTAGTCTTCT	3180
TAGCATCTGA CGACAGTTCA TTCATAACTG GAGAGACGAT TCGAATTGAT GGTGGTGTGA	3240
TGGCTTACAC ATGGCCTGGC GAGATGTTAA GTGATGATTC GTGGAAGCGG ACATTGGAAT	3300
AATTATTTAA AATCGATATC CAGTGGAAAA GAATTTGGCA TGAAGTAGGC AATGTATGCA	3360
TATTGTCGCA ATGAAAGACA TTAAAGCGG AGATTAATTA ATCTTTGAAAATCACATATT	3420
GTTCAATTGA AGTGTATTGC TTAAAGCTTG TTTTAACGTA TTGTAGGTCG TGCATCTAAT	3480
TTATCAGAAAT CTCGAGTTCA AACTTTTGGG GTATCTTTAA AATAAGCTGT ATTTTGTCTA	3540
TTCTAATAAA TTAAGGAGAA TTTTATGTTA AAAGAAAAAG AAAGTTTTAG ATTGCTATAT	3600
CAAGCTATAA GAGAGATTGC AGATAAAATT GGAGATAATC AGTTAGAAAC TAATTCGGTT	3660
AGTTTATtAT tATTGGACTT TGATTTTGAA CATGAAGTAT TTGATGAATT GTATCTTGTTG	3720
ATTTtAAAAAT ATTTAAATAC AGTAAGTATA GAGAACATAA GTCATAGTGA GCTT	3774

(2) INFORMATION FOR SEQ ID NO: 661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661:

TACTGGTTTT GGATTTTGGG GGTAATAAG TACCTAATAG TAATnATGGT GTCGTCAnAA	60
TTATATCTTT CCGTGATGTT CTTACTCATT AGAACATCnG CCTTCAGAGG AATCATGATA	120
CGAGGAATAA GAAATTTAAA TGTGAGCGAA GTCAATATAG TATTTGCGAT TATTTTTATT	180
AACTCCATTA TTATTGTTAG TTTGATTTTT CGAGGATAAC TTCAATTTTT GCtTTTGAG	240
GTTTTTTAAC ATATCTATTT GCATCAGTTG ATGGCAACCT TTTACTTAAA TCTATTGTGT	300
AGTTATTGTC TGCACCTGTT ATTTTAATTT GTCCTTTATT ATAAGAATTA TTATATAATT	360
TTTTACTTTT AATTAATGTT TGACGAATAC GAAAATCTAA TTCTTTTAAA GTTAAACAG	420
GCTTATTGCC TTCATAAACT GGAAATCCGC CAGTAAACGT TTCTGCTTTA TCTTTATATG	480
TTACATTCAG TTTATAGTGT TTATCGTTAG ATGTTGCTGC AGGAGTAACA CCACCAGTAA	540
ACGTTTCTTG AGATAATGCA AAAGaATCAA TGGTTTCTTG GTCTTTTATG CyAAAAATAT	600
CAACGCTTTT ATTTCTTAAT TGGTTGATAT TGCCCAACT TTCAGGTCCA TAAACTTGAA	660

TATGACTATA CCAAGaAAAC TGTAACAACG TTGCATGAAT CgTACCGTTA TCTTTTTTGCC	720
ATAACGTACT GTTAGAGAAG GTTAAATATT TTTGCGAGTA ATATTTAGTT AACTCATTAA	780
CGTTAGTTTC GTTTTGATTT ATATAAtAAG cTTTCGCTTC AGATGAAGAA TTGATAkGTG	840
TATTAGGAAA TTGTGTAGAT GCTGTACCTA ATAGTAACAA TGTTGTTGAT AAAATAATTT	900
TTTTCGTGAT GTTATTGTTT ATTCTGAATTT CTCCTTTGAG TATTGTTGGA ATGTTTAATT	960
ATAAAAAGGG GTTAATTAGA TAATTGAAAT TATCCGCATT TACAAAAGGT AATAGGTTAG	1020
TTAGATTTTT CGAGTATGAC TcAATTTCTG CATTACGAGG ATTTTAAACA TAACGGTT	1078

(2) INFORMATION FOR SEQ ID NO: 662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662:

AACTTGCTTT TTAGTATCTA CGTTAATATT AATAGCTTTA ATTTCACTTG TATTAATTAA	60
ATCAGCTGTG TAAATACCTG CTTTCAAATC GATAACTTTC TTTGTTCCAT TTTTAAAGTA	120
AACAGTATAT TTCGCTTGCT TCGATAGTCT TAAATCTAA TCACTAATAC CTCTGTCTGA	180
TTTTAAAACT GATTAACTC TATCCTCTAA ATCTTTATAA CTAATATTTT GATTCTTATT	240
AAATGTTAAG CTTGATAAAA TATTTTGGCT TGTACCGTTC ACAGTGaTTG CATATGGAAC	300
ATGGACTTTA GAATATCCAT GGTGTAACGA ACTTGATGAT TTATCTAATG GCTTAGCTGC	360
GGCAGACGCT TCATTATTTAT TAAAGTTTGC ACCTGTTGAT GCTAAAACAC CTAATGCTAA	420
AGTTGTTGTA ATCAATGACT TAAATTTTCAT AAATTATCTC TCCTTTTTTG TGTAATTCGT	480
ATTTGCAACT TAATTATAGC CAGACTTTCT CTATTTTTTG AATTAAGTGA ATATTAATAA	540
TAAATTATCT TTAACAATAA TTTTTTAACA CTGTTAAAAG TTCTTTTAAT TTTGATTAAC	600
TAATTAATTT ACAATACCTA AAATGTTGTT TGGTTTTGTT TATACCAAGC TTCAAACCTA	660
AATGTCATAA CAACATTCAT TTCTTAATTC CTATTAGATT TGTCGATTAT ATTTACAGCA	720
TCTTTATACT CAAAAACAT TTAAGTTAAA ATATAAATTC GATTAAATAA TTAATTTAAA	780
TTTAGTTAAT CAATTTTGCA TCTATTTTGT TGTAAGCTAT ATAAAAGGAG TGATAATGAT	840
GGTGAAAAAA ACAAAATCCA ATTCACTAAA AAAAGTTGCA ACACTTGCAT TAGCAAATTT	900
ATTATTAGTT GGTGCACTTA CTGaCAATAG TGCCAAAGCC GAATCTAAGA AAGATGATAC	960
TGATTTGAAG TTAGTTAGTC ATAACGTTTA TATGTTATCG ACCGTTTTGT ATCCAAACTG	1020
GGGGCAATAT AAACGCGCTG ATTTAATCGG ACAATCTTCT TATATTAAAA ATAATGATGT	1080

CGTAATATTC AATGAAGCAT TTGATAATGG TGCATCAGAC AAATTATTAA GTAATGTGAA	1140
AAAAGAATAT CCTTATCAAA CACCTGACT CGGCCGTTCT CAATCAGGGT GGGACAAAAC	1200
TGAAGGTAGC TACTCATCAA CTGTTGCAGA AGATGGTGGC GTAGCGATTG TAAGTAAATA	1260
TCCTATTAAA GAAAAAATCC AGCATGTTTT CAAAAGCGGT TGTGGATTCG ATAATGATAG	1320
CAACAAAGGC TTTGTTTATA CAAAATAGA GAAAATGGT AAGAACGTC AGTTATCGG	1380
TACACATACA CAATCTGA	1398

(2) INFORMATION FOR SEQ ID NO: 663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663:

TTGTAATTGG AACGTACGAA CTTTTCTAGG TAAGAAACGT CGAATCTCGT CCTCATTATA	60
ACCAACTTGT AGTCGTTTAT TATCTAAAAT AATTGGACGA CGTAATAAGC CAGGATTATC	120
TTGAATGATT GAATATAAGT CTTGTAATGG TAGTGAATCA ATATCAACAT TTAATTTTTG	180
GTATGTTTTA GAACGTGTAG AAATGATTTC ATCAGTACCG TCTTCAGTCA TTTTAAATAT	240
TTGCTTAATT TCATCAATTG TTAAATGTTT AGAAAAATA TTACGCTCCG TATACGGAAT	300
GTCcATGTTC tTGkTAACCA TGCTTTTCGCT TTTACGGcAA GATGTGcAaC TTGGtGaAGT	360
aAATAATGtT ACCATACATC TCACTCTCCT ATTTGAATGA ATAAAATTCA TTGCTTAAAA	420
TTTAGTTATA GATCAAGAAA AAACATTTTT TTCTAAAATT CTTAATCGTT ACTATTTATT	480
ATAACTATCT AACATTAAAA TTAAATGAGA AAAACCTAAT TTTTCAGATA AGTTTACATA	540
CTTATAAAAA AGATTATTAA TCCCTTTGTT AGTAGTAAGT TATACGTATA TTCTAACACA	600
TCTTACATTT TTAAGAAATA CTGTTATAAT GATAATTATT AAAATATTAC TAAGAAAGTA	660
GGCATTTAAA TGGAGACATT ATTTTCAGGC ATCCAACCTA GTGGAATTCC TACTATTGGA	720
AATTATATTG GCGCACTAAA ACAATTTGTT GATGTGCAAA ATGACTATGA TTGTTATTTT	780
TGTATCGTAG ATCAACATGC AATTACAATG CCACAAGATC GTTTAAAATT ACGTAAACAG	840
ACCAGACAAT TAGCAGCGAT TTATTTAGCT TCTGGTATAG ATCCAGACAA AGCAACATTG	900
TTCATACAAT CTGAAGTCcC TGCACACGTA CAAGCAGAT GGATGTTAAC TACGATTGCT	960
TCTGTTGGAG AATTAGAGCG TATGACGCAA TACAAAGATA AAGCTCAGAA AGCAGTTGAA	1020
GGTATACCTG CTGGTCTATT AACATATCCA CCTTTAATGG CAGCTGATAT TGTTCTTTAC	1080

AATACTAATA TCGTTCAGT TGGAGATGAC CAAAAGCAGC ATATCGAATT GACTCGTAAC 1140
 CTTGTAGATA GATTTAATAG TCGCTATAAT GATGTGCTTG TGAACCTGAA ATTCGTATGC 1200

(2) INFORMATION FOR SEQ ID NO: 664:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664:

TGTACCTTTT GCTTTAATAA ATACTGTTTC TTTATCATAA TTAGGTTTCAG TTAAGAAATT 60
 AAATTGTAAG CTTTGAGTAA TATTTTTTTG ACTATCACTT GTTGTAGCTG TACGTGTATA 120
 CATTTTAGTA TCACCATCAA GATTCTTCTC AGAAACTTGT TTGATTTTCAG AATTAATCTT 180
 TGCAAATGAA GTAGCTGGTA ATACAGTGAA AGTAGTCGAT AGTGCTAAAG wACAAATTGT 240
 GATATTTTTTA CATAGTTGTT TAATCATTAG TAATCCGCCC TTTCAATATT ATCCTTCTTT 300
 ATAAGGTTTA TTGTCATCAG AATATTTATC AACGACTTTAACTGTTTTAT TTTTCCAATC 360
 AACTTCATAA GTGACAATTA ATCTTTGACC ATCTTTATTT TtctCTAAAA TTGGAGGTGC 420
 ATAATGTATy CCAGGTCTGT TTTTCAAAAT ATCTTGATTT CGTGTGTATG TTACTTCAAA 480
 TTGCGTTTTT TCATTTGACT TTTTATTAGA TAAATAAGTT AAAAATTCTG GATTAAAGCC 40
 ACTTCTTACT AATGCTGGGT ATCTATATTT TGAAGCAAAG CTTAGTTCaG GGTTTTCTAC 600
 AGTAGCAATT CTCGTATTTT TATAGAATAA TAATTCATCA TTTCTATTTT TCACTTCTCC 660
 ACCATACTTC AAGTCATTCG CAATAACTGA CCAGTGTACA TGgCCAGTTn ATTTATTTTT 720
 ACCGCTGGCA ATTGTGTCAT AATTGCTGC ATCATCAACT AATCGTTTTG GAAGTAGCTA 780
 TTTGCTG 787

(2) INFORMATION FOR SEQ ID NO: 665:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665:

TTATCTGTCA TTAACCACTG GTACATGTGA ACCCGGChTn AATCAATATA TATATTTAAA 60
 AGCAAAGGCG CGCCATGTGC CTTTtTTnTA tTTTGTATAT CTGATCAAA ATCGATTTGA 120
 TAAAATCCG CTTTATTTTA TCATCTATTC AAATGATTTT AGTGCGCTTA TTTTACTATG 180

GCATTATTGC CTAACCTGTT TGAGATATAT TAATATTTGA TGATTCGTAT TCAAAGTTTT	240
CATTTAACAT GTATTTAGTA TCATGATAGC TGCTTCATTG ATGATATACT ACCTACTTTT	300
TCAACACTTC TTGTTGATA ATCGTTAATA CACCCTGCTT ATCATTACTT GGAAGCAGAC	360
CAGAGGCAAT ATTGAACAAT TCTTCATCAT GACTATTTTC CATCACATAA CTATGCTTAG	420
CGAACGCTAA CATATCTTTA TCATTATTCG CATCTCCGAA GGCCATGAGC TCTGAAGGAG	480
ACATTTCCCA TTTATCTAAC AATCGTTTA ATGCCTGnCC TTTAGTCATG TTT	533

(2) INFORMATION FOR SEQ ID NO: 666:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666:

GACTTCTCTT GCACTAAAAA TTGCTCAAAT TGCTCGCTGT CATAACCAGG CGGTGTTTCC	60
AACCATACAT ATATGCCACC TTTAGCATGA ACAAATGGCA AATCAGCTTT TGCAAGCATG	120
GCTTCGAATC GGTCACGACG TGTTTTAAAT ACATTGCTTT GTTCTTC AA AAAATCATCA	180
TAATGGATTC AAAGCATATA TTGCGGTCAT CTGTGAAATG CACCAAAACAT CCCAGCATTT	240
GTGTGCGTTT GGTACTTTTT CAAAGCTTGA AATCATATCT TTATTACCAA CTGCCAAAAC	300
CGACTCTGAA AACCTGGACA TGTTGATGAA CCTTTnAGAC AAGGGAAGAA ATTTGCAATC	360
GCAACATCTT TGCCCATTTT nCCGAAGCAA GTGnGACTAG	400

(2) INFORMATION FOR SEQ ID NO: 667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667:

TCTCCAATGC TACTCAAATT AAAAAGGTTT TAAATATTGT TAATTCTGAT CCAGAGCGAA	60
AGATTGTTAT CGTTTCTGCT CCAGGTAAAA GACATGATAA TGATATTAAA ACAACTGATT	120
TGTTAATCAG ATTATATGAA AAGGT ATTA ATCATCTTGA TTATCATGAT AAAAAAAGAG	180
AAATTATTCA GCGTTATGAT GATATTGTAA AAGAATTGCA AATGGATGAA AGTATTTTAC	240
GGACGATAGA TGTGACTTTG GAACATTATA TAAATCAATT AAAAAATGAA CCAAAGAGAC	300

TATTAGATGC ATTACTTTCT TGTGGTGAAG ATTTTAATGC GCaAyTGAtA GyTTATATA 360
ATAAtAGTCa gGTtACCAAC AAmATwTATA TCCcCGAAGG AAGCGGGTAT TT 412

(2) INFORMATION FOR SEQ ID NO: 668:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668:

TTACTCGTTA AAGATATTGT AAAAGATGAA GTGACAGAAT ATGACATTCA TCAAATGTTA 60
CCGCATCCGA TTAATATGGT AAGGGTTAGA CTTTTTG GTG TGAAATTAAA AGAGATTATA 120
GCTAAAAGTA ATAAACAAGA nTATATGTAT GAACATGCAC AAGGTTTGGG TTTCAGAGGG 180
AATATATTTG GAGGATATAT TCTTTATAAT TTAGGGTACA TTCATTCTAC AGGGCGTTAC 240
TATCTGAATG GAGAAGAAAT CGAGGACGAC AAGGAATATG TACTAGGTAC GATAGATATG 300
TATACGTTTCG GTCnTATTnC CCAACATTGA AGGATTACCA AAGAGTATTT AATGCCAGAG 360
TTTTTCAGAG GTATATTTAA nGAAAATTAT TGGCTATTTA 400

(2) INFORMATION FOR SEQ ID NO: 669:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669:

TGTTTCGATAT TTTTAAATTT ATCTTTTAAA TACAACA ACT GTTTCCGTAA TGATTTAACT 60
GTTTTATGAC TAATGCCATT GAATATTTCT AGCGTTTTAT TTAAC TTATCGATAATCGCA 120
TGTAATCCT TCAAATGTC TTTTGTTTCA AAAGTAAATA CATTATGGAA GCGATGAATA 180
TCATCATCAT AAACATCAGA ATCATTGATA ATCGTAAATA TCGTTGAGAA CAATTGCTCA 240
TTTAACTCAT GAATCTCATT CATACTAGCC TTCAAGCCAA AAATATCAAT TGGTGCAATA 300
TCTAATTTTT CCAAAATTCG CTGCTTTTCC AGTTGATCAA TTGCCTTTAA CAATTTTTCA 360
TTTTCGTTTT TACCAATCAA ACCAAGCTGA TATTTAATAT CAGCATAACT CAACTCATTT 420
GTCAC TTGAT TTAAGGCATA GTCTGGTAAG CGATGTGCTT CATCCACTAT ACAATCATCA 480
AACAA TTGAT ATATTGAATT TTCAACATCA GATG aATTA AATGTGCATG ATTTGTAATA 540
CCAATTTGaA TGTTCTGTGC ATTTGCTTA ATAAAATTAT aATAATGAAC ATCGTGACGT 600

GCCGGTACAT ATGTTTCAAT TTTCTGGTcA AAATACATCT TTTGACCACC TTTTAAATTT	660
AATTCCTGTA TATCTCCGGA CGGCGTcTCT GTAATCCAAA TCAGCAATTG CATTTTCAG	720
ATATTCACtT CGTAATTACT TGTGTCATCT TTTAAAATTT GACTAATAAG CCCC AATGAA	780
ATGTAATCaC TTtTACTTTT AATCAATAGT GCATTAATTT TAAAATTCAA CGCTTCATTC	840
ATTGCTGGAA TATCTTTTTT TAACAATTGA CTTTGCAGTA ATTTAGTATT GGTAGAAATC	900
ATGACATGCT TCCCAGTTTC AATATTATAC ATCAAGGCCG CAAGTAAATA TGCTAATGAT	960
TTACCACTGC CTAGTGATGC TTCAATCATT GCTTTTTT CAC TATGCATGAG CTGATCTAAT	1020
ATAGTTTCCG CTAAATATAA TTGTTGCGGT CGATATGTTA AGCCAAGTTG ATCTACAGCT	1080
TTGCTATATA AAGACTTCAA GCTGCCATTA TAATTTGTTGTCGGCTTTTT AAAATCAACT	1140
TGCTTACGAT AGATAATCTG TTCGAACTTT TCGTACGATT TATCCAATGG CTTTGCATCA	1200
TATTGCCTAA CCATCTCAAA GAAAATATCA TACAAA	1236

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670:

ACAsAATTAT TGACCAATAT GACTCGTGGA CTGATATGTT TAAAGCACTA CTGCATGAAA	60
CATTTAAAGC ATATGGCGTT CTATTTATAG ATGCGCAGTT TGAGCCGTTA AGAAAAATGG	120
AAGCGCTAT GTTTAAAAAG ATTTTGAAAA AACATCAGTT GCTTGATGAT GCTTTTAGAG	180
CAACACAACA ACGTACTCAA AATCAAGGCT TGAATGCGAT GATACAAACA GATACAAATG	240
TTCAATTTATT CTTACATGAT GAAAATATGC GTCAATTAGT tTCGTATGAT GGTAAGCAyT	300
TTAmATTAAA TAAAACAGAT AAGACATATA TAAAGGAAGA AATTATAAAT ATTGCGGAAA	360
ATCAACCKGA ATTATTTTCT aATAATGTAG TGACAAGACC ATTAATGGnA GAATGGTTAT	420
TTGAACACGG TGGCATTGTG TGGAGGACCG AGTGAAATTA A@aCTGGGC TGA ACTAAA	480
GATGTATTTG AACTATTTGA TGTTGAAATG CcTATCGTGA TGCCAAGGCT TAGAATTACT	540
TATTTAAATG ACCGTATAGA AAAATTACTT TCGAAATACA ATATTCCATT AGAAAAAGTG	600
TTAGTCGATG GTGTTGAAGG AGAAAGAAGT AAGTTTATTA GAGAACAAGC ATCACATCAA	660
TTTATTGAAA AGGTAGAAGG TATGATTGAA CAACAGCGTC GTCTAAACAA AGACTTATTA	720
GATGAAGTGG CGGGGAATCA AAATAATATT AACCTTGTTA ATAAAAATAA TGAAATTCAT	780

ATACAACAGT ATGATTATTT GTTAAAACGT TATCTTTTAA ACATTGAAAG AGrAAACGAC	840
aTCAGTATGa AGCmATTTAG rGrATTCAA GAAACACTCC ATCCAATGGG AGGATTACAA	900
GAAAGAATAT GGAATCCACT TCAAATTTTG AATGATTTTG GGACAGATGT GTTCAAGCCC	960
TCCACCTATC CACCACTTTC TTACACTTTT GATCATATTA TTATAAAACC TTAATATACC	1020
AAGGGTTTAG CCCGATTTAT CTTAATGATA AATCGGGCAT TTTTTTGTTTTTTAAAATAA	1080
ATTTACACAA TTTTGTATAA ATAGTGGTGG ATAGTGGGGA GATGTGGTAA ATTATATATA	1140
AGGTGAGGTG ATAAAAAATG TTCATGGGAG aATACGATCA TCAATTAGAT ACAAAGGAC	1200
GSTATGATTAT ACCGTCCAAG TTTCGTTATG ACTTAAATGA GCGTTTTATT ATCACAAGAG	1260
GCCTTGATAA ATGTTTATTC GGTTACACTC TAGACGAATG GCAACAGATT GAAGAGAAAA	1320
TGAAAACCTT ACCTATGACA AAAAAAGACG CACGTAAGTT TATGCGTATG TTCTTCTCTG	1380
GTGCTGTTGA AGTAGAACTT GATAAGCAAG GGCGTATTAA CATCCCTCAA AACTTGAGGA	1440
AATACGCTAA TTTAACTAAA GAATGTACAG TATCGGTGT TTCAAATCGT ATTGAGATTT	1500
GGGATAGAGA AACTTGGAAT GATTTCTATG AAGAATCTGA AGAAAGTTTC GAAGATATTG	1560
CTGAAGATTT AATAGATTTT GATTTTTTAA ATGGAGGAAT TGAAGtGTTT CATCATATCA	1620
GCGTTATGTT AAACGAAACC ATTGATTATT TAAATGTAAA AGAAAATGGT GTGTACATG	1680
ACTGTACGCT AGGTGGAGCG GGACAnGCCC TTTATTTACT AAATCAATTA AATGACGACG	1740
GAAGATTAAT AGCAATCGAT CAAGACCAAA CTGCAATTGA TAATGCTAAA nGGGTATTAA	1800
AGGATCATTT GCATAAAnG	1819

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671:

ACCAATTATT GGACAGGAAT TAGCAAAAAA TGCAATGCTT GCATTAATCT ATGCATCGAT	60
AGGTATCATC ATCTATGTAT CATTACGATT TGAATGGCGC ATGGGTCTTT CATCTGTAFT	120
GGCATTATTA CATGATGTAT TCATTATAGT AGCGATTTTC AGTTTATTTA GAATTGAAGT	180
AGATTTAACA TTTATCGCCG CTGTATTAAAC AATTGCGGT TATTCAATTA ATGATACAAT	240
CGTAACGTTT GACCGTGTAC GTGAAAACCT ACAAAGGTT AAAGTGATTA CGACAACAGA	300
ACAAATTGAT GATATCGTTA ATAGATCAAT tAGACAGACA ATGACACGTT CAATTAATAC	360
AGTATTAACA GTTATTGTAG TAGTAGTTGC TATACTATTC TTCGGTGCTC CTACGATATT	420

CAACTTTACT TTAGCATTAT TTATCGGATT GATTTCTGGT GTATTCTCTT CAATCTTCAT	480
TGCCGTTCCG CTATGGGGAA TAATGAAAAA ACGTCAGTTG AAAAAATCGC CGAAACACAA	540
ATTAGTTGTA TATAAAgAAA AGAAATCGAA CGATGAAAAG ATTTTAGTTT AAAAtGaATT	600
AAGCGGTAT	609

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672:

CTTAAACAG CAATTTGAAC GTTTACAAAA TGAACAAATC TTTGTTTATG TTTGTCATGG	60
TAATCACGAT CCTTTATCAT CAAAGATTTC ATCAAATGCG CCAGATAATG TtntTTGTATT	120
TTCAAATAAA GTTGAGACGT ATGAAGCAAT TACTAAAT T GGTGAAACAA TTTATATTCA	180
CGGATTTAGT TATGAAAATA GAGCAAGTTA TGAGAACAAG ATTGATGAAT ATCCATCAAG	240
TCAAGGCCAA AAAGGCATAC ATATTGGTGT CTTGCATGGT ACGTATAGTA AATCTTCAGT	300
TAACGAAAGA TATACCGAGT TCATTTTAGA AGATTTAAAC AGTAAATTGT ATCATTATTG	360
GGCTTTAGGT CATATACATG AACGTCAACA ATTAAGTGAT ATGCCTGTAA TTAAGTATTC	420
AGGTAATATT CAAGGTAGAC ATTTTAATGA GCAaGGTGAA aAAGGTTGCT TATTAATCGm	480
GGGTGACCAC TTAAAATTAA AGACTAAATT TTATCCTACA CAGTATATTA GATTTGAAGA	540
AGCAACTATT GAAACGGATA AGACATCTAA GCAAGGTTTA TACGAGGTCA TTCAAACTT	600
TAAAGAACAA GTGAGAGAAG AAGGAAAAGC CTTTTATCGT TTAACGCTTG TTATTAATAG	660
TGAGACATTA ATTTACCTC AAGATTTATT ACAAGTTGAA GAAATGATTA CAGATTATGA	720
AGAAAACGAA AATCAATTTG TATATATTGA TGAGTTAAAA ATACATATG CACAAAATGA	780
TGAGTCACCT TTAGTTAATG AATTTTCAGC GGAATTATTA GTCGATCAAA CTGTTTTTGA	840
TAAAGCGATG TCAGATTTAT ATTTAAATCC AAGGGCATCT AAGTTCCTAG ACGATTATGG	900
AACATTCGAC CATAACGCAT TAGTTAATCG TGCTGAAGAA ATATTAAAAG CTGAAATGAG	960
AGGTGAACAA AATGATAATT AAATCACTTG AAATTTATGG TTACGGTCAA TTTGTTCAaC	1020
GTAAAATTGa ATTTAATAAA AACyTCaCTG AAATTTTTGG TGAAAATGAA GCGGGTAAAT	1080
CGACGATTCA AGCATtCATC CATTCGATAT TATTTGGATT TCCAACATAA AAGTCTAAAG	1140
AGCCAAGACT AGAACCACGT CTAGGTACC AATACGGTGG TAAATTAGTA CTTATTCTTG	1200

ATGATGGCTT AGAGATTGAA GTTGAACGAA TTAAAGGCAG TGCTCAAGGT GATGTGAAAG	1260
TATATTTACC TAATGGTGCT GTGCGTGATG ATGCTTG GTT AAAAAAGAAA CTTAATTATA	1320
TTTCTAAAAA GACATATCAA GGTATCTTTT CATTTGATGT ACTAGGGCTT CAGACATTC	1380
ATAGAAATCT AAATGAAAAA CAATTGCAAG ATTATTTATT ACAAGCmGGG GCTTTAGGAT	1440
CAACTGAaTT CACGTCAATG CGCGAAGTGA TTAATCGTAA AAaAGATGAA TTATATAAAA	1500
aATCAGGTAA AAATCCGATC ATTAATCAAC AAATTGAGCA ATTAAAACAA CTAGAAAGTC	1560
AAATTCGTGA AGAAGAAGCA AAGCTAGAAA CATATCATCG CTTAGTAGAT GATCGAGATA	1620
AATCATCACG TCGATTAGAG AATTTAAAGC ATAATTTAAA TCAATTATCA AAAATGCATG	1680
AAGAAAAACA AAAAGAGGTT GCTTTACATG ATCATTCACA AGAATGGAAG TCTCTAGAAC	1740
AACAGTTAAA TATTGAGCCA ATCACATTCC CAGAAAAGG TGTGGATCGT TACGAAAAAG	1800
CACGAGCGCA TAAGCAATCG TTAGwAAGAG ATATTGGTTT AAGAAATGAG CGTTTAGCTC	1860
AACTTAAAGA AGAAGCGACT CAATTAGAGC CAGTTAAACA ATCTGATATT GACGCCTTCA	1920
TTAGTTTGAA TCAACAAGAA AATGAAATTA AAAATAAAGA ATTTGAACTT ACTGCAATCG	1980
AAAAGGATAT TGCGAATAAA CAACGTGATA AAGATGAATT GCAATCAAAT ATTGGTTGGT	2040
CTGAAACGCA TCATGACGTA GATAGTTCAG AGGCAATGAA AAGTTATGTC AGTGAGCAAA	2100
TCAAGAATAA ACAAGAACAA GCTGCATACA TTAACAATT AGAACGTAGT TTAGAAGAAA	2160
ATAAAATCGA AGATAATGCG GTTCATAGCG AACTAGATTC TGTTGAAGAA AAATAGTTCC	2220
TG	2222

(2) INFORMATION FOR SEQ ID NO: 673:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673:

TTGCAGGTAT CATTTTTTTTA ATGCCATATG GATTATGTTT TCTACCGTTT TATAAGCAAA	60
AAAAGAAAAA ACAGACATTT AAAAAATACA TGGTTTAAC TACGATTGGT TTGTCAATTT	120
GTCTAGGCTT ATCTCTAGTT TTGGTTCACA CTACGAAAAT TTATATGGAC GAAGGTGGCG	180
TAAGATACTA TTACGGTAGT TTTGTAATGA AACAAGCGGG CGGTTATGCT TATTTAGCTT	240
TAGCGGTACT TTCAACGTTG TTAATTGTTG CGAAAAAGC TACAAATAAA AATAAAGAAA	300
TCGAAACCGT CGACAATACA AATATAACGG AAAGATAATT AAGGGAGTGC TCATTCAGGA	360
GTGCTCTTTT TTGATGTCCA AATTTAGTTG CAAATGAAGG CATAGA	406

(2) INFORMATION FOR SEQ ID NO: 674:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 927 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674:

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CCACTTTGTG GATTTTCTTT ATATTCTCCA CGCTTGtACT ACAACTTCTT TCGTTTCTGT      60
TTCATCACCG ACTGCCGCAT TCGTTAGCAC ATGTAATAAC TCTTTTGCGG TTAATACATT      120
CTCATCTATA ATCTTATCTT TTTGTTCTTG TATATATTGC TTGATGTGCG GCTTTTTCAA      180
TAACCTACAC GCTGTCACAT GTGCGCTATT TGC GTTATAT CCTGyTTTTA TGGCACTTTG      240
TGTTACATTC AGTGTCTAA TATACTCATT CACAAAACGT GTTGCTTTG CAGTTAACTC      300
ACTCATTTTA TCACCCCCAC AATTTTATCT AATATGTTTT CATACCATAA TATTACAGAT      360
TGTTCTGAAC AATCTAAGGC ACTACTAATA TCTTGATAAC TAAGTCCTTG TATAAGGGAG      420
TCAAAAATAT AAAACTCTTT ATCGGTCGCT AATCTGTCAA CAATCATTTT TATGTGATTC      480
TTTATAATAT GATCATTGAC ATTATCGTCT GTCATCAATT CGTCAGAATC TTCATCACCT      540
ATTAAAAAGA AATCATCAGT ATTTATTTCA TCATCGCCCC GTTAACTAGC TTTGAAGTCT      600
TTAGCACACT TGCATATACC GGCTGTCGTG CTGGCkAGAT ACTAGCATTG AAGTGGTCTG      660
ATATTGATTT TGAAAACAAC ACgATTAGTA TTAATAAAAC ATATTACAAT CCAAATAATA      720
ACAAGAAGAA ATATCAGATA CTCCCCCTA AAACTGAAAG TTCTATCGGT AAGATTTCCG      780
TTGACCCAAA TGTAATAAAG GtGtTGCGtG ATTATAAGAT AAACGTTCAA AATAATTGGA      840
AAAACGAATT ATATAATGAT AACCATTGTA ATGAAAAAAC TATCAATG GATACAAACC      900
ATTATGTCAC GTACCAGCAT ACTCAA                      927
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(2) INFORMATION FOR SEQ ID NO: 675:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675:

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GATGTTAAnA TAAGTACATC ATTTTGACTC CCAAATATTG GCTTTAGACC TTGAAATGCT      60
TGTTGTGCGA TGTCTTCAA ATCTTTAGAA CGATGACCAA CCATAGGTGC TTGAATnTCT      120
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CTCATAATGG CATCAGGTAC cAGGGGTTGG GaCCAGGTGT TAATAACAAC GGTTGATGAT	180
AATACATTTA TATGCCTCCT ATAAATAAGA TTTCCTATT TTAGCAAATT TTCTGAAAAT	240
TTAAAAGCCT AAAAAgtGAT AACGCTATAT TGTCGAACAA ACGTTATCAC TTAACGATTT	300
TATTTGGCCT GAATGATGGG ATAGATTTTT ATGTCCACAT TATTTCTTAC AGCATTTGAA	360
ATCATGCAAT TATTATCTGC AATTGTTATC AATTTTGGTA ATCGCTTTTC TAATTGTGCT	420
ATTTGATCAC TTGGAATTTG AATTTGAGGA TGGTGCACAA TTTTGTGACAT ACTGAATTTT	480
CCGTTATTTA AACAAGCTGT TCCAATCGAT TGTTGTkCAA TTGAAATATC GTGAACTTT	540
GCACGTTCAA GAGTAGCTGC TAATGAGATG ATATAACATG ATGAAGCGGC TGATACTAAC	600
ATTTTCATCGG GATTTGTTCC TATACCAACA CCACCTAAAG AAGCAGGTAT AGAAATATTC	660
TCTGAAAGTA TGTCGCCTTG AACGTTTCCG ACATTGTTAC GACCACCTTG CCAAGAAGTT	720
TGGACTTTAA AGTCATGTTG ATGCAATTGC TTTAACCTCC AATATAATTG TGATAGTTTA	780
ATTTTAGAAT AGTTTATCAA AGTTTAACAG AAAGGTGACT TATCAATGAC TCTGAATAAA	840
CTGAAAGATG AATTACAAAT TGTTTCGCAC CGTGGATTGC CGAGTGATTT TCCTGAAAAT	900
ACAATGGTCG GTTATCGAGA GGTAATGGGG CTaATGTTG CTATGTTAGA AATAGATGTT	960
CATTTGACCA AAGACCAACA TTTTGTGTG ATACATGaTG AAACAATTGa TAGAACATCG	1020
GaTGGtArGG GGCgtAwTgc TGaTTACACA TTATCGCAAT TAAAATCATT TGATTTTGGT	1080
AGTTATAAAG ATGTTGCTTT	1100

(2) INFORMATION FOR SEQ ID NO: 676:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676:

ATTAATTTCA TATGGAAATA GTTGAACATA CTGCGCTGTA TAAGCTTCAA CAGTTTGATG	60
AATTAACGAT TGATCTTCAA TATATCCGTA GAACAAATCT TCAGTACAAA CTACTTTACC	120
TTTATCAGGT TTAATTGCAC CTGCCAACAA TTGACCTACC AACGCTTTGG AAGATTCAGG	180
TTCACCAATT ATACCTAATG CTTCTCCTTG ATAAATATGT AAATAATAT TGTTTAAATC	240
GATATCTTCA GCATCATATC CAAAAGGTAA ATACCATTTT TTATTCTGTT TATTCCTATA	300
GTAGTGTGTT ACTTTTAGTA ACTTTAAAAC AATTGAACTT CCCATCTATT TTCATCCTTC	360
TATAATTGTA ATAACGCTAT AGGtAATCCT TCyTCGgtT CATCGctATT AAAtCTAAAc	420
CCCCACGCaA AAATACCTTT TAATCTTnCT ACTTTAAAAT	460

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677:

GTCAAGTTTT CGGCTAGATT TTAAACGCTC ATCACTATGT AGAATGAAAC TTTCGAAAAA	60
CTGTAAATCA TCATAACCTT TTACATAAAC ATAACCTTCG CCACCAATTG CTTGAATAA	120
ACATTGGGCG GCCATTTGAA TTTCTAAAGA TTGTTTTTCT AGCCTATTAA AGATACCTAT	180
TAGTTGTGTG TTTAAGATTT TTGACATCTT TATCCTCCAA TCTACTTATA AAATATTGTA	240
ATTAATGACT ACATATTATG CAACGGCTTA AATTGTATAA AAATGTATAC GTTTGCATTT	300
AGTATAACTA TCGCATTTTT CAAAAAATAC ACATTTAATC TGCAGTATTT CAATGCATTG	360
ACGCTATTTT TTTGATATAA TTACTTTGAA AAATACGTGC GTAAGCACTC AAGGAGGAAC	420
TTTCATGCCT TTAGTTTCAA TGAAAGAAAT GTTAATTGAT GCAAAAGAAA ATGGTTATGC	480
GGTAGGTCAA TACAATATTA ATAACCTAGA ATTCACTCAAGCAATTTTAG AAGCGTCACA	540
AGAAGAAAAAT GCACCTGTAA TTTTAGGTGT TTCTGAAGGT GCTGCTCGTT ACATGAGCGG	600
TTTCTACACA ATTGTTAAAA TGGTTGAAGG GTTAATGCAT GACTTAAACA TCACTATTCC	660
TGTAGCAATC CATTTAGACC ATGGTTCAAG CTTTGAAAAA TGTAAGAAG CTATCGATGC	720
TGGTTTCACA TCAGTAATGA TCGATGCTTC ACACAGCCCA TTCGAAGAAA ACGTAGCAAC	780
AACTAAAAAA GTTGTGTAAT ACGCTCATGA AAAAGGTGTT TCTGTAGAAG CTGAATTAGG	840
TACTGTTGGT GGACaAGAAG ATGATGTTGT AGCAGACGGC ATCATTTATG CTGATCCTAA	900
AGAATGTCAA GAACTAGTTG AAAAACTGG TATTGaTGCA TTAGCGCCAc ATtAGGTTCA	960
GTTTCATGGTC CATACAAAGG TGAACCAAAA TTAGGATTTA AAGAAATGGA AGAAATCGGT	1020
TTATCTACAG GTTTACCATT AGTATTACAC GGTGGTACTG GTATCCCGAC TAAAGATATC	1080
CAAAAAGCAA TTCCATTTGG TACAGCTAAA ATTAACGTAA ACACTGAAA CCAAATCGCT	1140
TCAgCAAAAG CAGTTCGTGA CGTTTTAAAT AACGACAAAG AAGTTTACGA TCCTCGTAAA	1200
TACTTAGGAC CTGCACGTGa AGCCATCAAA GAAACmGTTA AAGGtAAAAAT TAAAGAGTTC	1260
GGTACTTCTA ACCGCGCTAA ATAATTAATA TTTAGTCTTT AAGTTATTAA TAACGTAGGG	1320
ATATTAATTT TAAAAGAAGC AGACAAAATG GTGTTTGCTT CTTTTTTATG TCGTATAAGT	1380
AATAAATAAA ACAGTTTGAT TTTAAAATGA AAGCGTAAAA ATGGTAAAAAT ATATCAAAAT	1440

TGATTGTGAT A

1451

(2) INFORMATION FOR SEQ ID NO: 678:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 668 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678:

nGTATTGAAG CGGTAAACA AACACTAAT GCAACTGACG AAGAAAAGCA GGCTGCTGTT	60
AATCAAATCA ATCAACTTAA AGATCAAGCA ATTAATCAAA TTAATCAAAA CCAAACAAAT	120
GATCAGGTAG ACACAACTAC AAATCAAGCG GTAAATGCTA TAGATAATGT TGAAGCTGAA	180
GTAGTAATTA AAACAAAGGC AATTGCAGAT ATTGAAAAAG CTGTTAAAGAAAAGCAACAG	240
CAAATTGATA ATAGTCTTGA TTCAACAGAT AATGAGAAAG AAGTTGCTTC ACAAGCATTA	300
GCTAAAGAAA AAGAAAAGC ACTTGCAGCT ATTGACCAAG CTCAAACGAA TAGTCAGGTG	360
AATCAAGCAG CAACAAATGG TGTATCAGCG ATTAAAATTA TTCAACCTGA AACAAAAGTT	420
AAACCAGCTG cACGTGAAAA AATcAATCAA AAAGCGAATG AATTACGTGc TAAGATTAAT	480
CAGGATAAAG AAGCAACAGC AGAAGAAAAGA CAAGTAGCAC TAGATAAAAT CAATGAATTT	540
GTAAATCAAG CCATGACAGA TATTACGAAT AATAGAACAA ATCAACAAGT TGATGATACA	600
ACAgTCAgCG CTgATAGcTt GCTTTAGTGA CcCTGACCA TATTGTTAGA GCgCTGCTAG	660
AGATGCGT	668

(2) INFORMATION FOR SEQ ID NO: 679:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679:

GATCCAAATT TAAAAGGAAA AATAGCCTTT AACGAATTTA CGAAACAAAT TGAATGTTTA	60
GGGAAAGTGC CATGGAATAC TAATTTTAAG ACACGTCAAT GGCAAGACGG TGAGATAGC	120
AGTTTAAGAA GTTATATCGA AAAGATTTAT GACATACACC ATTCAGGTAA AACAAAAGAT	180
GCCATTATAA GCGTcAAtGC AAAATGCTTA TCATCCAGTA AGGGATTATC TAAATAAAAT	240
ATCGTGGGAT GGACATAAAC GCCTTGAAAA GTTATTTATC AAATACTTAG GTGTTGAAGA	300
CcTGaAGTGA ATAGAACAAC TACCAAAAAA GCATTGACTG CTGGAATCGC TAGAGTAATG	360

GAGCCTGGAT GTAAATTTGA CTATATGCTT ACACTTTATG GTCCTCAAGG TGTAGGTAAA	420
TCTGCTTTGC TAAAAAATT AGGTGGTGCA TGGTTTTCTG ACAGTTTAGT TTCTGTTACA	480
GGTAAAGAAG CTTATGAGGC CTTACAAGGC GTTTGCTAA TGGAAATGGC AGAACTTGCA	540
GCTACAAGAA AAGCTGAAGT TGAAGCTATT AAGCATTTCA TATCTAAACA AGTTGACCGA	600
TTTCGTGTTG CTTATGGGCA TTATATTGAA GATTTTCCAA GGCAATGTAT TTTCATTGGT	660
ACAACTAATA AAGTTGATTT CTTAAGAGAT GAAACTGGTG GAAGACGTTT TTGGCCAATG	720
ACTGTAAATC CAGAGAGAGT TGAAGTGAAC TGGTCTAAAC TAACCAAAGA TGAGATTGAC	780
CAAATTTGGG CAGAAGCTAA ACACTATTAT GAACAAGGAG AAGATTTATT CCTTAACCTT	840
GAACTAGAAG AAGAAATGCG TTCAATACAA AGCAAACATA CTGAGGAATC TCCATATACA	900
GGCATTATTG ATGAATATCT TAACACACCm ATTCctAGCa ATTGGGATGA CTTAACTATC	960
TTTGAACGAA GACGATTTTA TCaAGGTGAT GTTGATATGT TACCaACAGG AAATGTaGAT	1020
TACGTTAAAA GAAATAAAGT CTGTGCGCTT GAAGTGTTTG TTGAATGTTT TGGTAAAGAT	1080
AAGGGAGATA GTAGAGGATC TATGGAAATT AGAAAGATTT CAACATCTT AAGACAATTA	1140
GACAATTGGT CTGTATATGA TGGTAATAAA AGTGGGAAAA TTCGATTGG AAAAGATTAT	1200
GGTGTACAGA TAGCTTATGT AAGAGATGAA AGTTTAGAGG ATTTAATATA AGAAATATTG	1260
AATAAATATG CATTTTAGAG TGTTGTATCA GATGTTGCAT CATTTTTTGA GTGATGCAAC	1320
ACGGGAGTGT AAAAAGTAAT CGTAGGTGTT GTATCATTTT TGGTGATGCA ACATTGATGC	1380
AACAAATGAT ACAACACCTC TTTCTTTCT AGCTGTAGGG TTCAACCCTG TTTGTTTCCA	1440
ATGTTGCATC AAATTCACTA TAAAGTTTAA AAAGTAGTGT TAGGGAGTAA AGGGGTATAG	1500
GGGTAACCTT CTAACAGCTA TTTTAAAAG TTTGGCAAGA ATTGATACAA CATCGGAACA	1560
CAAATATAAA TTTTGTATAC AAGGTGAATA AATGAAAGAA TCGACATTAG AAAAATATTT	1620
AGTGAAAGAG ATAACAAAGC TAAACGGTTT ATGTTTAAAA TGGGTCGCAC CTGGAACAAG	1680
AGGTGTGCCA GATAGAATTA TTATTATGCC AGAAGGAAAA ACATATTTTGTAGAAATGAA	1740
GCAAGAAAAA GGAAAGTTGC ATCCTTTTACA ArAATATGTG CATAGACAAT TTGAAAATAG	1800
AGaTCATAAA GTATATGTGT TATGGAATAA AGAACAAGTA AATACTTTTA TCAGAwTGGT	1860
AGTGAACATT TGGCGATTGA CTTTCAAACC ACATAGCTnT CCAAAG	1906

(2) INFORMATION FOR SEQ ID NO: 680:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 948 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680:

AATTATTTGA ATAAATTAGC AATTAAAGAG TTGATTTGTC AGTTTAAGyA TTTGAGTGCA	60
TTTGAAAAAG ATGTCATGTA TTTAATGTGT GAACAATATA AGCCGAGAGA AATTGCTCAA	120
TTGATGCATG TAAAAGAGAA AGTGATTTAT AATGCCATAC AACGATGTrA AAATAAAATA	180
AAACGTTATT TCAAATGAT TTGAAAAG CTTAGGACG TGAATTGAAT TATAACGTGT	240
TACTTACTGA TGGTTTGACA TTTGTTATAA ATTTTATGTA TAGTATACTG GTATTATAAT	300
GAATAAAGGT GAATTATTGT GAGAAAAATA CCTTTAAATT GTGAAGCTTG TGGCAATAGA	360
AATTATAATG TTCCTAAGCA AGAAGGCTCG GCAACAAGAT TAACCTTAAA GAATATTGT	420
CCAAAATGTA ACGCGCACAC AATTCATAAA GAATCGAAAT AAATACATTC GAAATAATAC	480
TTTGATAATA TGTTCAAAGG ATTTGGAGGT TGAGCAGATG GCTAAAAAAG AAAGTTTCTT	540
TAAAGGCGTT AAGTCTGAAA TGGAAAAAAC AAGTTGGCCG ACGAAAGAAG AGCTATTTAA	600
ATATACTGTA ATTGTAGTTT CTA CTGTTAT ATTCTTCTTA GTCTTTTTTCT ATGCCTTAGA	660
TTTAGGAATT ACAGCATTGA AAAATTTATT ATTTGGTTAG AGGAGTGAAG ACATGTCTGA	720
AGAAGTTGGC GCAAAGCTTG GTATGCAGTG CATA CATATT CTGGATATGA AAATAAAGTT	780
AAAAAGAATT TAGAAAAAG AGTAGAATCT ATGaATATGA CTGAACAAAT CTTTAGAGTA	840
GTCATACCGG AAGGAAGAAG GAAACCTCCA GTAAAnAAGnT GGCCAAGCCT AAAACGCGCT	900
GTTAAAAAAA ACCATTCCCC TGGGnTAnGG TTTTAAGTGG GAATTTAA	948

(2) INFORMATION FOR SEQ ID NO: 681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681:

ACAnATAATA ACAAAGCGCT TGCTAGTACC TCTTAAAAAG ATGATGCTAG CAAGCGETk	60
TCTATACTAT ATATTATTTT TCTAAAATTT TAACACCCTC TTGAGTGCCT ACAATAACTT	120
GATCTGCCAT ATCTAAGAAG TATCCTGTCT CAAACACACC TGTCAGATGA ATTAAATACT	180
CATGGAACCTT aTATGGGTCA ATTCCTTTTG GTA ACTTACA ATCTAAAATA TAATTGCCAT	240
TATCAGTTAT AAATGCGACA TCTTCGTTTA CACGACGTTT TACTTTTATA TCAGCGTATG	300
ATTCAATTTT ACGTAATATG TGATACCACT TAAATTTATC CACCTCTACT GGTA ACTTAA	360
ACGTCTCACC TAAGTATTGA ACTATTTTCG TTTCATCGAC AACCACAACA AAACGCGATG	420

CCATTTTCATC TATAACTTTC TCTCTGAACA GCGCACCAAC GCCACCTTTA ATTATATTTA	480
AAGATGGATC TACTTCATCA GCACCATCAA TTGCTAAGTC GATATGATCA ACATCATTGA	540
TTTCACATAT TTTAATACCT AATTCTTTTG CTAAAAATGC AATTTTATTA GAAGTGCATA	600
CACCTGTAAT ATTGTAACCA CGTTCTTTAA TTAGTTGCGC CATTTGAGGT AAGAGTAATT	660
CCATTGTACT TCCTGTACCA ATTCCCAGCG TCATGTCACC ATTGATTkGA CTTAAACAT	720
CATTTAATGT CATTAAC TTG AGTGCTTTGA CATCTTTCAT GAAGGTAGCC TCCCATATTT	780
AtGTAATCTA TTCAATTCAT ATTTTACATG ACTCGTATAA ATTAACATAC CCTTATnGCT	840
AACCATTTGT GTTAAACATA TCG	863

(2) INFORMATION FOR SEQ ID NO: 682:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682:

TTCATTTTTG TTGTTcAGCA ATTTTGGTCC GAATTTCAAT TCATCAGATG ATAGCTCTAT	60
TAATTCTGTA GAATATTCTG CtACAACAAT TTCATAAATA TGGCCTTTTT CTTCCATTAT	120
TATTTTCATCa ATTATTTTCAT AATTCAATTG TTGTAATGTT TtCTTAAAT TTTCAGTTTG	180
GATATTACTT TGTAAAATCA ACCTTGGATG TTGACTTAAC TTATCTTGCC CATCTTTTAA	240
AATTTTAGCA ATAAGTGGTC CGCCCATACC ACAAATTGTG aTATTATCGA TTACGTCCTC	300
AGGTTGAATA AACTTAAGC CATCCCCTAA ACGTACATCA ATTCTATCTA CTAATTGGTT	360
TGCAGCTACA TTTTTCACAG CAGCTTGAAA AGGGCCTTGA ATAAC TTCTC CAGCAATAcC	420
GaTTTCGCATA AATGGTTTTG AATTGCATAG ATTGGCAAAT AAGCATGATC TGAGCCAATA	480

(2) INFORMATION FOR SEQ ID NO: 683:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 689 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683:

CTGCAAAAAA TATTGGTATA ATAAGAGGGA ACAGTGTGAA CAAGTTAATA ACTTGTGGAT	60
AACTGGAAAG TTGATAACAA TTTGGAGGAC CAAACGACAT GAAAATCACC ATTTTAGCTG	120

TAGGGAAACT AAAAGAGAAA TATTGGAAGC AAGCCATAGC AGAATATGAA AAACGTTTAG	180
GCCCATACAC CAAGATAGAC ATCATAGAAG TTCCAGACGA AAAAGCACCA GAAAATATGA	240
GTGACAAAGA AATTGAGCAA GTAAAAGaA AAGAAGGCCA ACGAA E CTA GCCAAAATCa	300
AACCACAATC CACAGTCATT ACATTAGAAA TACAAGGAAA GATGCTATCT TCCGAAGrTT	360
gGcCCAAGAA TTGAACCAAC GCATGACCCA AGGGCAAAGC GACTTTGTTT TCGTCATTGG	420
CGGATCAAAC GGCCTGCACA AGGACgTCTT ACAACGCaTA AcTACGCACT ATCATTcAGC	480
AAAATGACAT TCCCACATCA AATGATGCGG GTTGTGTAA TTGAACAAGT GTACAGAGCA	540
TTTAAGATTA TGCGAGGAGA GGCGTATCAT AAGTAAACT AAAAAATTCT GTATGAGGAG	600
ATAATAATTT GGaGGGTGTT AAATGGkGGa CaTTAAATCC mCGTTCATTC mATATATAAG	660
ATATATCACG GTAATTGCGC ATATAACT	689

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684:

TTATTAAATT GGTATGTGTT CATTATACAT ATGaCAAATA TGaATGTAAA CCGATAATTT	60
AGATTTTTTTG GAATAACCTG AAAATTCAAG TTaTAGCGTT GCTTATATTT TAAAGGTGG	120
TGATAATGAG ACTTTTTGAA AAATAAAATT CAAAATACTT ATAGCATAATCAATATGCAC	180
ATTAAATAAA TGTA C TCTTT TAATGCGTTG ATA A CTGTAT TTGTAATTTA GAGAAGGGGT	240
GTTCACTATG CTGATGTGTT AAAAAATAAA ATAAAAAGGA CACCTCGATG CTATAAATAT	300
TAGCATCGAG ACGCCAGTT AATGTCTATT AAATTGAATA TAGTCTCGGA CATGAATCAA	360
TGCCCTAGGC CCTGCAATGT TATATTGACA GTAGTTGACT GAATGAAAAT GACTTTGTAG	420
CTAGCTTTTTT TCAATCCTTG TCGGTGCAAC ACATAGAGAA ATTGGATTCC TAATTTCTAC	480
AAACAATACA AGTTGCGGAA TAAGTCCCAA TATAGAAGGT GACAGTAAGC CA A CTTACAA	540
TAATGTGCAA GTTGGTCGGG CCTCAATACA G AGATTTTCG AAAAGAAATT CTACATATTA	600
TGTTTATTTT AAAACGCCGA TTTCTTGTA A ATATTCTTCA TATGGAATTT CTTTGA A AC	660
GCCACCTTGT TTATTTAAAT CGATAACACG GTTTGCGATT GTATTGATAA ATTC A AAGTC	720
ATATGAAGTA AAGATAATAG AACCTTTGAA TGATTTAAGT CCATCATTA A CAGCAG A AT	780
ACTTTCTAAG TCTAAGGGTT GTGGGTCATC AAGTAAAGA CGTTGCCCTG ATAACATCAT	840
TTACTAGCA n CACGACTT	858

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685:

TTAGTATTTT CAGGnTGGAA ATTGATGTTT GAAATTCACt GAAATGGGCC AGAACCTgAA	60
ATGaAACTTT ACCAACAATT TGGtCTTCAT CAATGAGGCC AAACGCACGG CTATCTTTAC	120
TTACTTCACG ATTATCTCCA AGCACTAAAT ATTTACCTTT TGGAAATGACA TTTGATTTAG	180
GATTCGCATT CGGTAAATCT TTAACCTGGA AAGTCCCAGT AATGTAATCA CCTTGTTTAT	240
GTTTTAAATT GTAGTTTAAA TATGGTTCAT CTTtTTTTT ACCATTGACA TATAATGTAT	300
CATTTTTGTA TTCTACTTTA TCACCAGGAA CACCGATGAC ACGTTTAACA TAGTCATCAT	360
TTTTGTTTGC ATGGAAGACA ACTACATTAC CTTTTTCCAA ACCACCTGTT TTATATCCAA	420
CAATGTTTAC AGCTACTCGC TCGCCATCTT TCAAAGTTGG ATCCATTGAT TCACCTTTAA	480
TTGTATATGG CGTAACAATA AATTTACCTA CTATAAATAA AATGACAAAA GCGACTGCAA	540
TTGAAATAAT CCATTCCAAT ATTTCTTTTT TCAATTTTGA CACCTCTTTT TAAGATTTGA	600
ACTGAACAGT CCATTTTGAA AAAGGATAGT ATCGTAAACt AACATTACCA ATAATAtCCT	660
TTTTATCGAT TAAACCAAAT TGTCTTGAAT CGTGCTTGt ATTATCTTGA TCATTTAGCA	720
CAACAAAATT GTTTGGCGGA ATAATATCAC CATCTAATTC TTTAAAATTG CGCAAACtAA	780
AATCTTTAAT TTTTCTGTTT TTGGCATAAG ATGCGTCAAC CGGTCCGTCA TCACGGTATA	840
ATTGTCCCTG ACGAAACGCC ATTGATTGAC CAGGTTTGGC ATAATTCTGA CTAGTATATA	900
TCTCGTTACC ACGCCTATAT GTAATGATAT CACCATTATT CAATTGATTA AATGTAACCT	960
TAATTTTATT TACAATAACA CGATCCCCTT TGTTAAGGGT TGGTGACATA TCATTATTCTG	1020
GAATGACATG ACCAACTATT ACAAAGTTT GTACGAACAG TACAATGATA ATAGCAAGTA	1080
TCAATGAAAT CAAATATTTT ACAACTTTTT TCACGATGTC ACTCCTTTTT CGATCCCATA	1140
AAATGCTGTT CTAACTTTTT TCCAACAATC CAAAATACAA CCAACACAAC TAACATTAAT	1200
ATCCCTCTTA AAGGATGCGT TAAAATTGTA GTAATTTCTT TACCTAAATA ACCTAAAATA	1260
ATTGTTGAAA CTAACTTTGA TGATGCCAAA ACAATGAAAT AATATTTAGG TCTAATATGA	1320
GATAGACTCG CTACAAAATT TATTAATGTA TTTGGCGTAA AAGGAAAAACA AAGTAAAATA	1380
AACAATGGGA TTAATCCTTG GCGATCAATA AACTAATCA AGCGTTGAAC AGCAGTACGT	1440

TGTTTAATTC GCTGCATCCT CTCAGTGTTT ACCAATCGTT TACAGATCA ATAGACTGTA	1500
AATGTTCCAG AAATTAATCC AAGCCAACTA ATCAATATAC CTAAAATAGG TCCATAAGCT	1560
TGAATGTTAA TTAAAATATA GAGTGCTAAA GGAAATACTG GAATTATAGC TCTAATATAT	1620
AACAATATAA ATCCAGGTAA ATAACCAAAC TGTCGAAATA TCTCAAACCA TTCTTCTACT	1680
TGATGAAACG ACAAATCATC AATCCCTTTC TTTGGTTGAA GATAATTATT CTTACATTAT	1740
AAAGTTA	1747

(2) INFORMATION FOR SEQ ID NO: 686:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 645 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686:

CGTAAAGATT ACTATTTAGG AGGGTGACTA TGAAAAAGAA ATTAGGTATG TTA	60
TACTTCTTG TACCAGCCGT AACTTTATCA TTAGCCCAT GTGGGAATGA TGATGGAAAA	120
GATAAGATG GCAAGGTAAC AATTwAAcGa CaGTTaTCCm TTGCAATcAT TTgCAGAGCA	180
AATTGGTGGG AAACACGTGA AGGTATCATC AATCTATCCA GCAGGGACAG ATTTACATAG	240
CTATGAACCA ACACAAAAAG ATATATTAAG TGCAAGCAAG TCAGACTTGT TTATGTATAC	300
AGGGATAAT TTAGATCCGG TTGCTAAGAA AGTTGCATCT ACTATCAAAG ATAAAGATAA	360
AAAAGTGTCT TTAGAGGATA AATTAGATAA AGCAAAGCTT TTAAGTATC AACACGAGCA	420
TGGTGAAGAG CATGAACATG AGGGACATGA TCATGAGAAA GAAGAACATC ATCATCATCA	480
TGGTGGATAT GATCCACACG TATGGTTAGA TCCTAAATTT AACCAAAGTT TCGCTAAAGA	540
AATTAAAGAT GAATTAGTGA AAAAAGATCC AaAACATAAA GATGACTATG AGAaAAACTA	600
CnaAAATTAA ACGACGATCT TAAGAAAATT GATAACGATA TGAAGCAAGT TACAA	645

(2) INFORMATION FOR SEQ ID NO: 687:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 956 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687:

TTTGTTACTG CTTCTAAAT AATATCCTTT AATTGTTTAA CATGTTGGAT TGTCATATGA	60
GGTGATGGTA CATTAAAAGG ATTTAATTCA TCTATTTGTG CATATTGATT TATGACATCT	120

TGATGCATTG AAATAGGGTT GATATCATTT GTTACTACTT TATTAGATTG GTCTTGTGAC	180
ATACTAATGG TGCCACCAGT ATGAATAACA AGTAGATGTT TCATATATTT CCTCCATAT	240
TTAATTTACC TAATTATGAT AAAATATTAT TCATAAAACG ACAAGGAAGG GAAATGACGC	300
ATGAAAGCCA TTAATATTGC ATTAGATGGT CCAGCTGCTG CCGGAAAAAG TACAATTGCG	360
AAACGTGTAG CCAGCGAACT ATCAATGATT TATGTCGATA CAGGAGCAAT GTATCGTGCA	420
TTAACATACA AATATTtAAA ATTAAACAAA ACTGAGGACT TTGCAAAACT AGTTGACCAA	480
ACAACATTAG ATTTAACTTA TAAAGCAGAT AAAGGTCAAT GTGTCATTTT AGATAACGAA	540
GATGTAACAG ACTTTTTTAAG AAATAATGAT GTGACGCAAC ATGTTTCATA CGTTGCATCT	600
AAAGAGCCAG TACGTTTATT CGCCGTTAAA AAACAAAAG AGTTAGCTGC AGAAAAAGGT	660
ATCGTAATGG ATGGTCGCGA TATCGGAACT GTAGTGCTAC CAGATGCAGA TTTAAAAGTA	720
TATATGATTG CATCAGTTGA AGAGCGAGCA GAAAGAAGAT ATAAAGATAA TCAATTAAGA	780
GGTATCGAAT CAAATTTTGA AGATTTAAAA CGTGATATTG AAGCTCGTGA TCAATATGAC	840
ATGAACCGTG AAATATCACC ATTAAGAAAA GCAGATGATG CAGTGACATT AGATACGACm	900
GGCmAGTCGA TTGAAGAAGT TACTGACGAn ATTTTAGCGA TGGTGAGTnC AATTnA	956

(2) INFORMATION FOR SEQ ID NO: 688:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688:

AAAAGGGAGG AAAGAGAACA GTTAAATATG AATACAAAAT AATTTTGTTT TCGGACAGCA	60
GGGGTATTAG ACGCGATTGA CAATGTCTGT TTAATTAAAC GTAATGTTTA TTTAAGCGAT	120
GAATATTAGG TGAAAAGTTT TTGAATTTGA ATGTAATTGA GGTTTATTGA TTAGACATTT	180
TATTGAATTG CGTGTTATTA TATAAATGTA AAAATAAGAC GACATGCGCG AACATGTCGT	240
CTAAGCAAGC CAAACGCTGG CTTCTAAAAT ATTTTTTTAAACCATTCCAAC TTGCCAAAGT	300
TAATGCGGAA TGGTTTTTTTT ATTTTCCGCT AATTGAAATA AAAATGACGT TTTAATATAT	360
TATGGGCTAG GTGGTTTGTA AGAAAGGGTT AGTTATTAAT GTTTTATGAA TTAAGGAAAT	420
TTGAGTTTAA GGTTTAATCA ATTGTGATTT TGTTGATGAA GCGTTTAGTT AGAGTATTTT	480
CGCCACCACT AGTTACTCCT TCTCCCACTT TACCCGAGAC TGGAGAAGAg CTATCTGAAG	540
AATAAATAGA TACTTTTTGG CCATTTTGTA GTAAACCAAG ACCTTTTAAC TkCTCGGTTA	600

GAGAAATTCCA TGTATTTTGA GCATCTAGCT TTTTGTAA GTCAYCGTAG ACATTTTCCT	660
TAGTTAAATC AATTTGTTTT ATCCTTTAA AGTCTATAGA TTGTGTTAGA TGGCCTCCAT	720
CATCATTTCC AGGAGCAGAA ACGCTGCTAG AATATCCATT GCTTAATAAA TAAGTAACGT	780
TGATTGTTTC GTACTCGTTA CTTAAAATAA TATCAGAATC ATGTAAgAAT CTTTAACTTT	840
TTTCCATAAT TGACCATCTG TCATTTTTTC TTCTGCTTTA GCCGTTTAA CAACTTTATT	900
TGTATCTAAT CCTAAGTATG AAGAATGTAA GCCTGTTCCCT AATGTTGTTA ATACTAAAGC	960
ACTTGCTACT aATGTTTTAC CTAAAAAttt TGTATTCATT TTTATTGCTC CTTtTTTTAT	1020
ATTGTAAACG TTTACAATGA AAATATAATA ATAATTTTTT AAAAGAACAA TTAATAAAT	1080
ATCAAAAATG TATTAATACT CTATTAATA AAAAATAGAA TAATTTTTTA ACATAGTTTT	1140
GTTGTTTTGA ATTATAAAAA CTAAAG	1166

(2) INFORMATION FOR SEQ ID NO: 689:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689:

AGCACTGAAG GATGGCTAGT TGTCATAGCA TATGCGGTCA TTGGTATAGT TATAACGAGC	60
GTTTCTTATA TGTTGTCTAT TAAATTTTTT AACAAACAAG AACTAKAATT GTCGATTTTG	120
GTGATGATAG TATTTGAAAT AATATTTAGA GCAGGTGATA AATCTTTACG ATTGTCATCT	180
GTTCTTTTtK GTGTGGAATG AAATGTGGGG GATAAGTATA GGTGACATAT CTATATTGAT	240
TTATTTGTTT TGAGGTGGTT ATGTTGTGTG GGAATTATTT CCTTTTAGATAGCGGGGATT	300
AGAGGATATA TGTTATTTAT AAGTATCATT TGATGATTGT ATAGGCTAAC GATTTCTCTG	360
GAAATATTTA AAAACCTCGA TCATGTAGCA TAACTGAAGT TTGTCACAAA AGTATAATGT	420
GAAGTTCGAC ACTTTTGgAT TCAGTTCAAA TACTTTGACC GAGGTAAATA CTATTTATTC	480
ATGTTTATTA CGTAGACGTT GATTTTTTAAA ATAAATCAGC ATGATGCAGA AGGTTGCAAC	540
TGATACTGAG ATAATCATT CATGGTCGTG ACCTTTAAAT AAAAGGCTGA CAATATAAGA	600
CATAACGAGT ATACCTAGTG AATATGAAAT ATACTTCGCG TTTGTCAGTT CATTATGGAA	660
ATAAGGCGTG ATTAACCATA ATCCAATATA GATATTAAA AACTGATAT ACATCATATT	720
AATTTCAAAC AAGTCATTTA GTTTATTGTT ATTACTAAA ACAATTGCAG CATTAATCAC	780
ACCTAAAGCG ATATTGATTA ATAGATGCGT ATACGATAAA CGGAAACCGA TAGATGTTAA	840
TTTATGATTA ATATAATTTT CAGTAATGAT CCAATATACA CCGAAAAGAC TAATTAAAT	900

CATAAATTGG AATATATAAA TGTAATAAA ATGATCAATG CTAAATGATG ACGAAGCTAA	960
ACCAACCAGT ACCTCGCCAr AGwTAtAATT GTTAGTAACG AAAAACGTCT ACTAAATGCA	1020
TCATATTAAC AGGTnTAATA CAAGTATTTT TGAAATGGAA TAAGnCTGTC GCTGCATGAT	1080
ACG	1083

(2) INFORMATION FOR SEQ ID NO: 690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690:

TTAATCATCT GGATGTATTT AGTATTnAGA ATAATAAnAA AACGATCATG TTGTATtTGA	60
GTAGCGATTG GTTTGCGGAA TTAGGCTTTA CTTTCTTTAA TTACCACTAT ACAGCAAAGT	120
TGATTAAATC ATCCTATAAT TTGAAATGTC TACTATAAA ATTGACATAT CGATACCTTG	180
ATAATCAGCC TCTTAATGAC GCTGATayTA GAAAATTACA GGATATTATT AAAATCATTG	240
CAAAAGAAGC AAGTATGGAT AAAAAGATTG CACAAAATCA ATATCGATAT GCGTATTATG	300
GTGATTTGCG TGATGAGCTC GAATATATTT ATCAAAATGT AAATCAACGA TTGACATTAA	360
AAAGTGTCGC TGATAAATTA TTTGTCTCAA AGTCAAATTT GTCATCACAA TTCCAATTAC	420
TTATGGGCAT GGGTTTTTAA AAATATATTG ATACTTTGAA AATnGGTAAA TCGATTGAAA	480
TTCTACTTAC TACTGATAGT ACTATTAGCA ACATAAGTGA nCATTTAGGT TTTAGTAGTA	540
GCTCCACTTA CTCTAAAATG TTTAAAAGTT ATATGGATAT CACACCGAAT GAATATCGTA	600
ATTTATCAAA ATATAATAAn TGTTTAC	627

(2) INFORMATION FOR SEQ ID NO: 691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691:

TTGAACGTAA TGCTAGCAAA TGACTTTGTG CCATAAAATA TTCTTCCCAT TTGATTCTTT	60
CCAAGATGTT CACCTTCCAT ACTTAAATTT TAGTAACATTTTCTAATAAT ATAAGATTAA	120
TCACAAAAAA TAAATTTTGC AATTAAAATA ATCCATTATG TCGTGAAATA AGATTTTCAGT	180

TTATCAAAAG TTTTACTTCC AAAACCTTTT ACTTTTTTCA AATCGTCAAT TTCTTGAAAT	240
GCACCTTGTT GGTTGCGATA TTCAACAATT GCATTAGCTT TAGCTTGCCC AACTCCAGGA	300
ACAGACATCA ATTCTGATAC AGATGCCGTA TTAAATTTA CTTTAGTATT ATTTGTGTTC	360
CCaTTTTTTTT CGTGCACACT GTTTACTTCA ATTTGTGGTT CAACATTCTT TTGTCCTTTA	420
TGAGGTATGA AAATCATTTT TTGATCTGTT AATTTTTCAG ACAAATTAAT TTGACTTACA	480
TCTGCATCCT CCAATAATTG TGCTTTATCA AGTAAATCAA CTACTCTATC CTTAGATGTC	540
ATTTTATAAA CATTAGGATG TTAAACAGCA CCTTTTACAT CGACATATAC AGGACCCTTA	600
TTTTTGGAAT TATCTCCATC TTTGACCTGG ACATCTTCTA C	641

(2) INFORMATION FOR SEQ ID NO: 692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692:

TATTAAAGnA CTTGATGAAC CAAATCATAA AAAGCnATAT ATGTATTTG CAGCTGGCAT	60
TGTGTTnGCA ACTATTTTAC TTATTTCTGGC ACATTTATAC AGCAGAAAGA GAGGTAACCA	120
AGTTTGAGAA TCATAAAGTA TTTAACCATT TTAGTGATAA GCGTCGTTAT CTTAACCAGC	180
TGTCAATCTT CCAGTTCTCA AGAATCAACT AAATCCGGCG AATTCAGAAT CGTACCAACA	240
ACTGTTGCAT TGACAATGAC ATTGGACAAA TTGGATTTAC CAATTGTCGG CAAACCCACG	300
TCATATAAGA CATTGCCTAA TCGTTATAAA GATGTACCGG AAATTGGTCA ACCAATGGAG	360
CCGAATGTTG AAGCTGTTAA AAAGTTAAAA CCAACACATG TTTTGAGTGT GTCAACGATT	420
AAAGATGAAA TGCAACCATT TTACAAACAA TTAAATATGA AAGGCTACTT TTATGATTTT	480
GATAGTTTAA AAGGGATGCA AAAGTCGATT ACACAATTAG GTGaTCAATT TAATCGTAAA	540
GCACmAGCAA AAGAATTAAA TGACCATTTA AATTCTGTAA AGCAAAAAAT TGAAAATAAA	600
GCAGCTAAAC AAAAGAAACA TCCCAAAGTA T	631

(2) INFORMATION FOR SEQ ID NO: 693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693:

AATTTAACTA TGTTTTCCAC ATTGTTTCAT GTCACGAAAA GGACAACGCG CGACTATAAG	60
TATCAACTAT TTCCACAAGT TTTATTGGTG TTTTATTAT TCATCGATAC GCTTCATTTT	120
CATCTCTCCA ACACAAAAAA GAAGCTAAGC AACTTATGTT GCCTAACTCC TCTATACTAT	180
CCATATTTTA CTATTATCCA TATTTTCATTG AATTATCTAA TGTTGGcTTC TATTTTTTCA	240
ATATTTCTAC CGTCAATGAC GTCACCTCATG CGATTTGTTT GTAATTTTTT ATTAAGTTCA	300
AACGTATAAT AGCCGCCATC TTTCATTATC ACTTTTATCT TACTATCTTT AGGAAACTTT	360
TTATACAGAT CAAAATTTTG AATTAAATC TGTCTCAATT TAAAGTCGAG TTCTTTAAGT	420
GAAATCTCTT CTTTATAAAT GTAGTGTACT CTACCGTACG TAGCAATACC GTCACCTTCA	480
TCTCTCTTGA TTTGAAATCT TGGTGCGTTT ATATAATCAT AATAAGCGTC TTGATTTTTT	540
TTAGTGACAC CACCATATGA AAACACTGTG CCATTACGGT TTTCCGCTTC TTACAACA	600
AATATGTCTA ATCCCGGATT TTTACGTGCT TTAAATCTTT CAATATCTTT ACCAAATATC	660
TGTACTCTTG TGAATTTTCT ATTTTATCA AAGATAAGGT AATGCTTGCC ACCTTTGCTA	720
TAACGATAAC CAGTAACATT TTTAAGTTCC TTAAGTGC CACTATAGTA ATCTCTTAAG	780
TCAAAGATAT CTTTGTGCAC ATTTTCATAT TTTGCTTTAT GTTCACTCGC ATTTACAGTT	840
TGATGCAATG ACGTTATTGT TCCTGTTGCT AAAATACCTA ATGCTAAACT TGCTTTGCGA	900
ATTGCTGTCA TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGCTTACG	960
TCTATTGAAT CATAACAGCTT TATTATAGTT AGCGATTTG ACCTTTCACA TTAAACCATG	1020
TTTAATAATC ATTGAATCAT TATTAAGTAA ATTAAGGATc TATAATGTTC GTTAAATAAA	1080
CTGAnCCCGT TGTGCTTCAC ACCCGnTnGA T	1111

(2) INFORMATION FOR SEQ ID NO: 694:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694:

TTATGGATGG ATTAAGAGGT CGTGTTGAAA AAATCAACGA TAACTCTGTT ATTGTTACT	60
TAACAATTAT GGAAAATTTT AATGACCTTG ATTTACCGGA AAAAAGTGT ATCAATCATA	120
AACGATATAA GATTGTTGAA TAAGAAGGTA AGTTATAATG AATAAAATCT CGAAGGCTTT	180
AACTTGGTTT ATTATAAGTT TCATTATATT TCATCTCATA TTATTTATTA TGTGGGGCGA	240
ACACCAAGAA TACTGGTATT TATATACAGG TATAATGCTA ATTGCTGGTA TCAGTTATGT	300

ATTTTATCAA AGAGATATTG AATCTAAGCG GTTGCTTACA TCAATTGGTG TTGGTATTAT	360
TACGGCAATT ATTTTAATTA TGcTtCAACT TTTATkCTCA CTTATAACTT CTAATTTAAG	420
TTATAG	426

(2) INFORMATION FOR SEQ ID NO: 695:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 737 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695:

AAAAGGGGnG TAAGGTTTAG CTCAAGTACG AGAAGTCTTT GGTGATGAAG CAATTGATGA	60
AAATGGTGAG ATGAATCGTC GTTATATGGG TGATCTAGTG TTTAATCATC CAGAAAAACG	120
CTTAGAATTA AATGCTATCA TACATCCTAT CGTGCGAGAT ATTATGGAAG AAGAAAAGCA	180
AGAATATTTA AAACAAGGAT ATAATGTAAT CATGGATATT CCATTATTAT TTGAAAATGA	240
ATTGGAAGAAAT GCAGTAGACG AaGTGTGGGT TGTATACACT TCTGAAAGTA TACAAATGGA	300
TCGTTTAATG CAACGTAATA ATTTGTCATT AGAAGATGCG AAAGCACGTG TCTATAGCCA	360
AATTTCTATT GATAAAMAAA GCCGAATGGC CGATCATGTT ATCGATAATT TAGGGGATAA	420
ACTTGAATTA AAACAAAACC TTGAGAGATT GTTAGAAGAA GAAGGTTATA TTGAAAaGCC	480
GAATTACGGA GAAGAAGATT AATATTACAC TATAAATAAG TCATTACTTT ACGTACGCGT	540
TGATGTATGT AAGTAATGAC TATTTTTTTAT AAAAAAGATA AAAAAATCAA CGGAAAACGC	600
TTTCAAATTT CATATAATAT GCTATACTAA TTCCATAAAG TATAACACAT AAAGATCAAG	660
GGGTGCTTTT AATGTCAACG AATATTGCAA TTAATGGTAT GGGTAGAATT GGAAGAATGG	720
TATTACGTAT TGCATTA	737

(2) INFORMATION FOR SEQ ID NO: 696:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696:

AACGATAAGA ACAAAAAGATA TATTACAAAG CGTTTATTTA AAACGTTATT TATTACGCGC	60
GATGATGGCA GGATTTATTA TCGGGATTAT TACGGTCTTC GTATTATCAG TTAAAGCAAC	120
ACACGAACCA GATTTACCGC CAGgCATTGT GAATATGGCC AGTGCCATTA CATTACGCTT	180

TGCGTTAGTA CTCATTTTAT TTACAAACTC CGAACTACTA ACCAGTAACT TCATGTACTT	240
TACTGTAGGC CTGTATTmTA AAGTAATTAA ACCAACTAGA GTATTGaAAA TATTTTTATT	300
ATGCTTTGCA GGAAATATTT TAGGTGCTGC TATTTyATTT AGTTTCATGC GTTTTTCAAA	360
TGTAATGACG CCAGATAwGt TAAAyCAGTT ATCAGCAGTT ATAGAGATA AAACGTTGTC	420
TACTGGTTTT GT	432

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697:

CTTTTATACG AAAGTTAAAnA TCAAATATAA CATTAAATGTT TGATGGGGAT TTTGCGGGTA	60
GTGAmGCAAC ACTTAAAACA GGTCAAAATT TGTTACAGCA AGGGCTAAAT GTATTTGTTA	120
TACAATTGCC ATCAGGCATG GATCCGGATG AATACATTGG TAAGTATGGC AACGATGCAT	180
TTACTGCTTT TGTAaaaaAT GACAAAAAGT CATTTGCACA TTATAAAGTG AGTATATTAA	240
AAGATGAAAT TGCACATAAT GACCTTTCAT ATGAACGTTA TTTGAAAGAA CTAAGTCATG	300
ATATTTTCGCT TATGAAATCA TCGATTTTGC AACAAAAGGC TTTAAATGAT GTTGCACCAT	360
TTTTCAATGT TAGTCCTGAG CAATTAGCTA ACGAAATACA ATTCAATCAA GCACCAGCCA	420
ATTATTATCC AGAAGATGAG TATGGCGGTT ACATTGAACC TGAGCCAATT GGTATGGCAC	480
AATTTGACAA TTTGAGCCGT CAAGAAAAAG CGGACnAGCA TTTTTAAAACATTTAATGAG	540
AGATAAAGAT ACATTTTTTAA ATTATTATGA AAGTGTTGAT AAGGATAACT TCACAAATCA	600
GCATTTTAAA TATGTATTCTG AAGTCTTACA TGATTTTTAT GCGGAAAATG ATCAATATAA	660
TATCAGTGAT GCTGTGCAGT ATGTTAATTC AAATGAGTTG AGAGAAACAC TAATTAGCTT	720
AGAACAATAT AATTTGAATG ACGAACCATA TGAAAATGAA ATTGATGATT ATGTCAATGT	780
TA	782

(2) INFORMATION FOR SEQ ID NO: 698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698:

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AAATCATTGG CAAAATATAC GAATTGCATT TAAATCGTCA ATTTACATAT ATTTTTCGCT      60
AGTAATCAAT CGTTATCATT GTTATTTATC GTTACATTAT TTCGAGTATC AGTATGTATT      120
TCGGGCTTCG TTTGATAACG ACATTTCTTT GTGACATCGC TTCATCAGTG TAACAACAAA      180
TACAATGATT TCGTGATGTT AGTTACCCAT TTTATGTGTT GCATAAAATA TGTTGTTATA      240
AAACATTTTA AATCATTTTA TATAACAAT CTATATATTT TTGGCATTTC CAAATATCA      300
CTTGTTATAT TAAAAACCGA CAAGACATTT TATCTTATCG GTTGAAATTT GTTATTGTTA      360
TTTGTAATGT TTTTAGGTTT CTTTTTAATA TAATATATTT CAGTGAAAAT ACATGATTGA      420
TTGTGATTTT ACTGAAACAT GGTTAATTGC GTTGTTGATG AATAACTTTA GCATAAATAT      480
AGGAAGTTAT TTTGTACATC GCCATATATA GAAACGAAAT TATAATGACA GCTAGTACGT      540
AACTTGTTAA AAATATATGA TGGTTATTAA TACCTATCAT ATTTAGTAAC GTATATACAA      600
TGTTACTAGA AATTAATGTG TGAATCAGTG CTACTGTTAT TGGTATtGCG AACAAGAAAG      660
TCATTTGATT TCGTGTTATC TTTGCTATTC TTCCATATC TAAACCAAGT TTTT      714
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(2) INFORMATION FOR SEQ ID NO: 699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699:

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ACTGAGAGCA ATAATTTAGT AACTTCTACT CAAGGAATTA TTAAAGAAGC ATTGCATAAA      60
TTGGGATTTG nnTTTAATTA AAGAACCTTT AAGAATGTTA CAAGTGCGTA TCCCTGTACG      120
AATGGATGAT GGCACAGTAA AAACATTCAC AGGTTACCGT GCGCAACATA ATGATGCGT      180
TGGACCAACA AAAGGGGGCG TCGGTTTCCA CCCAGATGTT GATGAAGAAG AAGTAAAAGC      240
ATTATCAATG TGGATGACTT TGAAATGTGG CATTGTGAAA CTTACCATAC GGTGGTGGTT      300
AAGGGTGGTG ATCGTTTGTG GATCCACGTC AAAnGAGCAT TCCATGAAGT TGGAACGTTT      360
A
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(2) INFORMATION FOR SEQ ID NO: 700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700:

GTCCTTAATT GGTATCCACC TTTAGCACCG CGTACACTTC GAATTAACCC CGCATTCTTT	60
AAAGGACCTA CAAGCTGTTT TAAATATAAA TCACTCAAAT TATTTCTTTC AGCAATTGAC	120
TTTAATGATA TACATCCTTG CCCCTCTTTT TTAGAAGAG AAATCATCAA TGTAAGTCCA	180
TATCTCCCTT TAGTAGAAAT TTTCATTGTA TAACCTCACT TAATTCGAAT ATTGATATTC	240
CCATTTTAGC ATTTTTTGAG TTAAGATAGT ATAAGAAAGG TGTGACAAAT GTGAGTACAG	300
AACCATTAGC ATCGAGAATG CGCCCAAAAA ATATAGATGA AATCATTTCC CAACAACATT	360
TAGTTGGACC AAGAGGCATT ATCAGAAGAA TGGTTGATAC AAAAAAATTA ACTTCAATGA	420
TTTTTTATGG TCCACCTGGT ATAGGCAAAA CAAGTATTGC CAAAGCAATT TCGGGCAGTA	480
CGCAATATAA ATTCAGACAA TTGAATGCTG TAACTAACAC TAAAAAAGAT ATGCAACTTG	540
TTGTTGAAGA AGCTAAATG TCTGGTCAAG TTATCTTGTT ATTAGATGAA ATACATCGAC	600
TAGATAAAGC TAAACAAGAC TTTTATTAC CTCATTTAGA AAATGGCAAA ATCGTCTTGA	660
TCGGTGCTAC AACTTCAAAT CCTTATCATG CTATCAATCC AGCGATTCGT TCAAGAGCGC	720
AAATTTyCGA GTTATATCCT TTAAATGACG AaGATGTGCG CøAGCGTTA ACTCGTGCAA	780
TAGAAGATGA TGAGAATGGT TTGAAAmCAT ATCaACCCAA AATTGATGAA GATGCCATGA	840
CCTACTTTTC TACACAAAGC CAAGGTGATG TTCGTAGTGC GTTAAATGCA TTGGAATTAG	900
CTGTATTAAG CGCAGATAAT GACAAAGACG GTTATCGACA TGT	943

(2) INFORMATION FOR SEQ ID NO: 701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701:

CATTAAGTGA AGTTGTTGAT ACACCCATGC ATCAAGTCAA TTGTTCTGTT GATTTAGATA	60
CAGAAAGCTT ATTAGGCTTT AAAACAATTA AAACAAATGC GGAAGGTCAA CAAGAAATTG	120
TCTTTGTAGA TGGTCCAGTT ATTAAAGCTA TGAAAGAGGG GCATATTTTA TATATTGATG	180
AAATAAATAT GGCTAAACCT GAAACATTGC CTGTATTAAA TGGGGTCTTA GATTATCGTC	240
GTCAAATTAC GAATCCATAC ACTGGTGAAG TAATCAAAGC TGTACCAGGA TTTAACGTTA	300
TAGCAGCGAT AAATGAAGGT TATGTTGGtA CTTTGCCAAT GAATGAAGCA CTAAAAAAaT	360
CGCyTTGTTG TTaTTCACGT kGATTATaTT GATGGGGaCA TTTAAAAAT GTGAnTAAGG	420

AGCAAGGTTT ATTACAAGAT GTTAA

445

(2) INFORMATION FOR SEQ ID NO: 702:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702:

TGCAAGATAA ACAAATTTGT CATTGTTTTG GTTGTAAGAA AGGTGGCAAT GTTTTTCAAT	60
TTACTCAAGA AATTAAAGAC ATATCATTTG TTGAAGCGGT TAAAGAATTA GGTGATAGAs	120
TTAATGTTGC TGTAGATATT GAGGCAACAC AATCTAACTC AAATGTTCAA ATTGCTTCKG	180
AyGATTTACA AATGATTGAA ATGCATGAGT TAATACAAGA ATTTTATTAT TACGCTTTAA	240
CAAAGACAGT CGAAGGCGAA CAAGCATTA CGTACTTACA AGAACGTGGT TTTACAGATG	300
CGCTTATTAA AGAGCGAGGC ATTGCTTTG CACCCGATAG CTCACATTTT TGTCATGATT	360
TTCTTCAAAA AAAGGGTTAC GATATTGAAT TAGCATATGA AGCCGGATTA TTATCACGTA	420
ACGAAGAAAA TTTCAGTTAT TACGATAGAT TTCGAAATCG TATTATGTTT CCTTTGAAAA	480
ATGCGCAAGG AAGAATTGTT GGATATTCAG GTCGAACATA TACCGGTCAAGAACC AAAAT	540
ACTTAAATAG TCCTGAAACA CCTATCTTTC AAAAAAGAAA GTTGTTATAC AACTTAGATA	600
AAGCGCGTAA ATCAATTAGA AAATTAGATG AAATCGTaTT ACTAGAAGGT TTTATGGATG	660
TTATAAAATC TGATACTGCT GGCTTGAAAA ACGTTGTTGC AACAAATGGGT ACACAGTTGT	720
CAGATGAACA TATTACTTTT ATACGAAAGT TA	752

(2) INFORMATION FOR SEQ ID NO: 703:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703:

nCGTTTTTGT nAAACnGCTT ATATGTATAA CTTTTCCCAA TTTATCATAA GTTTTGATAG	60
AAGGAGTTGG ATCGCTAAAG AAAATATCTC TAAAGATATC ATCTTCAATG ATAGGAATAT	120
TATGTCTTTC GCtATAAGTA ATTATATTT TCTTTTGCTC ATTCGTTAAA GAACGACCTG	180
TCGGGTATT AAACCTAGGT TCTATATAAA TCGCTTTATT TTTAAAATTA ATAAATCTAT	240
CAATGATGGT ATCAATTTCA TTAATTTGAT TATAAGGAAC ATCAATATGT CTAAAATTCA	300

ATTGCTCAAA AACATTTGTA GAGTGAATAT ATGATGGTGT ATTCGAAATT ATATGGCAT	360
CTTGACCTAA AAACCCAATA GATAAAAGTT GAATGGCATG TAAAGCGCCT GAAGTGATCA	420
TTACATTTTC TCTACCTACA TTTATACCTT GCTTTGACAT TCGTTCAACG ATAATATCTC	480
TTAACTTGAT ATAACCATAG CCATTATTAT AACCAAAAGA TAAGTCTTCA ATATGACTGG	540
CTGTATTAGA CATGGCTTTT TTCAATTGAA TATGTGGCAT TAACGATATA CCCAATTCAC	600
CTTTACTTAT ATGTATATAC GAATCATCTG TCTCAATTTT ATTAATTAAT TGCACCGTAT	660
ACTGACTTCT TTGTTGAGAG GACCATAACA TCATTTGAGA CCACTTATTT GTAATATGTG	720
CTTCATTCAA ATAGTCATTA ACATATGkTC CACTÆCTAC TTAGTATAG ATAAATCCTT	780
CAGCTTCTAA TAACTCAATA CTTTAAATAA TCGTTACTCT ATTTACGTTG	830

(2) INFORMATION FOR SEQ ID NO: 704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704:

AGTGGTGTTG GAAAAGCTAT TATGAAATTA TTACGTGAAC AACAAAGTTTA ATAAAAAAG	60
AGGGGTCAAA TATGAAAGGA TTAATTATTA TTGGCAGTGC ACAAGTGAAT TCACATAAA	120
GTGCACTAGC AAGATACTTA ACTGAGCATT TTAAACACA TGATATTGAA GCGGAAATAT	180
TCGATTTAGC AGAAAAACCG TTAAATCAAT TAGATTTTTT AGGAACAACA CCGTCTATTG	240
ATGAAATCAA ACAAATATG AAAGATTTAA AAGAGAAAGC AATGGCGGCG GACTTTTTTAA	300
TATTAGGAAC GCCAACTAT CATGGTTCAT ATTCTGGAAT ATTGAAAAAT GCATTAGATC	360
ATCTAAATAT GGATTATTTT AAAATGAAAC CTGTAGGCTT AATAGGAAAT AGTGGTGGTA	420
TTGTTAGTTC AGAGCCATTG TCACATTTAA GAGTAATCGT CAGAAGTTTA CTAGGCATTG	480
CTGTACCAAC TCAAATAGCA ACACATGATT CTGATTTTG TAAAAATGAA GATGGTTCAT	540
ATTACTTAAA TGATAGTGAA TTCCAATTAC GAGCAAGATT ATTTGTCGAT CAAATTGTAT	600
CTTTTGTGAA TAATAGTCCA TATGAACATT TAAAATAATA TTAAnAAATA TGTAATnT	659

(2) INFORMATION FOR SEQ ID NO: 705:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705:

nCACCATATA GTAACGGCA CCAACTACAT TACCGTCTTT TAAAAAGATT TTTTATAGT	60
TATTATCAAC ACTATTAAAT ATTTCAATAC CTTTAATTTT TGCATTTTCT ACAATTTGAC	120
CAGCACTATA CAAGTCACAC CCAGAACTT TTAATGACGT AAATGTTGTT GATCCCTTGT	180
ATCCGTTTCGT TTCTTTATTT GTTAAATGAT CAGCTAATAC TTTACCTTGT TCATATAGTG	240
GTGCAACGAG TCCATAAACT TTGCCGTTAT GTCTGCACAT TCACCAACTG CATATACATT	300
GCTATCACTT GTTTGCATCA CATCATTGAC AACAATACCA CGATTACATC TAGACCTGAT	360
CTTGGAACCTC CTGGGAAGGC GGAACCACTG CATACTACTA	400

(2) INFORMATION FOR SEQ ID NO: 706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706:

TTAAAAATAC AGCTACAGGT AATTTTAATG ATTTTTCAT AATATCAAAT TTGGGATTAT	60
GGTGTGGCGC TGTAATACCT TTAACCAGTC AGAAAGAATG CACCTGGTCG TACTTTCAA	120
TAATGTGAAA AATCTTCTCC AATCATCATT AAATCTGATT CATTAAAGCG TACATGTAAG	180
TCATTTGTTG CTTCTTTAAT AACTTGGATA TGCTTTCTCG TTTATTATGG ACAGGCAAAT	240
ACCCTTTAAT ATAATTCAA TCATAGTTAA TATCATTTGC TATTGCTAAA CCTGTAGAA	300
GCTTAATCCA TTTTGTCCAT ACATGATTCT GTATATCTGA AATCGAAAGT TCTnACTGTA	360
CCTTTACAAA ATGCCTTGnn	380

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707:

CAnAAAGGAT CAAAGTGATC GGTATAGTGA TAATTAGCTC CAAAGAAAGA ATATTCTAAA	60
TCAAATCCAT ACCAAGCAGA AAGTATTAGC GAATATCAAT TTAAATGGTA CCGATTCAA	120
TAAAGAAACA CGACATATAG AATTTTTACT TGATGATTTT AGTGAATCAT ATGAACCAGG	180

AGATTGTATA GTAGCATTAC CGCAAAACGA CCCTGAATTG GTGAAAAAC TAATATCCAT	240
GTTAGGTTGG GATCCGCAAT CTCCGGTGCC AATTAATGAT CATGGTGATA CAGTTCCTAT	300
TGTTGAAGCA CTAACATCAC ATTTTGAATT TACTAAATTA ACATTGCCAT TATTGAAAAA	360
TGCAGATATC TATTTTGACA ATGAAGAATT ATCTGAnCGT	400

(2) INFORMATION FOR SEQ ID NO: 708:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708:

TAATGCTGGT ACGGGTCATG CAGCATTATG TGAGTTGAAC TACACAGTTT TACAACCTGA	60
TGGTTCTATC GACATCGAAA AAGCGAAAGT GATTAACGAA GAGTTTGAGA TTTCAAAACA	120
ATTCTGGGGT CACTTAGTGA AAAGCGGTAG CATCGAGAAC CCAAGAGAAT TTATCAATCC	180
ATTACCACAC ATCAGTTATG TTAGAGGTAA AAACAATGTT AAATTCTTAA AAGATCGTTA	240
CGAAGCGATG AAAGCTTTCC CTATGTTCTGA TAATATCGAA TATACTGAAG ACATCGAAGT	300
AATGAAAAAA TGGATTCCAT TGATGATGAA AGGCCGTGAA GATAACCCTG GTATCATGGC	360
GGCAAGTAAA ATTGACGArG GTmCAGATGt AAmCTyCGGT GAATTACAC GTAAATGGC	420
TAAAAGCATT GAAGCACATC CAAATGC	447

(2) INFORMATION FOR SEQ ID NO: 709:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709:

GTGTCTACCT GTTTTGTG TTCAATTGTT AACTTTTCTT TTTGAATAGT AGTATTCGAT	60
AATTCTTTAT CGCTTATAAA ATCATCTAGT GGATGGCTTT CTTTGAAACT TTTATTTTCA	102
GTCATCAATC ATCTCTCCAA TAGTTGCTAT TTTACATCAA TCTTGATGAT GTTTTTGATG	180
TAACTTATTT AATTCCATTT CAATATCTAA ACGTTCATAA TCATCTTCGT TGAGACGCTT	240
TAAATCAGCG ATTAATGTTT GTTTGACCTC ATCCAAAGTA ATTCGTGTTT GTTCTAACTT	300
TTGCTGTTCA TTAATTGATT TTTGGGCAT TTTTGCTAGA CGTGTATATG CATCAACCAA	360

ATTTAAAGCA TTATCAATAT GAGAATAAAA AAAGCCTTCA ACTTTATAAA ATGATGCAGG	420
TCTCTGTCTA ACTGTCGTAT AAATAGAACG TGAAATTTGG TATATATCAT TAATCTGCCT	480
AAAATCTTTA ATTGATCTTA TATTGACATA CGTTTTTAAA ATACCTCTA GTTTTTGGTG	540
TGTATGATTT AACTGATTTT GAATATAGCG ATAGTCTTTT CTAGTCAAAC CAATTTTCGTT	600
TAAATATTTG CGTGAAGTGA GTTTTTGTAT CGGTAGGTAT GTCATTAAAA AGCCAACAAT	660
ACCAATAGAC ATATCAATTA AAAAAGATAC ATCAAGTGCA ATCATCCCAA ATATGCTTGT	720
TAAAAACGCT ACAGGAATTC CCACTAACAC CCCAAATATA TGAGAAATAT TATATCTCAC	780
TGTCATCTTC CTTTATTTAG CATTTTATAT TGATCGAAAA TCCGATAATT TTTGATTTAG	840
TTCTAACTCT TCAAGTTGAT GGCTTGTTAC ATTTGATGCT GGTGAGGCAC CTTCAATTAC	900
ACCTTGAATA AATCTCTCTA TATCTGCGTC ATCCCCTTGT GCATATATCT CTACATAGTC	960
ATCTACATTT TGAACAGTAC CGACAATGTT ATAGTTCATT GCAATGCGTT GTGTAAAATA	1020
TCTAAATCCG ACGCCTTGAA CGCGTCCGAA TACTTGTAAT TGTATATGtC TCaTTTTTAC	1080
CACCTCATAA TGTTATTATA CGTAGTTTTA CTTAAAAAAA CTAATAATTA CTATACTAC	1140
TACTTTGTTT GTTTCAAGTC GTCAAACCTG ATTTTCAGAG GATAAAGGTA TAAAAATAAG	1200
TATAGAGTTT TTGAAGTATG GAAGGGGTCT TTAATAATGT GGACAGTTAC CAAAATTAGA	1260
GCCGATTATG AGGGATGGTG GTTATTCAGT GACTGGCCAG AAAACATTGT TGAAAAATAT	1320
CAATATCAAG ATTTTGATGA CATGTTTAAG CACTATCAAC AATTGATTAA TCAATGTAAA	1380
GTTCAAGTTG ATAACATGT CACAGGCAAA TATAATATTT ATGCATTTTA TAATAATTGT	1440
GACATGAA	1448

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710:

GCTGnAAAAAT ATGTTAGAAG CAGATGCATG GGCAGCTG GGGTCCTTAT TTATTGTCAG	60
GTAAAGATGT CTTCAATTCA ACTATTGGAA TATATGGTAT GGGAGATATT GGTAAGCTT	120
TTGCAAGAAG GTTGCAAGGG TTTAATACTA ATATTCTTTA TCATAATCGA TCAAGACATA	180
AAGATGCAGA GGCGGACTTT AATGCAACAT ATGTTTCTTT TGAAACGTTG TTAGCAGAAA	240
GTGATTTTAT CATCTGTACA GCGCCACTTA CAAAAGAAAC ACATCATAAA TTTAATGCTG	300
AAGCATTTGA ACAAATGAAA AATGATGCAA TTTTATTAA TATCGGTAGA GGACAAATTG	360

TAGATGAAAC AGCATTAAATC GATGCACTAG ACAATAAAGA AATTTTAGCA TGTGGTTTAG	420
ATGTATTAGC AAATGaACCG ATTGATCaTA CACATCCATT aATGGGaCGT GaTAATGtTC	480
TGaTTaCACC aCACATTGGG TAGGCGCATT CAGTTAACn	519

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711:

CTATTACAGG TGGCGAACCA ATGTTTTCTA AAAAGTCTAT TAGAAATGTT GTTAAACCTC	60
TATTAAAGTA TGCACATCAT CGAGGTATAT ATACACAAT GAATTCAAAC CTAACATTGC	120
CTCAAGATCG TTATTTAGAT ATTGCTGAAT ATATCGATGT TATGCATATC TCACACAACT	180
GGGGAACAAC TGATGAATTC GCAAATGTTG GCTTTGGCGC AATGAAGAAG CAACCACCGT	240
TAAAAGCTAA GTTAAATTA TATGAACAAA TGATTTCGAA TGCACGTACA TTATCAGAAC	300
AAGGAATGTT TGTATCTGCG GAAACAATGC TCAATCAAAG TACGCTACCA CATTTACGAA	360
AAATACATCA AGAAGTCGTT CATGATATGA AATGTAGCAG ACACGAGATT CACCCTATGT	420
ATCCAGCTGA CTTTGCAAGT CAATTAAATG TGTTAACTCT AGCGGAAATG AAAAAGACAA	480
TTCATGATAT ATTGGATTTC AGAGATGAAG ATATTTGGAT GTTATTTGGT ACTTGCCTG	540
TGTTTCCATG CTTAAAGGAT GATGAAGATC AAAAGTTACT ATCACGTTTA AGAAATGCTA	600
AAAATGTAAC GACTAGAAAT GACCCGGATG GCCGTAGTCG TTAAATGTC AATGTATTTA	660
CAGGTAATGT AATCGTAACT GATTTCCGAG ATGAAACAGG TACATTTTCG AATATACAAA	720
AAGATAAATT AACAGATGTA TTTGATAAAT GGTATCCTC TGATCTTGCT AAATCATTA	780
ATTGTCATTG TTCCGAGTTT AGTTGTTTAG GGCCAAATGT TCTTGTTAAA AATATGTACT	840
ATCCGAATAT GGATTTTAAA GATAATGAGC GTCATATGCA CAAACAACCA CAAATTATAC	900
AATTTTAAAA ACTCTTAATT ATGCGGAGAA GCACTTTATC GATAAGTAGT CTCCGCATAT	960
TTTAATGCTA TTATAAATA AAAACAATT AATTGCTGGC AGTACTCTAC TTAAATAATA	1020
AAGGGCATT T AATAGGACTA ATAGTCTATA ATAAAAGGGG TAAATTTTAA CTAAAAGCAT	1080
AAACGTGCAT AATCAAAAAG ACAGaTGTA GGTGGAATAT TCGAaCATAA CAGTTCAATT	1140
CATCCTTAAC AATCTGTCTT TATATTTTAA GTCTCTAATA TGTTGCACTT GAGCTAAATA	1200
TTCAATTGTT gTTTACTTtC AaTGCGaCGt GCTTtCTtC GTtCAaCaCG TgwGGTGCTG	1260

TATCATAAAA CCATTTTTC AATCATCTT CTGGATATAC ACCAGGTACA GTTTAGGTT 1320
 GCCTTCATCA TCTAACGCAA CAAATGTAA 1349

(2) INFORMATION FOR SEQ ID NO: 712:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712:

GAAATTAAAA AAGCAATTGG ACAAGATGCA ACAGTGTCAT TGTTTGATGA ATTTGATAAA 60
 AAATTATACA CTTACGGCGA TAACTGGGGT CGTGGTGGAG AAGTATTATA TCAAGCATTT 120
 GGTTTGAAAA TGCAACCAGA ACAACAAAAG TTAAGTCCA AAAnCAGGTn GGCCTGAATG 180
 GAACCAGGAG GAAntTGAA ATATGCTGGG GATTACATTG TGAGTACAAG TGAAGGTAAA 240
 CCTACACCAG GATACGAATC AACAAACATG TGGAAGAATT TGAAAGCTAC TAAAGAAGGA 300
 CATATTGTTA AAGTTGATGC TGGTACATAC TGGTACAACG TCCTTATACA TTAGATTTCA 360
 TCGGTAAAGA TTTAAAA 377

(2) INFORMATION FOR SEQ ID NO: 713:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713:

AATGAAnCGA AAAATGACTA TAAAAAGTTT AAAGTGTTTT CACTTATTTT AACACTTGTC 60
 ATTGTCATTT TAGCAATTAT AAGATTTGTT CATAAAATGA TGTAATTAGA BGAGACATT 120
 GTTTTATGTC TCAGGATCCA GTTATTCATT ATATCTACAA TATTTACGAT TATATAAATA 180
 ACCCGAGATT TTAGTATGAT TCATTtCACT AAAATCTCGG GTTCTATTT GATAATTTTT 240
 AATGGGATAT GGCATGTATA CGTTCTTGCC TTTTATCTCA TTTCCAATGA TTAATCTGGA 300
 TATTGTTCTA AAAATGCTTT CGTTCTTTA TTAAGTGGT TAAATCAAT ACCTTGTTGC 360
 ATCGCTGCAA AGACACATCC ACAATAACAC TGCCTAAAGA TATTATAGTC ATTACACATT 420
 TCTATGGaAC GTCATAACC TTTACTTTTC yTAAATCAC TTGGcAAATA GTTCACaTCG 480
 TATATTTTTT GGACATCCAT ACCAAGTTCA TTATTAATT GTGCGTTC 528

(2) INFORMATION FOR SEQ ID NO: 714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 731 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714:

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TTTAATGGCA TGAAGTCACA GTATATAAAG AATCTGGTGT GACAATCAGT ATGACTAAGT      60
ATATAAAAAA AGAGCAGGTG cGAAATAATG GCGAAAGAGT CGAAATCAGC TAATGAAATT      120
TCACCTGAGC AAATTAACCA ATGGATTAAA GAACACCAAG AAAATAAGAA TACAATGCA      180
CAGGATAAGT TAGTTAAACA TTACCAAAAA CTAATTGAGT CATTGGCATA TAAATATTCT      240
AAAGGACAAT CACATCACGA AGATTTAGTT CAAGTTGGTA TGGTTGGTTT AATAGGTGCC      300
ATAAATAGAT TCGATATGTC CTTTGAACGG AAGTTTGAAG CCTTTTTAGT ACCTACTGTA      360
ATCGGTGAAA TCAAAAGATA TCTACGAGAT AAAACTTGGA GTGTACATGT TCCGAGACGT      420
ATTAAAGAAA TTGGGCCAAG AATCAAAAAA GTGAGCGATG AACTAACCGC TGaATTaGaG      480
cGTTcACyTT CTATcAGTGA AATAGCTGAT CGATTAGAAG TCTCAGAAGA AGAAGTGTTA      540
GAAGCAATGG AAATGGGACA AAGTTATAAT GCGTTAATG TTGATCATTC CATTGAAGCT      600
GATAAAGATG GTTCAACTGT TACGCTATTA GATATTATGG GGCAACAAGA TGACCTTAT      660
GACTTAACTG AAAAACGTAT GATTTTAGAA AAAATATTAC CTATATTATC TGATCGCGAA      720
CGAGAAATCA T                                                    731
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(2) INFORMATION FOR SEQ ID NO: 715:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715:

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TTTTAGrGGa AAGCGaATTA GtCaTATwCg CaGCAGATwG aATGATTGaA AAmGaAATTG      60
aTTcGATTCC AATTGTAAGA AAAAAAGATA ATCAAAAGTA TGAAGTAATT GGAAGAATTT      120
CCAAAACAAC AATAGCTAAG TTATTAGTAG CATTATATAA AGAATAGGTG AGAAGTAATG      180
GAAAAAATTA AAATTATCGT AGCTTCAGAT TCTATAGGTG AAACGGCAGA GTTAGTTGCT      240
AGGGCAGGTA TTTCACAATT CAATCCTAAG CAATGTAAAA ATGAATTATT AAGATATCCA      300
TATATTGAAT CTTTGAAGA TGTTGATGAA GTGATTCAAG TTGCAAAAGA TACAAATGCT      360
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ATCATTGTTT ATACACTTAT TAAACCTGAA ATGAAGCAATATATGAGTGA GAAAGTAGCA	420
GAATTCCAAT TGAAGTCTGT CGATATCATG GGGCCATTAA TGGATTTATT ATCTGCTTCG	480
GTTGAAGAAA AACCTTATAA TGAGCCAGGT ATCGTTCATA GATTAGATGA TGCATATTTT	540
AAGAAAATTG ATGCGATAGA GTTTGCAGTT AAATATGATG ATGGTAAAGA TCCTAAAGGA	600
TTACCTAAAG CTGATATTGT TTTACTTGGT ATTTTCGAGAA CTTCAAAGAC ACCATTATCT	660
CAGTATTTAG CGCATAAGAG TTACAAAGTT ATGAATGTAC CGATTGTACC AGAAAGTGAC	720
ACCGCCAGAT GGCTTATATG GATATTAATC CAAAGAAATG TATCGCACTT AAAATAAGTG	780
AAGAnAAATT AAATCGCATT AGAnAAGAGC GACTAAAACA ATTAAnGACTA	830

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716:

nGAAGAACAA GTTTAnCATC TAAATGCCCC TTAAAACTA CAACTACTTG ACGATGTTAA	60
ATCAGTGTTT AAnTCTCAA TGACGCAAAA TAGTGATTTT AATGAAGAAA AGAAAGTGTC	120
TACGAGAGTA TACTTAGATC AAATyCATCA ACGATTGTTT TTEAGCAAT CTTTAATTAC	180
AGAACGTATA AAAAAATACT TTAATAAGCA ACTCACTGAG CAAATTGCAC CAATCGTTCA	240
ACAATTAGCA GATTTACATG TCATTATTAA TCCTCAGTTT AACTTTGAAT CAGCTAATAT	300
AGAGCAACCA TTATTGCACA TCGATTTCAA CGATATGCTA AATGCATTGC CTAAACAATT	360
AACAAAACGT AAAATTTTGA ATCCAAATGG GCAAAGAGAT ATACATGAAT CAATTTGTCA	420
AAGTACGTTA GGATTATTAC AACCACAAAT GGGATTATTG AGGCAACAGC TTGAATTATA	480
TGTAAAGCAA ATGGCTGTAG AAGCTGAATC GCAATTTGAA AGTTTTGAAG CTAATATTCA	540
AACGCAAATA AACGATTTAT TAGCATTGA TTTAGATACA ACACTTATCA ATCAATTGAA	600
AGATAACAT CAACAACTGA AAATATTTT ATATTAAGAA AGAAGGAACG TTTTAAATGC	660
CTAATAAAAT ATTACTTGTA GATGGTATGG CGCTATTATT TAGACATTTT TATGCTACAA	720
GTCTTCATAA ACAATTTATG TACAATTCAC AAGGTGAACC TACAAATGGAATACAAGGAT	780
TTGTGCGTCA TATCTTTTCG GCAATACATG AAATACGCCC TACACATGTA GCTGTATGTT	840
GGGATATGGG ACAATCAACT TTTAGAAATG ATATGTTTGA tGGTTATAAG CAAAACGTT	900
CTGCACCACC AGAAGAATTG ATACCACAAT TTGATTATGT TAAAGAAATT TCAGAGCAAT	960
TTGGCTTTGT AAATATTGGC GTTAAAACT ATGAAGCGGA TGATGTTATA GGTACATTAG	1020

CACAACAATA TTCAACTGAT AACGATGTCT ATATTATTAC GGGCGACAAA GATTTACTGC	1080
AATGTATTAA TGACAATGTT GAAGTTGGCT AATTAAAAAA GGTTTAACAT TTATAATAGA	1140
TATnCATTAC ATCGTTTTn	1159

(2) INFORMATION FOR SEQ ID NO: 717:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717:

GATTTAATCA ATGCAGTTGC AGAGCAAGCT GATTTAACTA AAAAAGAAGC TGGTTCAGCA	60
GTAGATGCTG TATTCGAATC AATCCAAAAC TCACTTGCTA AAGGTGAAAA AGTACAATTA	120
ATTGGTTTCG GTAACCTTGA GGTACGTGAA CGTGCTGCAC GTAAAGGTCG TAACCTCAA	180
ACTGGTAAAG AAATTGATAT CCCAGCAAGT AAAGTTCAG CATTCAAAGC TGGTAAAGCA	240
TTAAAAGATG CTGTAAAATA ATTTTACTTA AAAAGCCCTG AATAAGGGCT TTTTATTTTG	300
CTTTTAATAC TTACAACCTG TACATAAATT GTAATGTTCT TCTAAGTTTT TAATCTTTGG	360
AACATTCATT GTTTAAGCGT TCAAAATATT ACATGACATA ATAGTTTTGA TAAAAATAGC	420
AACTACAAAA TATACATATG aATATTGaGa TTAATTGTTA GCGTTGaATT TACTTAAAG	480
GTAACCATGT CTACTATAGT ATTTTACGTT ATTTAAAAAG ATGAATAATG TAAATGAAGT	540
AAAGGTTATT ATGAGAATTA CAAAAGCTAC ATAA	574

(2) INFORMATION FOR SEQ ID NO: 718:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718:

AAGaTATTGA AAmtGmAaTG GaGCACGCCC TTATTTGATA GAAGTAAAAG ACATTTAATT	60
CTTACCGATG CAGGTCAAAT TTTTATGAG AAAAGTAAAG AAATTGTtGC ACTGTATGAT	120
TATTTACCAT CTGAAATGGA ACGCTTGAAT GGA CTGGAAA CAGGACATAT AAACATGGC	180
ATGTCGGCAG TCATGAATAT GAAGATTCTT ATCAATATTC TTGGTGCATT CCATCAACAA	240
TATCCAAATG TTACATATAA TTTGATAGAA AATGGCGGTA AAACAATTGA ACAGCAAATT	300

ATCAATGATG AAGTAGATAT AGGCGTGACC ACTTTGCCAG TCGATCATCA TATTTTCGAT	360
TATACTACCC .TAGATAAGGA AGATTTGCGA CTTATCGTGA GCAGAGAGCA TCGACTCGCA	420
AAATATGAAA CTGTTAAACT CGAAGATTTA GCAGGTGAAG ACTTCATTTT ATTTAATAAA	480
GACTTTTACT TGA	493

(2) INFORMATION FOR SEQ ID NO: 719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719:

GCATTGCCAA AACAATACGT TTATATTATT GAGGACTAC TGTATAAAAG TAATGAATAT	60
CAAAATAAAA AATCATATTA CGAAACACTT GTTAACCAAG TAATTGAACT TAAACAGGCA	120
GATGATTTAA TTATTGGACT CGCTTATTCC GTACAACGCT TAGTCGTCGA TCATTTACAC	180
GTTGTCGGTG ATATTTATGA TCGTGGACCA CAACCAGATA AAATTATGGA TACTGATT	240
AATTATCATT CCCTAGATAT TCAATGGGGT AATCATGATG TGCTTTGGGT TGGAGCCTAT	300
GCTGGGTCAA AAGTATGCTT AGCAAACTTA CTTGAATTT GTGCACGTTA TGATAATTTA	360
GATATTATCG AAGACGCTTA TGGCATTAAT TTAAGACCAC TGCTTACTTT AGCTGAAAAA	420
TACTATGACG CAGATAATCC TGCTTTTAAG CCTAAAAAAA GACCTGACAA ACACGAACGT	480
TTAACTCAAC GTGAAGAAAG TCAAATTACT AAAATTCATC AAGCTATTGC GATGATTCAA	540
TTCAAGTTAG AAATACCAAT TATTAAACGT CGTCCAAATT TCGAAATGGA AGAACGTCTT	600
GTGCTTGAAA AGGTTAATTA TGATACAAAT GAAATTACAG TTATGGTAA TACATACCCA	660
TTGAAAGACA CATGTTTCCA AACTGTCAAT CGTGATAATC CAGCAGAATT ACTACCTGAA	720
GAAGAAGAAG TCATGAATAA ACTATTATTG TCATTCCAAC AATCTGAAAA ATTACGTCGT	780
CATATGTCTT TCTTGATGCG TAAAGGCTCT CTTTACTTAC CATATAATGG CAATTTACTC	840
ATTCATGGTT GTATTCCAGT TGATGAAAAT GGTGAGATGG AATCATTTGA AATTGATGGT	900
CATACTTACA GCGGCCAAGA ATTATTAGAT GTGTTTGAGT ATCATGTCCG TAAATCATTT	960
GATGAAAAAG AAAATACTGA TGACTTATCG ACGGATTTAG TTTGGTATTT ATGGACTGGG	1020
AAATATTCGT CACTATTTGG TAAACGTGCC ATGACTACGT TTGAGCGATA CTTTATTGCA	1080
GATAAAGCTT CTCATAAAGA AGAAAAGAAT CCGTACTATC aTCTTCGTGA AGATGTGaAT	1140
ATGGkTCGTA AAATGCTCaG TGaTTTCGGA TTAAATCCAG ATGAAGGACG CATTATTAAT	1200
GGTCACACAC CAGTGAAAGA AATCAATGGC GAGATCCTAT CAAGGCTGATGAAAGA	1257

(2) INFORMATION FOR SEQ ID NO: 720:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720:

TGAGCACATG ACAGTGGCTG AAAACATTAA ATTTTTTAAA TCACTTTGTA AAAATCCAAT	60
TAACGATACA ACTATCAACG AATATTTACA GCAATTAAAC TTTGATGATA CGTCTGCCAA	120
AGTATCTACA TTGTCCGGTG GGAATAAACG TAAAATTAAT ATATTAGTAG GTTTACTAGG	180
TCAACCTCGA ATTCTCATTT TAGATGAACC GACAGTTGGT ATTGATTTAA AATCTAGACA	240
TGACATCCAC CAACTACTTA ACATCATGAA ATCTAAATGT TTAATTATAT TAACTACCCA	300
TCATTTAGAT GAAGTTGAGG CACTTGCAGA TG GTTATCAA GTTAATTGGG CCAGGTnCCC	360
TTTTnTTCAA CAGTTTTTGG GGGCCAACA TGGGCTTATA	400

(2) INFORMATION FOR SEQ ID NO: 721:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 570 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721:

CTTATTTATA TTATAATATA AATATTTTAT TTTTCAATAC TTAATTTTAA AAATCCCCTA	60
TGAAAATGTT GATGAGCTAC ATCTTTAAAT CTTATTATAC ATTGTATAAA ATTATATTGC	120
GAGGTAGTAA ATTGATATTA TACACTTTTG GTTGTGTATG CATCTCACCTATCTTTTTTG	180
CTTTTTTCAA ATAAGAAAGT ATTA AAAATy AATGCCTATA CAGGAACAGA CATGGCTAAA	240
CTTGATTTAA ATAGTCTTGA CGACGAGCAC GTAAAATTAT TAATAAATGA ATTA AAATAT	300
CCAGAAACTC ATATCGATGT AAATGAATTA AAAACAATAG TTGCTAGTCG AATAAATGAA	360
AGGCAAGAAA TAATAAGTTT TAAGTTAGGA ATAAAGTACT TATTAACAAT AAAAAGAGGG	420
AACATAGAAA AAGATAGGTT TTCAATTTCA ATCATTTTCA AAGATACCTA TCACACCCTA	480
GTTAGAATAG ATATTAACGG TGGTACTCAC GATAATCCAG ATGGAACAAT CGCTCCGAAA	540
AGTCATATTC ACATATATAA TGATAAGTAT	570

(2) INFORMATION FOR SEQ ID NO: 722:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722:

ATTTTAGTCT TAGGTGTTGA TTGCATGATG AATGCAGAAG TTATACCTGC AGCCATATTA	60
GCACCTTCAT TATTGTGTAT AATTGAATA TTATTGCTT TTAAAGTATG TCCAATTAAG	120
TTTGAAGTCG TTGTTTTACC ATTTGTTCCA CTGATAAATA CAATATCATC AACTGCTCT	180
GCTAATTTTC TTAATATATC TGTATCCACT TTTCTAGCGA TTTGTCCAGG TAAATCTGTT	240
CCTCTTTTAC CTACTGCTCT ACTTGCTTTA CGCGCCAATT TCGCTAGATG GATTGCCGTC	300
CACTGTCTCA TGTGTTTCCT CCTCAAATt CCACTCGCAT CATTATAACA TGACAAGGCA	360
ACTTCAAAAA AGTTTCTCAA TCACAAATnG ATACCAGTGT	400

(2) INFORMATION FOR SEQ ID NO: 723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723:

GATTATATGC TGTGGCAAA ACAATATACC CAGATGAATT TTTATTTTTA GTAATAGTAT	60
AACCATGCTT TGTCTTACTA ACTTTGACAG CTTCTAATGA ATTTGAAGCG TCTTTAAGCG	120
TGGTATAATC TTCGCCGTAT ATCCCTTTTAAATTTACTCG ATACTTACCT TTAGGCAATG	180
ATAATCTAAT TCTATCTGGA GCTTTAATGC GTATCGTTAC GGGTGTTACA ACGCGTCGAT	240
ATTTATAAGT GAGTTTATTT CTTTCTTGTG TATATTCATT CACTTTAACA TCATGAGCTT	300
TATCCGGCGA AAGTAATTCT AAATCCATTT CAAAATACAA ATCTTTAAAT TGATTAAAA	360
CTGATTTTGG CAACTGTACA GTTAGACCAC CATTATTTTG TTTAACTTGT AATAAATGTT	420
TTGTAGGAGA TTGCCAGGCT GCACTATTTA ATTTAATTGT TGAATCTGAT AGTAAATTTT	480
TATTGGCTTT AAAATGTGTA TTAACATCTT TAATATTGTT AGAAACAATC CCTTGCAACA	540
TTGCTTGTTT TTTATCTAAT GGAGATTTTA ATTCTTTATT GGAAAAGACC TTATTTGTAA	600
TATGTGCACT TGGATAATGG ATGGTATTTT TAGAATGAAT CCAACGAAC TATTGTCTT	660
TGTGTTTCTA CTTAATTTTA AATCCATATG GtAAGTTGTC ATCATGATtC ACTCTAATTC	720
GATCATTAAC ATTCCAAAGT GATAGTaAAT TTgACGAjC CAAGTAATCT ATAAGTGCTG	780

TTTTTATCGA TTGGCATATT AATTTGGAGT GTCTTGTCAT AATATTTTAA AATGTCTCCA	840
TTAAAAATAC TAGAATATAA TGAAATGCCA TTATAATGAT ATATAAATGG TGAATTTAAT	900
GCATAGTCTG ACATATAATC AATGCGATTA AATGAGCCTG TTGCATTTTG ATTTATCTTT	960
TTTATAAGCT GGTTTACATA GTTACTATGG TAATCATGTT GTTCAACGT TGATAATGAT	1020
TGTTGATAAG GTTTGATTGC CATGTTTTTG TTGTTATCTA AAATGACGAT TTGTTGAATC	1080
ATaACGATTA ATACTAATAT TGCAACGGTT AAT	1113

(2) INFORMATION FOR SEQ ID NO: 724:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724:

TGCCGTTTAG CAAAATCTAG TATCGCTTGA TGATCAGATT CTGAAATTC AGTGTGTACT	60
TCAGCTATAG GTGTCATTGC CTCATTACCT GGAATGACAA ACACTTGTTT AACTAGATTC	120
GATTGATTAA GTTTATATGC AAGTGCATGT TCTCGTCCAC CAGCACCAAT TACTAATACA	180
TTCATTTATG TTACGCCCCCT TTAAAATTAG TGTTTAAAAT GCGAGTGCC TGTGACTACC	240
ATTGCAATAC CATGTTTATT AGCCATATCA ATTGAATCTT GATCTTTAAT CGAACCACCC	300
GGTTGGATAA TTGCCTTTAT ACCATGTTGT GCTGCAAGTT CAACTGTATC TCCCATAGGG	360
AAAAATCCAT CAGATACTAA CGgCTACATG ATCATTGATT TCAATAGCTC TCTCTAACGC	420
AATTTTAGCA GCACCGACAC GATTCATTGG CCAGCAnCTA TACC	464

(2) INFORMATION FOR SEQ ID NO: 725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725:

GTAAATnCA nTATTTnAAA TaTATTACCT TATTAGAAAA AGTCGTAATA TGAGGTGTAC	60
AAATGACGCA AATTTTAATA GTAGAAGATG AACAAACTT AGCAAGATTT CTTGAATTGG	120
AACTCACACA TGAAAATTAC AATGTGGACA CAGAGTATGA TGGACAAGAC GGTTTAGATA	180
AAGCGCTTAG CCATTACTAT GATTTAATCA TATTAGATTT AATGTTGCCG TCAATTAATG	240

GCTTAGAAAT TTGTCGCAAA ATTAGACAAC AACAACTCTAC ACCTATCATT ATAATTACAG	300
CGAAAAGTGA TACGTATGAC AAAGTTGCTG GGCTTGATTA CGGECAGAC GATTATATAG	360
TTAAGCCGTT TGATATTGAA GAACTTTTAG CAAGAATTCG TGCAATTTTA CGTCGTCAGC	420
CACAAAAGGA TATTATCGAT GTCAACGGTA TTACAATTGA TAAGAACGCT TTTAAAGTGA	480
CGGTAAATGG CGCAGAAATT GAaTTAACAA AACAGAGTA TGATTTACTA TATCTTCTAG	540
CTGAAAATAA AAACCATGTT ATGCAACGGG AACAAATTTT AAATCATGTA TGGGGTTATA	600
ATAGTGAAAGT AGAAACAAAT GTCGTAGATG TTTATATAAG rTATTTACGA AACAAGTTAA	660
AACCATACGA TCGTGACAAA ATGATTGAAA CAGTTCGTGG CGTTGGGTAT GTGATACGAT	720
GACAAAACGT AAATTGCGCA ATAAC E GAT TATTGTTACC ACGATGATTA CGTTTGTAC	780
GATATTTTGG TTTTGTTTAA TTATTATTTT TTTCTTGAAA GATACACTGC ATAATAGTGA	840
GCTTGATGAT GCaGAACGAA GCTCaAGCGA TATTAATAAt TTATTTCaTT CTAAGCCTGT	900
TAAAgATATA TCTGCaTTAG ACTTGAATGC aTCTTTAgGT AAtTTTCaAG A ATAATTAT	960
TTATGATGAG CATAATAATA AATTATTTGA GACATCGAAT GATAACACAG TGAGAGTTGA	1020
ACCAGGTTAT GAACACCGTT ATTTTGACCG CGTAATAAAA AAACGCTATA AAGGCATTGA	1080
ATATTTAATT ATTAAAGAAC CAATTACAAC GCAAGATTTC AAAGGGTATA GCTTGTTAAT	1140
TCATTCACTA GAAAATTATG ATAACATCGT AAAATCATTG TATATCATTG CGCTGGCATT	1200
TGGAGTGATT GCAACAATTA TAACTGCCAC AATCAGTTAT GTATTTTCAA CACAAATTAC	1260
TAAACCGCTT GTCAGTTTAT CAAATAAAAT GATTGAGATT CGACGAGATG GTTTTCAAAA	1320
TAAATTGCAA TTAAATACAA ATTATGAAGA AA A GATAAT TTAGCAAATA CGTTTAATGA	1380
GATGATGAGC CAAATTGAAG AATCATTTAA TCAACAAAGA CAATTTGTTG AAGATGCGTC	1440

(2) INFORMATION FOR SEQ ID NO: 726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726:

TGATATTCCG ACTTGCGAGG ATTATTGCGC ATTAAGGATT AACGCAGTAT GAGTCCAAAG	60
ACGCGCGACA CCTGGAAAAA GGATTACCTA ATGCCTTATT TACAGTAACC TTGTAGATA	120
AAGATCGGTT AATTGGTATG GGTAGAGTGA TTGGCGATGG CGGAACTGTT TTTCAAATTG	180
TTGATATTGC AGTTTTGAAA AGTTACCAAG GTCAAGGTTA CGGCATCTAA TTATGGAGCA	240
TATTATGCAA TATATTAAAG GTGTGGCTGT TGAGAGTACA TACGTTATCT GATTGGCAGA	300

CTACCCAGCG GGnTAAATTA TATACCAAAT TTGGGTTTnA TACCTACCGA ACCAGAnTCC 360
AGGCGGTGAT GTATG 375

(2) INFORMATION FOR SEQ ID NO: 727:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727:

TAAAAAACTT AGAGATGAAA ATCATATTAT TTATCTGTTT TTGGGACAAT TTTTACTAA 60
 AAATGAAGAT CCATGGCATC AAATACTTAA TGATTAGAA GTTACAAATT CTGTTGATAA 120
 TTTTTTAAGG TCAATAAGTA ATAAGGCCAA AGAAACAAAA AAAAGAGCTT TTATTATTAT 180
 TGATGCGCTT AATGAAGGTG AAGGTAAAAG GTTATGGGGA AATTATTTTC AAAGCTTTAT 240
 CAACCATATA AAGAAGTATT CTAATATAGC TTTAATATTT TCTATTAGAA CCCCTTTT~~TC~~ 300
 AGATGTTATA TTACCCAAAA ACGCAATACA AGATAACAAT ATTGTAGTAT TTCAGCATGA 360
 AGGTTTTAGT AAGGAAGAAA ACTATAATCC AATTGTATCT TTTTGTGATT TTTATGGATT 420
 AGAGCTACCT AAGTTACCTA TATTAAATCC AGAATTCAAC AATCCATTAT T 471

(2) INFORMATION FOR SEQ ID NO: 728:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728:

TAGGATGTTC CACCCTgGCA ATTGcTCTAA GACATcTACa GCAGTAGAAT ayCCTGTTTT 60
 CGTcTtTTTtA ATAACAGGTA ATTGTAATGT CTCAAACAAT ACAACACCTA ATTGCTTAGG 120
 AGAATTTATA TTAAAATCTT CACCAGCTGC ATCATGGATA TTTCGAATCA AGACGTCTAA 180
 TTTTCTTGA ATTTCTTTTT CCATTTCTTC TAAATaTGA ACATCTGTAA ATATACCAAT 240
 TTCTTCCATT TCACTTAAAA TCTTAGCTAG CGGTAGCTCT AAATCAGCCA AGAGTTCTAC 300
 CTGATTGTAT TCTTCTAATT GTTTATCCAT ATTTGGTTTC GCAAAGTAAA TTGCATCAGT 360
 AATAGAAGCA ACATATGGAT TTAAACATC ATCTTCAGGT ACCTTAAATT TCTTACCTTT 420
 TCCATATATA CTCACATCGT CTTTCACAAA ACTTTGACCG TACAATGAAA CAACTGATTG 480

AACATCACTA ATCGTACGAG ATGGATCAAT TATATAACTG GCCAACATAA TATCGAAAGA	540
AATATTTTGA ATATCAATCC CCAATCTATG TGATGCTACA TATGTTTTTT TAGCATCATA	600
TACGACTTTT TTCGAATTCG GATTTTCTAA CCATGAAACT AGTTCGACAT AATTATTTAT	660
GTCATCCGCA TTAATTACAA TATGTTTCTC ACCTGtAAAT aAAGAGAATT TAAAAtATT	720
ATTtCGCAAA TAGtTACCAC CGtCTAATTC GAAATGGATG GCCGCTTCTT TcAATGAAGT	780
AAAATCcAAT ATTATCAAAA GACGTTTCcA ATTTCAAATG TCTtTCTAT TGCATCTTCA	840
ACGcTtGCTG ATTGaTCAAT GTCAGCCAAC AATTGTTTGA ATTCTAACTT CTTAAACAAT	900
TCGATTTTTT CTGTGTGTTT ATCTtGakGA GTCATTAAACG TATCTTCaAG TTTTACTTCa	960
ATCGGACTAT CTACATTAAt CGTTGCTAAT TCTTTACTCA TTAATGCATC TTCTTTGCTA	1020
TTTTGAAGTT TTTCTTTTAA CTTTTTACCT GAAATTTTCAT CTAAATGTTC ATAGACACCT	1080
TCTACTGTGT CAAATTGGTT TAGCAATTTT ATTGCTGTTT TCTCTCCAAC ACCTGCAACA	1140
CCTGGTATAT TATCAGAAGT ATCTCCCAT T AATCCTTTCA TATCAATAAT TTGATTAGGT	1200
GTTAACCCGT TGTATTTTTT CGCAATAAAG TCAGGTGTAT AATGATCAAC ATCAGTAACA	1260
CCTTTTTTTAG TGTAATAAAT GGTTACATTA TCCGTTGCAA GTTGTGTTAA ATCTCGGTCT	1320
CCCgTAATAA TAATTGTCTG AAAGCCCGCT TTATCTGCTT CTTTACTTAA AGTTCCGATA	1380
ATATCATCTG CCTCATAGTT ATCTAATTCA TAACGTTTAA TATGATAAGCATCTAATAAT	1440
TGGCGAATAT AAGGAAATTG CTCACTTAGT TCAGGCGGCG TTTTCTGGCG TCCACCTTTA	1500
TATTCACTAT ATTTTTTCATG TCTGAAAGTC GTTTTACCTG CATCAAACGC TACTAAAAAA	1560
TGATTTGGCT TTTCTTCTTT TAAAATCTTC TCTAGTAACA TTGCAAAACC ATATACTGCA	1620
TTGGTATGAA TGCCTGCTTT GTTTGATAAC AAAGGTAATG CATAAaAAGC TCTAAACTT	1680
AAGCTATTAC CATCGaTTAA TACTAATTTA TTCACAATTT TAACCTCCAG AACTAATTTA	1740
TATATnTGTG	1750

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729:

AAATTAATTT TAACATCCTT TCAAAATAGT TTTAACGGAT CcTCCcAAAA CGTAAACTCA	60
CATCAGTTAC TTGTAACATG CATTTTCTCC TTTTTTTCAT TCGATATTCT AACGGAAGAA	120
TTATATCATA TTATCGTCAC AGTTTCGACC TCATATAAGT TGTAATGATA GAATGACTCA	180

CACATGTTAT AATAATAAAG AATACAAGAA TCGAAGGAGA ATAAACATGG CATAGACAA	240
AGATATAGTA GGGTCTATAG AATTCCTTGA AGTAGTAGGG TTACCAAGGT CAACTTACCT	300
TTTAAAGGAC CAACGGTGAA ACGTAAAGTT AAACCAATCA GAATGAACGT GATGATTGAA	360
TTAGAAGTAG GGGAGnATAT AGTTCCTCAT TTATCCAACC GGTCAGGTGG ATTATTGCAC	420
TCAAATATGC nGnTATACG	439

(2) INFORMATION FOR SEQ ID NO: 730:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730:

GGATCAnCAG GTTcAAAaGG TATACTGACT AACATTTTAC CGAGGTATGT CCATGTTCTCT	60
AGTTTAGGAT TGATGACAAA GCCATTACGA CCAACAAATC CTAAACCTGC ACGTTCTGCT	120
ACTGCCCTAT CTGATAATAC ACCCGTATCT ACATAGATT TGATTTCAAC ATCTGGAACT	180
TTAGATTCAA TAAATGCAGC TAACATGTCT AATCGTTTAC GCATAATTGT ATGATAATCT	240
TGACCCACG ATGCTCTAGC AAATAAGCCT CTGCGATCAC CTCTAACACT CTTAGGTGCA	300
CCTTTCAGTT TGTTAGGATA ACCAACTGCA ATTGCTATGA TTGACCTTGC TGTGTTAG	360
GATAATTTAG GCTCCGTTTCG TAAAGCAATA TCAGATTCTT CAAaTCCTGA GGCATAACCA	420
TTTGCATGAT ATGCTTCTAG CTTTTGCTTC AATTCATCAA AGGGnTCGGC AGTAGTAAAT	480
C	481

(2) INFORMATION FOR SEQ ID NO: 731:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731:

GTGATGAAAA ATCTTTTTCT ATTGATTGAG AAAATAGTTA TTTATATAGT TTTTAAAGAA	60
AAAAAGTGAT AATATTTAGC TAATCTAATG AAAATTGATT TATTGGACAA AAAATACATT	120
TTAAATGAGT AGAGGAGGCT GCAAwTGGGT TACAGAACTT TAAAAAGTAT TTTTCATGAA	180
CACAATGAAA GTAAAAATGAA GGAAGAGTAT ATTAAAGAT TTAATTCTTT mGCTTCTTTC	240

AATACTAATA TTAATATCAT ACCTATGGAA AATGGAAAAA AAGTTAATGA TTTGGAATAT	300
CCTCTATTCT TTATGGTGAC TAAAAATCTA TCAAAAAAAC AAGAATTAAT ATCAATTAAT	360
AGTAGAAAAA TTGATAGAGC ACTTAATTCT TTACCATATG CAGCTAGAGA ACAATATTTT	420
AATGATTTAT TAATCGATGA ATTACAAAGT ACTAATGAAA TTGAAAATGT ATTTAGTACT	480
AAACAAGAGA TTGCACATGC GTTAAATAAC CAAGCATCAG AATTTCTTAA GTTCAGAGGC	540
CTCGTGGATC AATATAAAGA GATAGAACTT AATAAAAAAA TTAAAGTTGA TAATGTAAGA	600
GACATTAGAG CGATTTATGA TAAATTAGTT TCAAATGAAA TTAACGAACA AGATAAGTTA	660
GATGGAGAGC TATTTTCGTAA AAATTTTGTG GGTGTGCATG ATGGGTCAAC GAATAAATAT	720
ATACATGTTG GGTTACAACC TGAAACCAAA ATTGTTGAAT TTATAGGTGA AATGCTAACA	780
TTTTTAAAT ATTTTGATGC GCCTCAGCCG TTCAAAATCA TGGTAGT	828

(2) INFORMATION FOR SEQ ID NO: 732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732:

CGTATGTTTC GAATTTTATG nATTGCATTG GATAATAGTA CCAGTTAAAA GAACTAAGAT	60
TGTAATTATC CCCCTTAAA ATTCAAGAAT ATATTTTCTT AATCTATCAG CAAGAGGTTA	120
TATTTCAAAG TGTTTATTTT TAAAACAACA TCTAAAAGCC ATTTcATAAt AAwGTTAAT	180
CaTTAGaATG TATAAAGATT CCaATTAATA AAAATAGATA AAATGCAATA AAGTTCCAAA	240
TACTTATTAT TATTCATCAC AAATTACGTG ATGCCCTCTA CAACACTAAA TCAAGGATGA	300
TATTTATTTT ATATACATTA GCATTCATTG TTTGCTTACC CACATTATCC TGTTTAGTCT	360
TTTTTATAAC TCTAGTCTTG AATGTCATAT TTACAAAGAA AAAAACAATA AAATATTTAA	420
AACTAACACT ATTTATTCAC TTTGTTCTTT TATAGCACCT TTTATGTTTA TTTCTTGTA	480
TTCAATAAAT AGTATGGAGA TGATAATTTA AAGTAGATAT ATTTGAAGTA TACTATAGAG	540
TAAATTATAT TGGGGAAATA TGTAACGAA CCGGTTGATT TTATAEGGA TTAACACTTC	600
ATAGAGAATA TAATCAAGAA CAAAAACAGT CAATAGGTGT GAATTTTTTTT AAAGACGGAT	660
CTGTTGCTAC TAAAAAAGA AGTATACAAT TCAATAGTTA AACCTTAAAA CAAGAAATAT	720
TATTCAAAT CAATGAATTT CCTATCTTAT TAGTTTTAAC AATATTTATT CTCATAGAGT	780
TTGTCCAATT AAATATAGAT GATTCAAATA TTTATAAGCA TACAAAAGAG CAGTAAGACA	840
TTTTCTAATA GAAAATAACT TTACTGCTCT TTGTACATTA CTCATCAACT ATTGTAAATT	900

AAATAATAAA TAACTACCTA TTTTATTATT CAGCTAAAAA ATGCTCTGCT AAATATTTTG	960
CTGCGCCATC CTCTTCATTC GTGTATGCG TTACATCTGA AGTTAATGCT TGGATTTCAG	1020
GGCGTGCATT TTTCATAGCA ACTGTATAAT GACCAAATTC AAACATTGCT CTATCATTGT	1080
CGCTATCTCC AATAACTAAC GTTTCTTCTT GATGAATACC AAAATGTGCA ATCATTCTT	1140
TAATGCCTGT ACCTTTATCA GTTTGATAAG CCATTGTTTC CGCATTAAAT CTGATGAAT	1200
TTGArACACT AATCTGTAGT TGCACATGAT TTTGCTTTAA TTCATCTCTA AATGCTGTTA	1260
TTTTTTCTAA ATTAGAAGT AATAGATAAA TTTTGAATA TTCACCTTCA GGAACTTAG	1320
TTACCCAATC TATCTTACCA GCAAGCGCAT CTTGTCTTGA AGACCATTCA CTATGACTTA	1380
CGCCATTAAT AGGATCTTGA CTACGAATCA TATCTCGCAT CCATGTTTCA TCTTCTTTTA	1440
AAGAACTCT ATTACCTTCA AAAGGAAATA CCTCATAATA AATTTGTTGG CGCTTAGCTA	1500
AATTAGTAAT TTGTTGCACT TGAGCCAATG ATAAACCATG CTTGAAGATA ATTTCTCCAT	1560
CTACTTCTCC AATTGTTCCA TTTGAACTAA TGATGCATT AACCGCAAAA TCTTGAGGTA	1620
CA	1622

(2) INFORMATION FOR SEQ ID NO: 733:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733:

AATGCCAnAT AAATCCAAAT TCTTTTAACG AACAAGAGTG CCCAAGTTAT TGCTGATCGT	60
TATGCCAGAT AnGCATATCA ATGATAATTA TGGTTTAGAA AGAATTTCTA AGACAAACA	120
TGGATATAAT TATGTGTATT CCAATGATAA TTCAACTAGT AAGCAACATG TAAGTATTTT	180
AAATCAAGGC ATAATAACGA AATAATAGAT GGAACAGTGT ATTCTAATTG GATATACTGT	240
TTTTATTTTG CAATAATTTA ATTTAAAAAG GTGAATTCAA CTTATAAAAT GATGTAAATG	300
TTATGTCAAA ATCAACCAAT CCGTAATGTA TTTTAAATG TTAATATAGT TCTGAAGAAG	360
TATAAATGAG GTGTTGAAAT GGCTAAAAAT AAGAAAACgA ACGCGATGCG TATGCTTGAT	420
CGTGCAAAAA TTAAATACGA AGTTCATAGC TTTGAGGTAC nTTAAGAACA TT	472

(2) INFORMATION FOR SEQ ID NO: 734:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734:

CATAGCCCCA AATTTTTTCT ATTATTTGTT CACGÆTAAA GATTTGCTTA GGACGTGCTG	60
CAAGCATAAA TAATAATTGA AATTCCTTGT TCGGTAACGT CATCGTTTTA TTAGATACTT	120
GGAGTTCCAA ATAGGATTGG TTTAGCGTTA AGTTGCCAAT AGTCATTTCT GAATTTGAAT	180
TGATATTATA TCGACGTAAT ACAGCACGAA TTCTAAAAAT AAGTTCCTTA ACCTCAAAGG	240
GTTTGGTTAC ATAATCGTCA GTACCGCTTA TAAACGCACG CTCTTTGTCA CTAAGTGCAT	300
CCCGCGCTGT TAACATAATA ACTGGTATAT CATAATCATT TTTTAATGTA TTACATAATT	360
GAAAGCCGTC CATACCATCC ATCATAATAT CTACCACTGc AATATCGaCA CGCTGTTTTT	420
CtAAAAGGTT TTAATGCAGC TTCACCACTT GGTGTGTGG TATGCATCCA ATGGTGCTCT	480
GTTTTGTnAA ATGGGCTAGC TATAATAATT TAGGGGATT	519

(2) INFORMATION FOR SEQ ID NO: 735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735:

ACTTGAAAAC GATAAACAGT ACTTTCCAGC TACACATTGG AAAGCTATAA ATGGGATACC	60
TTATGCAGGC AGTAGTGATA TTGATGGATT GCCTCAAGÆ GGTATCATTT CGGTAAATGA	120
TAAAAATAAA TTAGATAATT TAAAAATAGG CGAACAGGAA TTATTCAAAA TAGCATTGTA	180
CAGAAATCCC CAAACGGTAA ATTGTGGAAA ATAACAGTTG ACGATAGTGG GAACTTGGT	240
ACAGTGCTAT TTTATTAGAA AGGAAGGTGC ATTATGGAAA ATTTGTATTT AATAAAGGAT	300
TTGGGAGCTT TAGCAGGTCG AGATTATAGA GCTAAGGAAA TACAAAACCTT ACAAGGAATA	360
GGCATTGCGC TGGGCTGACC ACCAGGGTTT AnGTGnCCnC	400

(2) INFORMATION FOR SEQ ID NO: 736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736:

CTTTTTTATT GAAAAAGTGG TATTTGATTA TCTATTTACT ATTTATATTA GCGGCACTCC	60
TTATTACATT AACGACAATC CAACATGTAA CAGAAGATGA CAATCATnTT AATATAGGTG	120
TCGTAGATAA AGATCAATCA AGTGAAACGA AATTAATCTT AAACCTCTATT GGTAAAGGGA	180
GTAACCTAGG AAAAAACGTG AGCATTAAAG CATATGATGA TAAGCAAGCA CATACTTTGT	240
TAAAAAAACA TAAACTTCAA GGCTATTTTG TTTTGTATAA AGTATGACC AAGGCATTTT	300
ATAACAAGG CGAACTACCA ATTTTCAGTAT ATACATATGA TCAACAATCC ATGAAAAGTG	360
TCGTGCTATC TCAGCTAACA GATTCTGTTT ACCAACGTCT TATGCGATCA ATGGGTGGCA	420
TCTTAGCTTT TCAAGACTTA GCACCGAAAG CATCACATTC TGACAGTATC AATGTTATGA	480
CTGATTTGCT GATTACAGGA TTAAACCGTT CAGGTGCAtT TAACTTAGAA CCGATTCATT	540
TATACGATAC GGGCAGTTAT TATGCAATTA CAGGATTTTT AACAAACGGTA TTCATCTTTG	600
CACTATCTTT ATTTACAGTT TTGAAAATGA ATCAAGATAC TGTATTGAAA GCGCGATTGA	660
AAATGTTTCA TTTTCTTAA GAGGTTTAT TAATCATTCG TACGTTGATT ACATGGTTTT	720
ATACTATGTT ATGGGnGTAT CnTGnTGTA GTTTGAATG TGGTTCAGTA TTCCGAATnA	780

(2) INFORMATION FOR SEQ ID NO: 737:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737:

TATTTAATTT CTnATTnTG GTTTTTAATT nTAAGATGAC CATAAATGAA TTTCTTCTGC	60
TGTCATAGAA TTAGAGCAAA ATACGAGCAT AAATTTAACT AATTTCTGC TTGTCTTATA	120
GTCTTGATTG CCTTGTA AAA ATGTTAGTAT TAATTGCTTC ATCGTTTCGA ATTGTTGTGT	180
TGATTTAATA GCGATTGCTA AACCTATATT TTTTTCGAAA AGCTTTTCAA AACATCTATT	240
TAACAGGTTG TAATTCGTTT GGCTAATCTC AATATCGTGA ATATCGTCAA TGAAAACGAC	300
AGGTTTTGGT AAGTGCTCAA AGTTAATATC GTAATATTCA TTGAAAAtAA ATTGAAATAG	360
TTCATTGAAA TTAATAAATC GAACAAATAC TTTGGCACGC TGACTTCGAT CTTTCGGATT	420
AAAATCATCT ATATGAATAT CTGTTGTATT TGTAGCCAGT TGAGCTGTTA AATCAATTGT	480
TGAAATTAAC TCAGTGAATT GTGATACtT ATCTTGTTGG AAGTGTATTT GTGGTGGTTC	540
AGTAATCTTG GAAACGAGTG AACGGAAGTG TTTAGGACTA AAATGCAAGT AATTCTTAAA	600
TTGATTTGCA AAATTTGTAT GACTGTTAAA ACCGGCCAAT TCAGAAACAG TTGTAATAGA	660

ATGTTTTGTA GAAAGTAATA AATTGATGGC GTTAACAAGT TTAATACTTG TAAATAATC	720
TTTAAAATTC ATACTCAAAT ATCGAACAAA AAGATTAGAA CAATATGATT CAGAGATGTT	780
GCAATGCATC GCTATATCTT TTAAAGACAA GTGCGCATCA ATATkGTCAT GAATATAGTT	840
TACACAGTCT ATGAACACCG GATTGCTTAA AGCAATATTT GGTAAATATT CATGATCTAT	900
TCTTATAAAA GCTTCTTTAA GTAAAGTGTC TATnATACTT TGACCT	946

(2) INFORMATION FOR SEQ ID NO: 738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738:

TTTATTTGAT GATGTACTAA AGCAAGATGA AAGATTTGTT ATTGTAGTTC AAGCATTAGA	60
AGAAAAGAAC GGACAATTAT TAAAGAGAAC TTTAAGGGAA TATCCCGGTT TAAACCATAA	120
ACAAATGAAT GATTTATTTA TGCACTTAAA GAATTATTT TCCGAAGAAT CATTTGCTGA	180
AAACCAATCA GCGTTCAGTA TTACAGTTTA TACAAATTTA GATTATACTG CTGACCAAAT	240
ATATGCTCAT GTAAAACGTT TCAGAGGTAA GCATGACTGG ACACAAACAG CTAAATAAAA	300
TCAAGATGCT TGCAGTGgAT TkTAACmATT AATGtTAGaT gTCmCyGcAT TTTTaAGCC	360
ATTCGGTAAT TAATCCGGAT GGTCCAATTT AATTAAC	397

(2) INFORMATION FOR SEQ ID NO: 739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739:

CAAGGTATTT CATTTGACCC ATTCACACCA TTAATAGTGG CAGCAGCATT ATACTTTGTC	60
TTAACATTTG TACTTACACG CATTATGAAC ATGATTGAAG GGAGATTGAA TGCCAGTGAT	120
TAAAATAAAC AATCTTAATA AAGTTTTTGG AGATAATGAA GTTTTAAAs ATATCAATCT	180
TGAAATCAAT CAAGGGGAAG TAGTAGCAAT AATAGGTCCA TCTGGTAGTG GTAAAAGTAC	240
ATTGTTAAGA TGTATGAATT TATTAGAAGT ACCTACTAAA GGTCAAGTGA TTTTGAAGG	300
CAATGACTTA ACGGAAAAAG GGACACAAGT AGATAACTA CGTCAAAAAA TGGGTATGGT	360
ATTTCAAAAC TTCAACCTAT TTCCACATAA AAAAGTTGTC GATAATATTA TTTTAGCTCC	420

TAAATTATTA AAGAAAGATA ATAACGATGA ATTACATAAG GAAGCATTGT CGTTATTAGA	480
TAAAGTGGGA TTAAAAGAAA AAGCAGATGT ATATCCGAAT CAATTATCAG GTGGTCAAAA	540
ACAAAGGGTA GCAATTGCAA GAGCTTTAGC AATGCATCCA GATGTTATTT TATTCGATGA	600
ACCAACTTCA GCATTAGATC CTGAGGTAGT TGGTGATGTA TTAAAAGTAA TGAAAGACCT	660
AGCCAAAGAA GGTATGACCA TGGTGGTTGT GACACATGAA ATGGGATTTG CCAAAGATGT	720
AAGTGACAAA GTCATATTTA TGGCAGATGG CGTTGTCGTA GAGTCAGGCA CnCCAGTCGA	780
AATATTTGAA CAACCGCAAC ATGAAAGAAC ACAAATTTT TTAGCAAGAG TATTATAACA	840
ACCTAACGAG GCTTGAATAT ATGATACGCA CCACAAAGTT ATATCATATA TTCAAGCTTT	900
TTATTATTAA nATTA	915

(2) INFORMATION FOR SEQ ID NO: 740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740:

AGTAAATGCG ATGTTGCATG GAGGCTATAG CAATGAGCAA TAAAGCTTGG GGCGGTAGAT	60
TTGAAGTACA ACCTGAAGAG TGGGTTGACG ACTTTAACGC ATCCATTACT TTTGATCAAA	120
CGCTCATAGA TCAAGATATC GAAGGCAGCA TTGCACATGC AACTATGCTT GCGAATCAAG	180
GCATTATTAG TCAACAAGAC AGCGAACAAA TTATACAAGG ACTAAAATCT ATTCAACATG	240
ATTATCATCA AGATCAAATT CAATTTAGTG CATCATTAGA AGATATTCAT TTAAATATTG	300
AACATGgAAT TAATTAAACG TATCGGTGgA TGCTGGTGGT AAGTTGCATA CTGGACGCgT	360
AGtAAACGAT CAAGTTGcAA CAGACATGCA CTTGTACACT GAAGAAACAA GTGCAAGnnn	420
TCATCGCATT GGATG	435

(2) INFORMATION FOR SEQ ID NO: 741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741:

AATATCATAA CCAAAGCTTG TCATTACTTA TATGTAAAGA TTAGAGGCTA ATTACATAAT	60
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CCTAACTTAT TTAACAGGAA GTCATGAAAA CTATATTACA ET AAAAAGTA TAACTTTCCA	120
TCACCAAAGT CAGAATTTAT TGAAACACTC AACTGATAAT ATAGAAGGCT AATTATAAAA	180
ATACCTGGCG ATTAATAAAC TGTTCCTGTT TTTTAGCACT TAATATATTT AAAAAGACAA	240
ATAGAGCCCT TTCAGGCTCT ATTTnCTGTA TCCTTAACAA CAGAAGCTGT TAAACTACC	300
CGTCTTTTCa CAaCCAAaGc TaCAAAAAaaG aTgGCTAGTT ATTCTTTCGT CACCCGCTGA	360
ATCATTAGTG TTGTTATTTc CTTTAACTTG CACGTCTAAA TCAAGAAcTT TTTCCAAaGA	420
TaAAACCCCC TATTTAAAG TTGAAGTTAA GACCCcTTCA ATTGTCATAT TAATCATTAC	480
CACACAATAA ATCAATGAAT TT A ATAATAA TTATTTGTTA TTAATTTGTA AATCGTCATT	540
AATTTTATGG TACTATTGTT AGTTTAAACA AATAATGTAA CTTCTTTTTT TAATATGTTG	600
TGAATATTTT TTGTTTAACT CTTAAATTTC GGGTTTAACT TCCTCTATTT CTAACAGTTA	660
TACTCCAGGA TTAGTTTCTT TAGAATCCGT ACCGATTAAT TTAACAGT E GGTTTTGCCA	720
GTCAACTTCA TAAGTAGATG TAAACGTTAC TGTATTTTGA TnTTTGTAGT TATTTCCAAC	780
CCAGTGTAGT CGATTCCATT GATTAGTATA TCTATCCATT TCTCTTTGGT AAGTTACTTT	840
GATTTTAGAT TtTTTTGTAT CATTTTGTTT ATGAGAAAGT ACGCTTATAA ATTCTGGGTT	900
AAAGTTACCA CGCGCCAATA AAGGCATTTG ATGTGTTGGC AAGAAATTTT GACCAGCATT	960
TGAACTACTT TGTCTACCAC CTAAAAACAG TTCATTACCA TATGTTGGGT CATAACTATC	1020
TCTACCATAT GGTCCCCAAC CATTATTCAT AATTTTGTGC GCCTCAACAC CCCAGCCAAT	1080
TGATTTATGA TTTGTTTTTC TATCAATCGT AGTTCTGTAA CTTTCTTGTT TATAATTTAT	1140
CGTTTCTGAA AATGATTTTG ATCCATTTAA TCCACCTGAT AAGCCATTAG ATATATTA	1198

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

GTGGCATATn CAAACTACTA CTGAAAGATC AATTACATAC GTACAGATTT TGCAAAATGA	60
TCAAGATTAT CCAACAATTT TTAGATGAGa CAAAACGTAA ATCTGTAATT A ATcAGATG	120
TTAATGTAAC GGTA A AAGAT AGAATAATGA CTTTATcAAC GTGCGAAGAT GCATATAGTG	180
AAACGACGAA AAGAATTGtT GTTGTGCGAA AAATAATTAA GGTAAGTTAA ACAGAAAmGA	240
GGATAATTAT GAAATTTATG GCAGAAAATA GGCTGACGTT AACaAAAGGA ACAGCAAAAG	300
ATATTATAGA ACGATTTTAC ACGAGACATG GGATTGAAAC ATTAGAAGGC TTTGATGGCA	360

TGTTTGTTAC ACAAACCTTA GAACAAGAAG ATTTTGATGA AGTGAAAATT TTAACAGTTT	420
GGAAATCAAA GCAAGCTTTT ACGGATTGGT TAAAATCTGA TGTCTTTAAA GCAGCGCATA	480
AACATGTTAG AAGTAAAAAT GAAGATGAAA GTAGCCGAT TATAAATAAC AAAGTAATTA	540
CATATGATAT AGGCTATAGT TACATGAAAT AATTGAATTT AAAGAGGTTG CAGTACTTGT	600
TATGACAATT GGTATTGTTA GCTTTTGTAA CGACCATACA TGATACCGAT GATGGTCGTT	660
TTTTTAATGa ACACAAACAT GCTAACAACA AATTGCTAAA ACATAGTTTG aTTTGAATGT	720
GgCTTTGGAA AATAATCATC CaTtATATCa TTtTGGATTn TATTTTGGAA GAAGAAAAGA	780
ATTAATAATG GATATTTTGG GGGGCGTATG GATTTTnA	818

(2) INFORMATION FOR SEQ ID NO: 743:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

TGCTGGTAAA TCTTCCCTTA TCAAGTCTTT AATTGGTGAA TTTAATGCTA CCGGTACTAA	60
ATTGTTATAT AACAAACCTA TACAACAACA ACTGCAACAT ATTACATATA TTCCACAAAA	120
AGCACATATT GATTTAGATT TTCCTATAAG TGTGGAACAA GTGATTTTAT CAGGTTGCTA	180
CAAAGAAATT GGATGGTTTA GACGACCTAA TAAATCAGCA AGGGATAAAC TCAAACAGTT	240
ATTAAGCGAT TTAGAATTAG AATCTTTACG TCATCGAAA ATTTCAGAAT TAAGTGGTGG	300
ACAATTACAA CGTGTGCTAG TAGCAAGAGC ATTGATGTCC GnaAGTGAAG TTTATTTTCT	360
AGATGAGCCG TTTGTGCGAA TTGATTTTAG TAGCGAAAA tTAATCATGA CAAAAATcGA	420
GAACCTAAaA CAACAAGGAA AACTTATTcT TATCATCCAC CATGATCTAT CAAAAGCAAA	480
GCAATACTTT GATCGCATTa TTCTATTAAA TCAAACATTA CGATACTTTG GTGATAGTGA	540
AGAGGCTATG AGTGTCACtC GCTTAAACGA AACATTTATG AGTAGCACTG ACTGTAGTGA	600
CCCTAGTCAA AGGAGCAATA TAACATGTTA GAGTTTGTcG AACATTTATT TACATATCAA	660
TTCTTGAATC GAGCATTGAT AACTTCAATT ATTGTAGGGA TAGTTTGTGG TACAGTTGGT	720
AGTTTAATTG TATTACGTGG TCTTTCATTA ATGGGAGATG CAATGAGTCA CGCAGTATTA	780
CCTGGTGTTG CCCTATCATT CTTATTTGGT ATTCCAATGT TTGTAGGCGC ACTTATAACT	840
GGTATGATCG CAAGTATTTT TATCGGTTAT ATCACATCTA GTAGAAAAC GAAACCTGAC	900
GCCGCTATTG GAATTAGTTT TACCGCTTTC TTAGCTTCGG GGATTATTAT TATTAGCTTA	960

ATAAACACTA CGACAGATTT GTACCATATT CTGTTTGGTA ATTTACTGGC AATCACAAAT	1020
AGTGCATTTT TAACAACTAT TGTGATTGGT TCAATCGTCC TTATTCTAAT CATTATTTTC	1080
TATCGTCCAT TAATGATTTT TACATTCGAT CCAACGTTTA GTAGAATGAG TGGTCTAAAT	1140
ACGACGTTAT TACATTACTT TGTGATGTTG tTACTCTCAT TAGnAACAGT AGCAAGTatT	1200
CmAACGGTA	1209

(2) INFORMATION FOR SEQ ID NO: 744:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 675 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

CCGCCTTTTCG TAAACCTAAT ATAATACGAA ATTTTCGTAT TGTCAACATT AAATACGTTT	60
TTTTTCGTAAA AAACCTTACT ATGATATGAA AATTTTCGTAT AATAAGAAAA AAGGAGGTAA	120
GTAATATGAA CAAAGAmAGm AATATTATTA TAGCCAAAAm CATTAGAAAA TTTCTCAACG	180
ATTCAAATAT GTCTCAAAAG AAACCTTGCTG AaCTCATTA CATAAAACA TCTACTTTAA	240
GCGATTATTT AAATTTACGT TCCAACCCCT CTCACGGCGT TATACAAAGG ATAGCTGATG	300
TTTTTCGAGGT TGGTAAAAGC GACATAGATA CTACATACAA AGACGATAAC GACATCACTT	360
CCATATACAA CAAACTCACA CCTCCCCGCC AAGAAAACGT ACTTAACTAT GCAAATGAAC	420
AATTGGAAGA ACAGAATTCT AAAGGAGATA ACGTTGTAGA TATTAATTCA TATAAACAGG	480
AGAAAACCTCC AGTTAACGTC AATGGTTGCG TCTCTGCTGG TGTAGGAGAA CGTTTACACG	540
ATGAAACGCT ATTTACTGAA ATGGTTAAAG GACCTATCCC CACACACGAT TTAGCGTTAA	600
AAGTAAATGG TGATTCTATG GrACCTATGT TTAAAGATGG CGAAATCATA TTTGTGGAGA	660
AAACTCACAA TnTGA	675

(2) INFORMATION FOR SEQ ID NO: 745:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

CAGGTGTCAT AGTTGAACTT GGtGGTTTTG GACTAATCGT TAAATCATCA ATTTGTGTCA	60
TCCAAGGTTG GAATTTACTG CCTTGTGTCT CCAGTGCCT GAAAATACCT TATCTTGAA	120

ATAAGTCAAC TAACTCTTGG ATACCTTTAA TTAATGCTGG GTTACCACCA GAAATTGTAA	180
CGTGGTTAAA TAAATCGCCA CCAATTCGTT TTAATTCATC ATAAATTTCT TCAGCGGTCA	240
TGAGTTTTAT ATCGCCTTTA GCACTACCAT CCCAAGTAAA TGCAGAATCA CACCAGCTAC	300
AGgATaATCA CATCCAGCTG TTCTCACAAA CATCGTTTTT CTACCGATTA CTCGACCTTC	360
ACCCTGAATG GTTGGACCGA ATATTTTCGAG TACAGGAATT TTAGCCATTA GTTACACCTG	420
TTCCTTTGGT CTAAATACGA CATAACTTGT TGGTGTTTCT CTTACAAATA CTTGAATACA	480
TTTTGGTTGG TGTTTCGAGCG ATGCCAAATT TTCTTAACA ATTTGATAAA TTGTTTCCGC	540
TACGATTTCA GTTGAAGGGA TTTTGTTTTT AAAAGCAGGT AAGTTATTTA ACAGTTGATG	600
GTCAAATTTA CCGTGTATCA TCTTTTTCAA ATGGCTAAAG TTCACTAAGA AGCCAGTGTC	660
ATCTAGTTTA TCACCGACAA TTGTAAaya cAAAGTAAGT ATGACCATGG ACATTTTGA	720
AAATACCTGC TTCTTCACAT GGAATGTGAT GTGCAGCCGA AAAATTAAAA TCTTTATTTA	780
ATTCGAATTG ATATGGATGC GTTGTACTAG GATAGATTTG TTGTAACATT TTAAAGCGCT	840
CCTTTACTTT CAAGATATTG ATTTAGTCCA CGTTGACGTA AATGACAAGC TGGACATTCA	900
CCACAGCCAT CCCCATGAT ACCG	924

(2) INFORMATION FOR SEQ ID NO: 746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

ATCTTTTGGG TATTTTCTAT ATTAGCTGTT GTTTTCTTAG TATTATTTAG TTTTGCTGTT	60
GGTGCATCAA ATGTACCAAT GATGATTTTA ACATTTATAT TACTCGTTGC AACCTTTGGA	120
ATTGGATTTA CTACAAAGAA AAAATATCGA GAAAACATT GGCTATAAGT TATATCGACA	180
ATAACACGCG TTGATTTAAG ACCACACATG TTCATGATGA ACATTTAACT GGTTTTATAT	240
TGGCGCGTGT TTTTATTATT TAAGGTATAA AAGCGTAATA TGTTACCTAA TTGTTAGGAC	300
TACATATTAC GCTTTTGGTA ATTATTTTGA TTTTCTTTTA AATCGTTGTT CATGTAATTG	360
TATTAACGCA TCATGGTGGG GCTCTAAaTA ATCATtGCTA ATTcTTGATG GAGACCmCGA	420
TTtCCAACTA rGATkGAATT kGGACCmCTA AtkGTTAATG GTcctCCTAG TAAATTGGAA	480
GCTTGTCAT TaCTTCcATA TAAAtAACCA ATCCGCCAGC AAAtCCCcAT GGTkGAAGTC	540
TTGGCGTCAT ATATGCTTCT AAaTTACCTG TAGCAACTGA AACGATTTCA AGCGCTGCAC	600

TACCATATGC CCTTGCACTT CTAGAATCAT TAACAATTTC TTTAAAGATT TCTCCTAAAA	660
TTGGTTTtagT TAACCAGTTC GGATTGATCC CAATAATGCT TTGTCTTAGA TTAGAATCAT	720
TCAATGGTTT CAAGGGTTGG CTACCACGAT ATGCACCTTC CCCACTTTA GCATGATATA	780
AGACATCAGC CATAACATCA TATACAAAAC CTGCATAAGG TTTACCATCG ATATAAATAC	840
CAATTGAAAT TGCGAAATTT TCTTGTTGAT GAACAAATT CAATGTACCG TCTATTGGGT	900
CAACAATCCA TACCGTACCT TTGGAAGTAT CGATGTCATG ACCATGCCCT TCTTCACCTA	960
ATACTTGATG A	971

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

TTCTCGTCAC TGTACGTTGT ATTGCGGCAT CATCCATTAT GATACGTTCA GACATATTCT	60
CACCCTTTCA AAATTTAGAA ACAAAAAACC TCATGTCTTT AATATCGACA TGAGGTTTAG	120
TATATACAAT CAGCCTATTT AATAGAAGA ATCGTAGTAT TACTACTTAT TCTTGCATAT	180
GTGAAAGTGT TATGATCATT TTAGTATATA TCTATATTTT CATGTCTTTG ACGTCTCTCT	240
GGACGCTCAA TTAAAGACTC TTTATGTTGT ACTTAACTG TTATAAGGAT AATACTAATC	300
AGGCGCTTTG TCAATCTATA TTGAAAAATT AACCATACTC AGTAAAAAG TTAACCTTAA	360
TCTATTTTAT AATGTGTTTT CATTTAAAAA AAACGAAAAC GATAAACACT TATAGTTTAC	420
ATAATAATGT TATCGTAATT ATAGCACGAC ACAATTATGC ATCTCTTTTT CGAATTGTAT	480
CTAATAAATC TTCAAAGTCT TGTGGTAATT CAGCATGTCT TTCAATATAT TCACCTGTTA	540
CTGGATGTTT GAATCCAATA AGTCCAGCAT GTAGAGCTTG ACCACCAATA TCCAATGTCT	600
TTTTCGGTCC ATACTTTGGA TCACCAACTA ATGGGAAGCC AATATATTTT ATGTGAACAC	660
GGATTTGaTG CGTACGTCCT GTTTCAAGTT GACATTCAAC AAGCGTATAA TCTTTAAAT	720
GTTCTAGTAC GTTAAAATGT GTCACTGCTT CTTACCATC ATCAnCAACA GCCATAGATT	780
GACGATCATT TTTGTTTCTA CCAATTGGCG CATCGATTGT ACCGTAATCA TGAGGAATAT	840
TCCCGTGGAA CTAAAnCGAT ATAGT	865

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

ATAACATTGT GGAGCCTATG ACATTGATTT ATGTCTCGGT CTCAAATGTT TTGTAAAAA	60
AACTAAGTAT AGTTGAATTT TAAGTTAAAA AAATTGTTTT TGCAAAAATA AAATAATCCA	120
TCAACTGCAA AAAAAATATGC AATGATGGAC TAATGTCAA AAATTGTTAC ATCCATTTTA	180
TTTTAGGTTT TTCGCCTCTA AAAATCCTTG CGaTATTAGA GCGATGTCTA ATTATCAATA	240
TGATTGAAAC TAAGAACTA ACGACTAATA AAATATAGTC TTGAATGATA AGCGAGCCAA	300
TCACACAGCA AATTGCTGCA ACGATACTTG CTAAAGAAAC ATATTTAAAA ATCTTCAATA	360
CAATAAGAA GATAATTGCA AGTATTAGTA AAAGTATCGG ATTGACTCCC AAGACGACAC	420
CTGCACTAGT TGCAACAGCT TTGCCACCTT GGATTTTAA ATAAACAGGA TAAACGTGTC	480
CAAGTATAGC GAATAAGCCA ACAATTAAAC CATTTGTAAA AAAAGTACTA ATAGGGCCAT	540
CTGCGTGAAC TTGTAACCAT AAAGGGAAGA AAACAGTTAT GAACCCTTTG AAAATATCTA	600
GAAATGTTAC CAAGAATCCT GCAGGACGAC CTAATACTCT AAAGCTATTA GTAGCGCOA	660
TATTACCACT ACCAAATTGT CTAATATCTT TTTTGAAAA TAATTTTCCA ATTACGAATC	720
CACTTGGGAA AGCGCCGATA AGATAACTTA GTAGTAACAT GACGATTATC ATCATAAATA	780
TTACACATCC TTTAATATCT TAGGACTATT TTATCATA	818

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 971 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

ATATCCAATa ACTGTTcATT GTCTTGATAT TCCTTAAATG TTTcATAATG CTCATTAGAA	60
ATGACAATTT CAAGCAACCA ACCCGTGCCA CTTTCCTCTT TATTAATTAT TACGCCATCT	120
TCTAATTCAT ATTCTATAAT TCTGCCGTGT TCATTcACAA TTTGAAACCT TACTGCTTTA	180
AAAGTTTTCA TATTCCCACA TCCCATTAGT TTAATAATTA TGATTTTTGA ATTATTTAGA	240
AGATTTAAGG TCATTTcATG ACTAATTTCT TTAAATATAA CAAATAACGA GATGCTATAG	300
CTATTAATTA TATAAAATTT GcCATTTTgA CCATTTTTAA GCTAGTAATT AAGATATAGG	360
cATAGGAGGT GAATCACACA CTACATGCTA AATAAAATCG TAATTGTCGG GAGcTGACGA	420

AAGACGCACA AATATTTGAA AAGGAGGATA GAAAAATTGC AACGTTTTGT GTTGCAACGC	480
ACCGAAATTA TAAAGATGAA AATGGAGAAA TCGTCTGTGA TTAATTATTC TGTAAGCAT	540
TTGGCAAGTT AGCTTCTAAT ATAGAAAAAT ATACTAATCA AGGTACATTG GTTGGTATAA	600
CTGGTCAAAT GAGATCAAGA AAGTATGATA AAGACGGACA AACACACTTT GTCATTGAAT	660
TATATGTTGA AACAAATAAAA TTTATGTCCC CTAAATCCCA AAATAATGAA ATTCTCTCAG	720
ATAGTATTTT AGATATTGAC TCTCAAAATA TAGATAATCA TGACTTATTA GAAATTTAAA	780
TCCAATTATC CTAAACATCC TTAATATACA TTTAATCCAT CCTAATTTT TTATAGATCT	840
AATTAAGTTG AAATATACTC ACTTAAAAAC GACTTACATG ACCTAGTACT GTTGGTAAGG	900
TCGnCTTTTG GTGTAGTTTT CCTAATAGAn AATAGACnTA GGTTGCCAAA CCGATTACAT	960
AAAAAATTGC C	971

(2) INFORMATION FOR SEQ ID NO: 750:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 832 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ATAGATTACT CTTTTGATCT GTAGATCCTA CTGTAACGAC ATTGTCCATA GATGCAGGAA	60
CATCTTTCAC TTCGCCATTA CCTTGATATT CACGCTGTAA TTTTAGTTTC TGTTTGTCAT	120
TGACATCAAT ACCATCATT A CCAGCTGCAG CAACAACGAT AGATTTTTTC TTCTTGGCGT	180
AATTGATTGC TTTCTGTAAC GATCGTATT CTACTTTTTC ATCTTTTCTA AATGTTTGAT	240
GGTCATTTTT GTCCAAAATA ATATAACTAC CAACACTAAT ATTAATGACT TGAATTCCAT	300
CATTTGCAGC TTGAACAATC GCTTTTGATA CCCAAAGCAG TTCTGTTTTT TTAATACCA	360
ACACGCGATA CATTGTAAAT TTGTTATTCG GTGCAACACC TATTAATA CCATTAGCAC	420
TCGTTTGACC CGACACCATC GTGCCATGTC CTTTCCTATC ATTGACATCG TGAACATCAC	480
CTGTTTCCTC CGGTTTCAGTA CCTCTAAAAC CGTTTAAAGG TACTAAATTT TTAGAATCAG	540
TCGAGAAATT ATTTTTCAAA TCGTCATGGT TTTTCATCAC ACCTGTATCT ATGATTGCTA	600
TTTTGGTGTT AGCATGTTTT GGCAAATCAT CATACGATGC ACCATTATTG GTTATTTTAT	660
TCATATCCCA TTGTCTTGAA AATAATGACT CATTGTATGT TCTGTCTATT GTTTTCTCGC	720
TAGTAATACA AGTTGAACAT GTGGCATTGA TATATTTAA ATCATTTTTA TAGTTTGCTA	780
AAGCATTAGC ATGCATTTTC GTCATTTTAA TCTGTGCCAC ATGGAATTCC GG	832

(2) INFORMATION FOR SEQ ID NO: 751:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751:

GTAATATCAA TCTCTTCATA AGCTGAATTA TTTTCATGCA CTTCTTGATG TGATGATTTG	60
TCACGAACCG CTACAATAA CATTTTATCG TCTAAAATAA GTTGTTTATA TTTTCTAAT	120
TCATCAGGCG CTAAGTTGTA GCGTGATAAA ACTGCATGTT CACCATCTTC CTCTGTTAAC	180
AGTTTAGTCA TTCTATCACT AAATGTTCCA CTTGTTGAGA TAAGGGAGAT TTCAGAGTCG	240
TGTAAGTCAT TTAGGTGTAA TTTACTTTTA CTAATAATTG TTAGCTCTGA TTCTAAATAA	300
CCTTCAGATT TCTTTTGATT GATTACGTTG TATAATTGCG CAGTGTCATT TACTACAGTA	360
ATATCTGCCA TAGTTGTCGC CCCTTTAAAA ATTTGTTTAT tTAATCTTTT ACCCTTCTTA	420
TnATAAAGTA AAACCCTTAC ATTATTAAGT nATAAGTCTT CATTCGCATT AAACG	475

(2) INFORMATION FOR SEQ ID NO: 752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1019 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

GCGACACTTG TGAGTTCTCC AGCAGCAAAC GCGTTATCTT CAAAGGCTAT GGACAATCAT	60
CCACAACAAA CGCAGTCAAG CAAACAGCA ACACCTAAGA TTCAAAAAGG CGGTAACCTT	120
AAACCATTAG AACACGTGA ACACGCAAAT GTTATATTAC CAAATAACGA TCGTCACCAA	180
ATCACAGATA CAACGAATGG TyATTATGCA CCCGTAACCT ATATTCAAGT TGAAGCACCT	240
ACTGGTACAT TTATTGCTTC CGGTGTAGTT GTAGGTAAAG ATACTCTTTT AACAAATAAA	300
CACGTCGTAG ATGCTACGCA CGGTGATCCT CATGCTTTAA AAGCATTCCC TTCTGCAATT	360
AACCAAGACA ATTATCCAAA TGGTGGTTTC ACTGCTGAAC AAATCACTAA ATATTCAGGC	420
GAAGGTGATT TAGCAATAGT TAAATTCTCC CCTAATGAGC AAAACAAACA TATTGGTGAA	480
GTAGTTAAAC CAGCAACAAT GAGTAATAAT GCTGAAACAC AAGTTAACCA AAATATTACT	540
GTAACAGGAT ATCCTGGTGA TAAACCTGTA GCAACAATGT GGGAAAGTAA AGGAAAAATC	600
ACTTACCTCA AAGGCGAACT ATGCAATATG ATTTAAGTAC AACTGGTGGT AATTCAGGTT	660

CACCTGTATT TAATGAAAAA AATGAAGTGA TCGGaATTCA TTGGGGCGGT GTACCAAATG	720
AATTTaATGG TGCGGTATTT ATTAATGAAA ATGTACGCAA CTTCTTAAAA CAAAATATTG	780
AAGATATCCA TTTTGCCAAC GATGACCAAC CTAATAACCC AGATAATCCT GATAACCCTA	840
ACAATCCTGA TAACCCTAAC AACCCAGATG AACCAAATAA CCCnGACAAC CCTAACAACC	900
CTGATAATCC AGACAATGGC GATAACAATA ATTCAGACAA TCCAGATGCA GCTTAATTAA	960
CAATTAAGTT CGTCTAGATA AAATAGGAAG CAAAGTCTTA GCAACGTAAA ATATTTTGA	1019

(2) INFORMATION FOR SEQ ID NO: 753:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

ATTCTTATCC CAGGTAGGTG nTTTACTTCT TATATTAGGT GCAATAACTC ATGCCACTCA	60
TCTTGTGGCA CAACATGAaT CGCATTTTCA AAAATTGCAT GTCCTGCTTG ATCAGTCAAA	120
CCGGCAGCAT GATCAAAATG CATATGTGTC ATTAGCACAT AATCAATATC CTTTGGCGTT	180
AAATTATAAT TTGCCAAATC AGCAATTATA TGACTTTCTT CATCTACTCC AAAATTACGT	240
AATTGCTTTT CAGATAATTT ACCATTACCA ATACCTGCATCTATAATCAA ATTATATTGA	300
GCCGTTTGAA TCAAAATTGG ATGTGTCGGT AAATTGATTT GATTTCGTTC ATTTGCATTG	360
TATTGCTTTG ACCACAACGG CTTCGGAACA ACACCAAACA TTGCACCGCC ATCCATTTTTT	420
GTATTGCCAC CATTTAGaTA ATGAATAGaT ATATCCCCGA TTTTCATAAC ATCACCTATT	480
CTTTCTGTAT TCGTTATTAC AATTAGCATG TGTTTATTAC ATCATATCAC TAT	533

(2) INFORMATION FOR SEQ ID NO: 754:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

ATCCCCTGCA AGTGATAAAA TTATTGAAAA AGGCGACATG ATTACATTAG ATTTTGGCGC	60
GTATTATAAC GGCTATTGTT CAGATATTAC TAGAACATTT GCTATTGGAG AACCAGATCC	120
TAAACTGAAA GAnATATATC AnATAGTACT TGAATCTCAA ATGAAAGCAA TTAATGAGAt	180
TAGACCTGGC ATGACTGGTG CAGAAGCTGA TGCCATTTCA AGAAACTATt TAGAGTCAAA	240

AGGGTATGGA AAAGAATTTG GACATTCACT AGGACATGGT ATTGGTTTAG AAATCCATGA	300
AGGGCCAATG CTGGCTCGTA CGATACaAGA TAACTTCaA GTAACAACT GTGTTACAGT	360
AGAACCTGGT GTTTATATAG AAGGTTTGGG CGGTATAAGA ATAGAAGATG ATATTTTAAT	420
TACAGAAAAT GGTTGTCAAG TCTTTACTAA ATGCACAAAA GACCTTATAG TTTTAACATA	480
AGCGTGTAAT ATGAGGAGGA AACTGAATGA TTTCGGTTAA TGATTTTAAA ACAGGTTTAA	540
CAATTTCTGT TGATAACGCT ATTTGGAAAG TTATAGACTT CCAACATGTA AAGCCTGGTA	600
AAGGTTGAGC ATTCGTTCTG TCAAAATTAC GTAATTTAAG AACTGGTGCA ATTCAAGAGA	660
AAACGTTTAG AGCTGGTGAA AAAGTTGAAC CAGCAATGaT TGaAAATCGT cGCATGCAAT	720
ATTTATATGC TGACGGAGAT AATQATGTAT TTATGGATAA TGAAAGCTTT GAACAAACAG	780
AACTTTCAAG TGATTACTTA AAAGAAGAAT TGAATTACTT AAAAGAAGGT ATGGAAGTAC	840
AAATTCAAAC ATACGAAGGT GaAACTATCG GTGTTGAATT ACCTAAAACT GTTGAATTAA	900
CAGTAACTGA AACAGAACCT GGTATTAAAG GTGATACTGC AACTGGTGCCACTaAATCGG	960
CAACTGTTGA AACTGGTTAT ACATTAAATG TACCTTTATT TGTAACGAA GGTGACGTTT	1020
TAATTATCAA CACTGGTGAT GGAAGCTACA TTTCAAGAGG ATAATCTCTA ATTTGTTAAC	1080
AAATAGCTTG TATTCATAT ACTGATTTAA CGTAAGAnAT TCTAAATAAG TCTCATAAAG	1140
CTATTGCCTA AAATGATTAT AGGTTATATG CTGATATGAG GCTTTTTATT TTTAAATAA	1200
TTTTTAAAT ATAAAACGAA TCGTC	1225

(2) INFORMATION FOR SEQ ID NO: 755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:

ACAAACAAAT CACTTAGTTA AAATTGACAG TGCATTATAT TCCGATAAAT TATTCAACAT	60
TGTAGAAAnn AGAATTGATA CACCAGATAT TGGCTATAAT ACAGTGGTTT TATCAGAAAA	120
ATGAGTGTAG AAATTAAAGG GATACCTGAn GTGTTGAATA AATTAGAATC GGTATACGGT	180
AAACAAGCAA TGCAGGCTAA GAGTGATAAA GCTTTAAATG AAGCATCTGA ATTTTTTATA	240
AAGGCTTTAA AGAAAGAGTT CGAGAGCTTT AAAGATACGG GTGCCAGTAT ASAGAAATG	300
ACTAAATCTA AGCCTTATAC AAAAGTTGGT AGTCAAGAAA GGGCTGTTTT AATTGAATGG	360
GTAGGTCCTA TGAATCGCAA AAACATTATT CACTTGAATG AACATGGTTA TACAAGAGAT	420

GGAAAAAAT ATACACCAAG AGGTTTTGGA GTTATTGCAA AAACATTAGC TGCTAGCGAA	480
CGTAAGTATA GAGAAATTAT AAAAAAGGAG TTGGCCAGAT AAATGAATAT ATTAAACACC	540
ATAAAAGGAA TTTTATTATC TGATGCAGAG CTCAAAACAC ATATAAATTC TAGAATATAC	600
TATTACAAAG TCACTGAAAA CGCTGAAACT TCCAAACCCT TTGTTGTTAT TACACCTGTT	660
TATGATTTGC CTTCAGACTT TATGTCTGAT AAAATCTCA GTGAAGAATA CTTAATTCAA	720
ATAGATGTAG AATCTTCAA TAATCAGAAA ACAATTGATA TAACAAAACG AATAAGATAC	780
CTGTTATATC AACAAAATTT AATTCAAGCA TCTAGTCAGT TAGATGCTTA TTTTGAAGAA	840
ACTAAACGTT ATGTGATGTC GAGACGATAT CAAGGCATAC CCAAAAATAT ATATTATAAA	900
AATCAGCGCA TCGAATAGGT GTGCTTTTTA ATTTTAAAG AGGAAATAAG CAATGGCAGA	960
AGGACAAGGT TCTTATAAAG TAGGTTTTAA AAGATTATAC GTTGGAGTTT TTAACCCAGA	1020
AGCAACAAAA GTAGTTAAAC GCATGACATG GGAAGATGAA AAAGGTGGTA CAGTTGACCT	1080
AAATATCACA GGTTTAGCAC CAGATTTAGT AGATATGTTT GCATCTAACA AACGTGTATG	1140
GATGaAAAA CAAGGTAATA ATGAaGTTA AGTCcTGaCA TGaGTaTTTT CaATATTCCa	1200
AGTGaTGaTT TAAaCACaGT TaTTGGaCGT ACTAAAGATA AAAATGGGTA CATCTTGGGT	1260
AGGAG	1265

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

CATATACCCG GGTCCAAGA ATCCTCTATC CATATGGTCC CCCAATTTTG ATTCCACCAT	60
ATTGTTAAAT ATCACTTTCC CAGCCTACTT TTTTATnCAG TTGGGCTCTC TAAATTTGTT	120
TTGAAATCCA GGTGAACAT ATTTCCAGTG TATGACCAAT CGAAACATTT GCACCAATAA	180
GGCCGCCAAT TTTTCCTGTA TCATCACCAG TAACATTACC GTTGAATCCA TAAGTTAAAG	240
TACTCATATA CTCTTTTGTA TCAATCGAAT TTCTTGATA GTAATCAGAT ATTTGAGCTA	300
CTTCATTATC AGGTAGTTGC AACTGTACCT TAAAGGCTGA AGGCCAGGCT AAACCACTTT	360
TGTTAGCACC TTCTTCGCTA TAAACTCTAT ATTGACCAGC AATGGTACCT TTCGTTCTAA	420
TAACTAGCAG TTTTTTATTA TGATTTTTAT CATCGATAAA ACTATAAAAT ACTTTTTTGT	480
GCATGCCATT TTCTTTATCA TAAGTACTA AATCACCTGT TTTTACTGTA GTATTGCTTC	540
CAATATCTGT AGTACCGGTT TTAATATTAA TATCAGAATC TGCGCATTG GCGACAGGAT	600

TCATTAATAT GGAACCTAGC AATAGTGTG TTGTTACTGA GCTGACTATA CGTGTTTTCA	660
TTTTTCATCAT CCTTCTATTT TTTAAAACGA TTTGAGGAAA CAATAATCAA TATGTCAATT	720
TAGAATATTG CAGTTGAGAC ATATCAAATA TTTATAATCG TTTATATTAG TATATTTAAT	780
GTAGCAACTG ATAAATTACT GAGTGATGAT GAGTGATTAT TTTAAGAATA TGTTTTTAAC	840
TTTTATTTAA AATTTGAAAG GAAGCATTTT AATTTTCGAGG GTTAGTCAAA GTTGAATAAA	900
TTCTTTATGA AACAAGGAAA AGACATAGCT AATTTtATTG ATTAATTTCT TTAAAACATA	960
TGATTTGTTT GATTTAATAA TGTAATCGAT TACAATATAA AAATACAAAT ATCTTAGAAT	1020
TAAATCAATT AATTAATAT TAAATAAAAA TTAATATAT ATTAATAGT GTAAATTAAT	1080
AAATAGAAAT AGAGAAAAAG GGTATTAATT A	1111

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

TATCTATTGT ATGTAACAAT AGGTACATAA TATTTTTAGG GTGGGTTAA TGAGCATAAT	60
TACAAGATTG TTTAATAACA GTGATTTTGA AAAATTAAAT CAACTATGTA AATTATATGA	120
TGATCTAGGT TATCCAACAA ATGAGAATGA TTTAAAAAAG AGACTAAAGA AAATAACGAA	180
TCATGATGAT TACTTCCTAC TGCTTTTGAT AAAAGAAAAT AAAATAATTG GTTTAAGTGG	240
TATGTGTAAA ATGATGTTTT ACGAAAwAAA TGCAGAGTAT ATGAGAATCC TTGCGTTTGT	300
TATACATTCT GAATTTAGGA AAAAAGGTTA TGGAAAGAGA TTATTAGCTG ATTCTGAAGA	360
ATTTTCTAAA CGGTTGAATT GTAAAGCmAT AaCACTAAAT AGTGGTAATA GAGATGAnAG	420
ACATCTGCAC ATAAACTATA TAGTGATAnTGGGTATGTTA GCAATA	466

(2) INFORMATION FOR SEQ ID NO: 758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

CGTACAGCAT AACCAAATAC ATATCTGCCA AAATCGCCAT ATGCCCCAGT TCCTCTTCCA	60
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TATTCCGTTG TCATTGAGTT TTTAATTTTA TCGATAGAAA AATGTAAATG GCTATCTAAT	120
TTGTTTTTTA AAGATTTTAT GTAATCtCTA TATTTAAATT CGAATATTCT TTTTATACC	180
AATTACTTTT ATAAGGTGGC CTAATTTTTT CTAAATTTAT ATTAGATATA TCTwTwGATA	240
AACTAATATA TwCAATTGTA TGCCTAGCAT AATCTCTCAT TAAAAATATGA GGATATACCA	300
TTTCTTTATC AAATATtTCT TCATAAATAT AATTAGCAAT CTCTATATGT ATTtCACAAA	360
TGTCGATTCG AAGTGTCGCC CCTAAAACAG rAGCATATAA TC	402

(2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

AAGTTACTCA ACAGCCATTT GACACGTCTC GATTAGAGCG ATTAGGTATA ACCGAGCGCC	60
AAACTAAAGA CATGTATCGT TTATTAGGAC TAGCCAAATA TGAAGATCGA TTTGTTATTC	120
CAACATCACA CAAAGAAACC TATTTAGATA CGTATCACGC ACAAGGTAGT ACAGGATACA	180
ATTACGGCGG CGAGCATTTT GGAGATAACT GTGAAGGCTG TGGCGTTGCA GTAGGTTTACG	240
GGAAAACCTGG TCAAGAAATT TATAATGGAG AATTCTATGG AGGGATTTCG GTGGTTAATT	300
TCGATAATTT AAAAAATATC CAAGAAAGTT TGGGTnnn	338

(2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

CTCTATTATA TTTAGAGTTA TAGCTATTGC aGTTGTTTAT TTATTGAAAA TAAATGTACT	60
ATCATTAGtT TTAGCAAGTG TATTAGGCAG TTTgGTATCt AGGCTACTAT TATCTATTAT	120
TTTAAATTTA CCTGTGTGGG TAGTGTTGTT AAaCGCGATT CCAGGCGTAA TATTCACTTT	180
AATTGTAGcT ATTCCTTTAT ATCTCACATT GAGAAAAAGA ATGGCAGTAT TACTAAGATA	240
ATAAATCAAA ACACGGTCGT CACAATTACT GTTGGCGACC GTGTTTTACT AGCTATTTAT	300
TGTTTTTCACT TTCTTTTGTA TCTAACAATT TCACTTTGTG ATTTTCCCAA TCAATTCAT	360
ATGTTGaTTT AAATGTTCTA GTTTTAAAGT TTTATAAT	399

(2) INFORMATION FOR SEQ ID NO: 761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

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GCATATnCAA AACAAAGCT GCTTTAGGTG CGGGGGCTAT TAGCGTTATT TCTGCACTAA      60 ,
CAGGAGGTTT AGTTGGCGCA GGTGTTGGTG GTTTCCTTGG ATCTATAGCT GCATCGAATA      120
TTGATACTAG TAAGGGAATA TATATAAAAT TAAAACTAA AAAGTATGCA GCCGGGAAT      180
ACGTTCTGAC AGGAGAAAAA TGGGGATATC AGTAAGGGTG ATTTTATGGA TAGATTAAAA      240
TATTTACTTA AAGTTGGAAT TTTAGCATT TATTATTTT GTACTTTAAA TTATTTAGTT      300
CCAATGCAAA GCAATGCTTT TTCAATAATT ATATATTCGG CAATTTTTCG TGTGTTACTT      360
ATGCTTTTAG TTTATATATT TTTAGGAATT TTAAAGAAAT GACATGAAAC AAATTAGCAT      420
TGGCTATGAA GAAATCTATG GGGATAGAAT TTTTCATAGC CATTTTTTAA AAGAGCATGA      480
AGTAAAAAAT TGGAAAACCG TCAATCAAAT AATTGAAAAA GAACACTTGG ACAAAAATGA      540
ATATGnAAGC GGAACCGCCG TTATTTTCT TTTGCAGAT CGTTAGATTA GATTnCGGTT      600
GTATAGTATA ATGAAAAATA TTATAATAAA TTTATAAAA      639
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(2) INFORMATION FOR SEQ ID NO: 762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

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nTGTTGTTG TCTGGATCCA ACGTAAACAG TCGCTTCATC TAATACAATG ATAGGCGCAT      60
CTTTTAATAT CATTCTTGCA ATAGTGACTC GTTGTTTTTC ACCACCAGAC AATTTATCT      120
CCACTGTACC AACATTCGTA TCATATCCAT CTGGCAACTT TTCAATAAAT TCATGACATT      180
GTGCTAACTT GGcAGCTTTT TCAACTGCCT CATCCGTAGC TTCTGGATTG CCAAGTTTAA      240
TATTTTCTTT AAAAGTAAGA TTTAATAAAA AGTTATCTTG TCCAACAAAA CCAACTAAAT      300
CGTTAAGTTG TTTTCATTCA ATATCTTTTA TATTTATACC GCCAATCGTA ATTTACCTG      360
AAGTCACATC CCAGTATCGT GATATAAGCT TGGCAATGGT TGACTTACCG CTACCAGaTG      420
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CCCCGACGAT AGCTGTGAAA TTATTTTCTG GTACTGTAAA TGATAAATGC TTAAAGACCA	480
GATCGTCCTT ATCTTTGTTA TATGAAAATC CAACATTATTAAAAGCAATT TCATAATGTT	540
GAGGCTTCTT AAATTTTGTG GACAATACTA ACTCTTCTAG ACTTAATATT TGATTCACTT	600
CAGTTAATGC GTATTGTATA GACTTTAAAT GATTTACATA ATTAGTAAAA TTCTTAATCG	660
GTGCTACTAC ACCTAAAGAT AATACGATGC ATAGGAAAAA TTCCGCATAG TTTAATTGGT	720
TGATAGATAT CAAATACATG CCGACCGGTA AAATCCCTAA AAATGTTGAA GGTAATACAC	780
TAGCTCCTAA ATTCATATAC CCCCATGTAT TTTTAAACCA ATTCAAAGTG TGAATCTTAT	840
AATTATCTAC TG	852

(2) INFORMATION FOR SEQ ID NO: 763:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

CTCTTCATGC GTCATACGTT GTGTCGATTG ATCAGTTGTT TTGTCTAAAT CACTAGCTTT	60
AAATTTAGAT TGATTTGATT GACGTGTCGT AAATnGTTGT TCCTTTTGTG GCGGTTTGCC	120
TTTTTTTCTT GATCTTATTA AAAATAAATT GATAACCCCA ACAATAATGA GCGCTAAAT	180
AATGTAGCTA ATAATGAAGG TCGTAGTCAT TTAATGACCC CCTAATTTT TATGGATTTT	240
TACTTCAGCG TTCaTTCCaG GAACAACCTG TTTAGACGGT TcTGATTCTA GAGTGATTTT	300
AACAGGTATT ACTTGAGAAA CTTTAGTGTA GTTACCATCA CTATTTGATG ATGGCATTAA	360
TGAAAgtTG CAGCAGTTGC TTTTCCAATA CTATCAACTT TACCTTTAAT AGAAGCTTTT	420
TGACCGTCAA TAGTCACATC AACATCTTTA CCTACTTCAA CATCTTTAAT ATCTTTTTTCG	480
TCAATATTTG CTGTTACATA TAAATCATCT AAATTGTATG CATAAGCGAT TGGGTTACCA	540
GCTTGCACCA TTGAACCTTC CATAACATCT AATTGGCAA TTGTACCTTT TTGAGGCATT	600
TTAAGATCCA TATCTTTCGT TTCGCATCT TGACCTTGTA CAGTAACAAT TGCTACTTTG	660
TCACCTTTAT CGAGTTTGTC ACCTTGTTTA ACATTAAGTG ATTTAATTTG TCCAGATGCA	720
GGACTTGCTA TTTTAATTTG ATCGCCATTT ACTTTTGCAT TATCAGTTGT TACATAGCTT	780
GTTGTTTTAT TCCAAAAATA AAAGCCAGCA ATCCCAATGG CTAACnGTAC ACAACCGTA	840
ATGACATTnA AT	852

(2) INFORMATION FOR SEQ ID NO: 764:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

ACATATTCGA CATTCAATTTT AAATTGCATA TAACTACATT AACCATTCAT TGTGCAGCGC	60
CTGTTGTTTA GATGATCATT TATTGACTTT TTGCTCTTAT nCCAnGCAAT TTTTTGATTT	120
ATTGCTTATA ATACATTTTA AGACAAATGT TTGTTTCAAC ATCGCATGCG ACATCATTA	180
yTATTCATTT AAATTTATCC AGTTTCTATT TGTCTGCAAT TGCTGAAAAT TAAAGGAGCT	240
TATTTTTAAT AATGGAACAA ATTATCACTG AATTTATTAG CCGTTTTGGG TATGCAGCCA	300
TTTTTATATT AATTTkATkA GAAAATGTAC TACCTaTCGT aCCATCGGgA AATTATTCTG	360
ACATTTGCTG GTCTTATGTC TGTTAAATCA CATTTATCAA TTTTAACTTT ATTTATTATT	420
GCAACTATCG CATCGTTTAT AGGGCTGTTA ATTTTATATT ATATCTGCCG TTTGATTTCA	480
GAAGAACGTC TATATCGTTT TATTGATCGA CACGGTAAGT GGATTAAATT GAAAGTAAG	540
GATTTAAAGC GAGCAAATGA TTGGTTTAAA AAGTATGGCG TATGGGCTGT ATtkATCTGT	600
CGTTTCATAC CTGTATTACG TGTAtTGATT ACCATTCCAG CTGGTGkaAA CCGCATGAAT	660
GTTGTGAcAt TtACCgTTAT TTCATTAATA GGTACTACAA TCTGGAATTT CGGTTTAATT	720
TTACTAGGAC GCACTTTGAG CGATAGC	747

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

TTTACCTTTT AACCAATCAT GCATTAATGC AATGTGTACT GTCTTAACAA ATGTTGCATA	60
TtCATCTTCT GCACTCCACT TTTTCAATTC CTGTTGATTA ATGGCATGTT TTTCTCCATT	120
TTCCAACATA TTGACATACA ATTTATAATG TTTTCAACT GCCTGAATAA AAGCGAGTTG	180
ATTTTTATTT AAATGTGATT TTAACCTTTC TAAATCTGAA TTAATAAAGT CTTCTATAGT	240
CGAATAAGAC ATATCTTGGT ATTCAACTAC TGCATTAATT TCATCTAATA ATTGCGATTG	300
TGATTTTAGC GTTATATAAC TCTCGTCTCC ATAAGATATT TCTGTAGTAG CTGCTGTAE	360
AGGATTTGGA GAACTGACTA AAATATGCTC GCCTAATAAT GCATTTATCa AACTACTTTT	420

ACCaGCACTA AAtGTTCCAA ATACACCTAT TTTTATTAAT TTATTATCTA TACGTGTAA	480
TGTTTCGTGG ATATCTTGCT TTGTACGCTT GAACAAAGGC ACATCCGAAA TTATATCAAG	540
CGCTTTTTGA ATATCIATAG ACATATTTGT TG TAGCTGTA TTTTGATTTA GCTGCTGATT	600
ATCACGATTA TCCTGAGCAT TATCAGTAGC CACTTGATAT GTTGTCTCTT GTCGACCTAT	660
TAATTTATCT AGAGATTCAT CTAAATGAAT ATAGTAGTGA CGATAATTCT TAGTCGTCAA	720
TGACTGACGC AGCTCATTTA ATTCTGTATA ACGTTGATATTCTTTTAAAT CATCACTTTC	780
TTCTGTTGGn AATTCATCTG CCTGCACATT TTCTATnATT	820

(2) INFORMATION FOR SEQ ID NO: 766:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 672 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

TCAACATGAC ATTAATTTAA TAGCGATGCA TACAAATTTA GATGTAAATC CGTATGGTGT	60
CAATATGATG TTGGCGAAGG CGATGGGTTT GAAGAACATT TCAATAATAA ATAATCAACA	120
AGATGTATAC TATAAAGTTC AAACATATAT ACCTAAGGAT AATGTTGGAC CATTTAAAGA	180
TAA GCTTAGT GAAAATGGAT TAGCGCAAGA AGGTAATTAT GAATATTGTT TCTTTGAAAG	240
TGAAGGAAGA GGGCAATTCA AACCAGTTGG TGAAGCTAAT CCAACAATAG GACAAATTGA	300
TAAAATTGAA TATGTAGATG AAGTTAAAAT TGAATTTATG ATAGATGCAT ATCAAAAGTC	360
AAGGGcTGAG CaATTAATTA AACAATACCA TCCATATGAA ACACCGGTAT TTGATTTTAT	420
TGAGATAAAA CAAACATCCC TTTATGGACT TGGCGTTATG GCAGAAGTGG ATAATCAAT	480
GACATTGGAA GATTTCGCAG CTGATATTAA ATCTAAATTA AATcCCCAA GTGTCCGTTT	540
TGTTGGTGak TCTAATCAGA AAATTAAACG TATTGcAATT ATTGGTgGTT CAGGTATTGG	600
ATATGAakAT CAAGcGTCC AACAAGGcGC AGATGTCTgT TACGGTGATA TTAAACATCA	660
GATGCCTAGA TG	672

(2) INFORMATION FOR SEQ ID NO: 767:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767:

GAAAAAGTTA AACCTACTGT AACTACAACA AGcmAAGTTG AAGACmATCa CTCTACTAAA	60
GTTGTmAGTA CTGaCACAAC AAAAGATCAA ACTAAACaC AAAGTCTCA TACAGTTAAA	120
ACAGCACAAA CTGCTCAAGA ACAAATAAA GTTCAAACAC CTGTTAAAGA TGTTGCAACA	180
GCGAAATCTG AAAGCAACAA TGAAGCTGTA AGTGATAATA AATCACAACA AACTAACAAA	240
GTTACAAAAC ATAACGAAAC GCCTAAACAA GCATCTAAAG CTAAAGAATT ACCAAAACT	300
GGTTTAACTT CAGTTGATAA CTTTATTAGC AcAGTtGCcT TCGCAACACT TGCCCTTTTA	360
GGTTCATTAT CTTTATTACT TTTCAAAAGg AAGaaTCTAA ATA	403

(2) INFORMATION FOR SEQ ID NO: 768:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

TTCAATGCTC GTTTTGCTTG CGTTAGTAAT TTCTAACATA TTCATTCACA TTTTGGAGCC	60
TAAACTATCA ATCACCCTC AAATCATCAT CGTTTTGATT TTAATTGAAG CACTAATTGG	120
ACTGCGTTTC TTGAAAGCGT ACGATGTAA GCGTGGCAA GATAAAGAAA ATAAGAAAAA	180
TAGTAAGGAT TTCGTAAAC TAAAATCAAT TTTAGTAGCA ATTTTATTTA CATCATTTGGC	240
GCTGACAGCA GGTACTGTAG CTGATATATA CGGTTTCACT GACTTAGGAA ATACTAGAAG	300
TGATTTAATC GTTTGGAGCA TAGGTGGTAT TATATTGGC CTCGTATGTT ACACAATGGA	360
AGATAAAAGA TAACGATAAG GAGCTGCGA TTATAAAGCT AGCTCCTTTT TTAACCTaTA	420
TATGTAAAGA aCTaTCCTAA GGGkTTTTAA TCATATGTCA ATAATTTCTA TAATACATTA	480
TTA	483

(2) INFORMATION FOR SEQ ID NO: 769:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

ATTATATGTC TGATGTATTT CATGTCGTTA AAAATAAAGG TACGGAAET TTAAAGAAG	60
ATGCCATTCA AAGATTTGTG AAACATGATT ATAAAGTAAC GAGCAAAGCA AATCGCATGG	120

GGATGATGCT TGAAGGTGAA AAAATCAAAG CTTTTTATGA AGATATGCCA CCGTATCAGA	180
CTGTCAAAAA AGGAACGATA CAAATTAAGC GTGATGGCAC ACCTATTATC CTATTAAATG	240
TCATTATACG CTnGTAGCTA CCCGCAAATC GGTACAATCG CAGTTATCAT TTACGAATTA	300
GCACAAAACC GCAGGATCAC GTTGAATTCC ATTATAGTAT TTACGGCTGA AGACTGTAAG	360
nTAnACTGGT AACCATATCA TGGATGATTG ATCATAGATG	400

(2) INFORMATION FOR SEQ ID NO: 770:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

ATCTCTTCTA CTTCTTTTAC AAATTAGAA CGTCTTAAAA TGGCTTTCAC ACGGGCAACA	60
ACTTCTCTAG GTkAAAAAGG CTTAGTCATA TAGTCATCGG CACCTAATTC TAAACCTAAT	120
ACCCGATCAA ATTCATCATT TTTCGCCGTT AACATTAATA TAGGGACTAA ATTTTTATTT	180
GTTCTTACAG TCTTACATAC GTCAATGCCA TCTTTTTTTAG GTAGCATAAC ACTAAAATA	240
ATTAAATCTG GCTGTTCACT TTCTACCTTT TCTAAAGCCT CATCACCATC AAATGCGACA	300
ACAACCTTCaT AACCAGCTGk TTCTArGyTA TATTTAAGTA ATGgTTaCGa TTGaATGtTC	360
GTCATCTACT wCCaACACTT TTTGCGACAT GgAtGCCTC CTAACttAk AATTATATTT	420
cATTATAACC GAACTATTTA TAAAAATAmC ATCCTACACA TTATCTTTAC ACATTTTTTTA	480
CATTACTTTA CATATAAATA AAATACTTCT TATATTTTCCT TCTmTCATTT GCATGACTTA	540
CTCTGGGACA ACGAAATAAA TTTTGTAATA ATAGCATTTT TATCCCACTA CCTATGCATG	600
AGTTTTACTC ATTTATTCCT AAGCTTATGT ACtATTTCGC TTTGTCTAAT GTGTAAGAAA	660
CACTACATAA TCAATCATTG GTGACTCTTT ATTATTTCTA TCCTGTTGCC AaCTTCAATT	720
CATTTAAAAA GGCGAACCTA GCAATTAAAG	750

(2) INFORMATION FOR SEQ ID NO: 771:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771:

ATTTAATTAT TATTTTTCCA AATCAATACG ATATAATTTT ATGTTTTTAT CTTTGGTG	60
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TGaGGCAAAT TGATAAGtCG TTTTGCCTTT TTCAATATAT CCAAAATTAC CAGCAACTTT	120
GCTATATTCC GTATGTGTTA CTGCTTTGCC AACATAATTT TTAACAGCTT GATATGTTGG	180
ACCATTAGCA TCATTATACA TCATTGAAAT ATGAGTTACT TTACCATTGT TTTTCTTACC	240
ATCAGTAGTT ACTAATAACA TACCTTTTTT AGTATGGAAT TCGTAATAAT GTTCAGTTCC	300
ATCTTCATTG TAAGAATACA TCGGATTTTT GTACTTAGTT AAAACATCTT TAATAGATTC	360
GCCAATTTTC ACATTTTCTA ATGACTGATC ACCCTTAATT AATTGTTTAA CAGTATCAAT	420
AGAGTTGCCA CTTGCTGCTT CGGCACTAGT GTTCAATAAG CCTACTCCCA TTACAACAGA	480
ACATGCAATT ATACTTGCCG TTAGTAGCTT TTTCATAAGC ACTCTCTCCT TTTATTTATA	540
TCGTCTTG TG CTCACAACCA TTATACAACA ATCATTTCTA AAACAACAGT CATATTACAA	600
TTATATTACA AATAATAATT ACTACTTTTA TATTTCACTT ATCACTAAAA ATTAAACATG	660
CTTTTCATCG TGATGTTTGT TGATAAATGC AGCTGTATCT TCGACGAATC TTTCTTGCTC	720
TTcAACAAAT GGGAAATGCAC TTGATTCTTG ATATACTTCA AAGTCCGCAT TTTGGATTAA	780
ATCAGCTACT TCTTTAGCTT CTAATCTTGT TGTTCTTTCA CCGAATTCTC CTGCAATAAT	840
TTTTGTGCGT ACTACGACAT TTCTATAAGT TTGAGAAATA TCAGCGTTTT TGAATACCTC	900
TTTAACTGCT TGAATTTCTT CTTTAGTTGA TATTTCACTT GTATCTACGA CATGTTTGAG	960
GAATCGATTC ATTTTTCTCG GACGATAATA CTTACGCTTA TTTAAAAATT TAwCyTGtTT	1020
TTCaGGATCC CaGTTtCGAA TAATATGGGC ATaTTTTCTA AAaAACGTT CTTCCGGTAA	1080
TTCACCTTCA ATAGATGTTG GATTTACCAA CGTAAGTGAT GATGTAAATT CAGGATAACG	1140
TACTGAAATA TCCGCACCAA TGATTCCACC CATTkCATGG cATACAAATG CAACTTCTTC	1200
AATATATAAAA TATTTAAGTA ATTCAACAAT GTCATCAGAA AAATCTTTTA TTTCAATGTG	1260
ACGAGGTTTA TCAGAATAGC CATGTCCACG TAAATCAATT AACACAACCTT GAAATGATTT	1320
TGCTAATTCT GCTGCTAATT TATTAAACAC AGAATAATTA TCAAGTACAG TATGAATCAA	1380
TACGATAGGA TAGCCTTCAC CTAAngTACT GTAATGTATC GATGTTCCAT CTTTTCTAGT	1440
AAATAGATCC ATAATTTTCT CC	1462

(2) INFORMATION FOR SEQ ID NO: 772:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 704 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

ATTATTATAA GGAGTTATCT TACATGTTAA ATCTTGAAAA CAAAACATAT GTCATCATGG	60
GAATCGCTAA TAAGCGTAGT ATTGCTTTTG GTGTCGCTAA AGTTTTAGAT CAATTmGGTG	120
CTAAATTAGT ATTTACTTAC CGTAAAGAAC GTAGCCGTAA AGAGCTEAA AAATTATTAG	180
AACAATTAAA TCAACCAGAA GCGCACTTAT ATCAAATTGA TGTTCAAAGC GATGAAGAGG	240
TTATTAATGG TTTTGAGCAA ATTGGTAAAG ATGTTGGCAA TATTGATGGT GTATATCATT	300
CAATCGCATT TGCTAATATG GAAGACTTAC GCGGACGCTT TTCTGAAACT TCACGTGAAG	360
GCTTCTTGTT AGCTCAAGAC ATTAGTTCTT ACTCATTAAC AATTGTGGCT CATGAAGCTA	420
AAAAATTAAT GCCAGAAGGT GGTAGCATTG TTGCAACAAC ATATTTAGGT GGCGAATTCTG	480
CAGTTCAAAA CTATAATGTG ATGGGTGTTG CTAAAGCGAG CTTAGAAGCA AATGTTAAAT	540
ATTTAGCATT AGACTTAGGT CCAGATAAA TTCGCGTTAA TGCAATTTCA GCTAGTCCAA	600
TCCGTACATT AAGTGCAAAA GGTGTGGGTG GTTTCAATAC AATTCTTAAA AGAAATCGAA	660
GAGCGTGCAC CTTTTAAAC CGTAATGTTG ATCCAGTAGA AGTA	704

(2) INFORMATION FOR SEQ ID NO: 773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

GACCACGACA CCACAAGCTA TGAAGAATGC CyTTGTTAAG CCGCcTTTGaATtGCATAGA	60
GATGAAAATA CCAATATTAA TAAAGAAGTT ACAGAAAATA CCTTTTGTAA AAATATTCAA	120
CCATGTTGAA TCAACAGTCT TTTTCTGAAC TAAAGCTGTT AAAGCTTGTT TCATTTCAGG	180
TGTCATGACA TGCGCAAATT TCATTAAGAA AAATAACACA AACCCACCTA AAATATTTCC	240
TAAGAAACAA TATAATAAAA TCCAAGTCAT CTTCTTAACA GAAACGACTT TATAATACCA	300
GCCTACTGTA AAGTACATGA AGTTACTTGT TAATAATTCA GAGTTAGTTA ATACAACTAA	360
AATCAAACCT AAATAAACG CAATGGCTCC CATTAAATTG ATAAGTCCAT CTACGTGAGT	420
ACTCGCA	427

(2) INFORMATION FOR SEQ ID NO: 774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

AGGTGAGCAT TATTAAATAT TGCCAAGAAA TCAAACTAA AAACATGCA AAAGATGTAG	60
ATATATTATT TATTCTTGCC GGTGATGGCA CGGTTAACGA ACTTATAAAC GGTGTTATGA	120
CACATGACCT TCAACTCCCT ATTGGCATT TACCAGGCGG TACTTTTAAT GATTTACAA	180
AAACGCTAAA TATAGCACCT GAATCATAAA CAAGCTAGTG AACAAATGGA TTTCTGCACA	240
AGTTGGTACA TACGATGTAA TTGAAAATGA AATGAATCAA TATGCACTCA ACTTTGTGGG	300
CTTAGGTCTC ATGTTCAAAA CGCGGAAAAC GTACAAGAGG TTCAAAAAGAT GTATTGGGTA	360
AATGGAGTTA TATTGGGTCC ACCGTCCAAA ACnCGGCnAA	400

(2) INFORMATION FOR SEQ ID NO: 775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

AATTATTCCT CAATAGGAGC ATTACCCGCT CTCTCACCAA TTCCCCAAAA TGTAGTTTCT	60
ATTTGCTTTG CACCATT TAA AATTGCAGCT AATGTATTTG CAGTAGCCAA CCCTAGATCG	120
TTATGACAAT GAGCAGAAAa AATTATGT TA GATATTTTT TTACAAAGTA ATTAAAAATA	180
TCTCCGTATT CTAATGGTGT CGAACATCCT ACAGTGTCG CAAATGTAAC TGTTCTAACT	240
TGATATTTTG AAATAATTC CATGTATTCT TTCAATTTTT CTCTAGAAGT CCTTGTTCCA	300
TCTTCAAAAC AAATATCTAC TCCTTTTTTA TCTTTCTTTA ATATATCCAA GCAGTCTTG	360
ATTTTCTGAA TATAATATTT ATTTGAAAAA TTAAGCTTTT CTTTTATATG CAAGTCAGAT	420
ATTGGCAATA GTATTTtTAC CACTAAATTA TGAATTTtCA ATtTGACTAT TTTTgGTATG	480
TCnT	484

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

CGCAAGATGA AGTTAAAGAA CTTAATCGCT TATTAGGTAA AGTCATTCAT GCATTTGATG	60
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AAACAAAGGA AAAATAATTA ACTTTTGTCA TGACAATTAA AGTAATGTTT AGAATTTATT	120
AAGAATAGAA AAACAATTAG CACGCGTAAC TTGTTAGTnA AAAAAGTCT TGAAAGGTTT	180
CTTAGCCTAT CAAGCAGTTT TTTTATGCAT TATATBAAT CATATTCCAT AAAGCACCTT	240
GATTAGCTAG TAATTGTTGA TAGTTTCCCT TTTCAACTAT TTTACCATTT ATCATCACAA	300
TGATGGTCTC AAAACGTGAC AATAAAGTTA AATCGTGTGT AGCAACAATT AATGTTTCTG	360
CATGTGCTTC AATTAAATCC ATAACCTTTA AACTATTTTG TTTATCTAAT GCAGTTGTTG	420
GTTTCATCTAA AATCCATGTT GATGCAGTAT CTTTTAATAA CATCCTCGTA ATCGCTAAAC	480
GCTGAATTTT TCCGCCAGAT AATGTATGAC CATCTAAGTC AATTTGACGT tCTAGTGCCA	540
AATGTTCTAA ATCTAATTGC TTAAATATTG CTTGCACCGC TTCATCTTTT TCATCGGTAA	600
ATAAATTTTG ACGTATTGTA CCATCAAATA ATTGTTGAGA TTGTAGCAAG ACATTTAACG	660
ATTCAAACTT ATCTTTGTcA TCTATTTCAA ACATATCCAT ATTTTCGAAA CGAACAGAGC	720
CACTATCTAA TTGATATAAC CCTGCCATAA TTTGTAGTAA TGTACTTTTT CCTGAACCAG	780
AAGGACCC	788

(2) INFORMATION FOR SEQ ID NO: 777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

TTACAAAAGA AATGCAACAA AATTTTTGAA TCATTACATT TTTTATAAA AATTTCACTT	60
TAGATTACACA ATAATTACTT ATTTTGTCAA TTTATTTAAT GTCAATATGT TGATTAATTA	120
ATAGTGTTGT CTAATGTATA TAATATTTAG GTCATCGTTA TAGTCAACAA TAATAAGGTA	180
TTTCGAGTTG AAATTTATCT TATTATTTTT CCACTTTTAC GTGCTATCCC ATTACACAAA	240
AACAAATAAG TAAAGATATT AAGTACAAAA AAGTGGAACA CCTTGTAGAT GCTCCACCTC	300
AATTATATTA AGTTATATTA TTTTGCTGCT TGGTATAATT CATCAACTTT TTTCCAGTTA	360
ACAATGTTCC AAAATGCAGT CATATAGTCT GGACGTTTAT TTTGATATTT CAGATAGTAG	420
GCATGCTCCC AAACATCAAA TAGTAAGATT GGTGTTTTGC CTTCTGTTAA TGGATTATCT	480
TGGTTTGGCG TTGTCACAAT TTCTAATTTG CCATCATTAA CAACTAACCA AGTCCAACCT	540
GATCCAAATA ATGTTGTTGC TTTATTTGCA AATTCATTTT TAAATCATC TAAAGTGCCC	600
CACTGCGcTT TGATGTCATC TATTACGCCA CCTTTTTCTT CAGAATTAGG TGATAGTATT	660
TCCCAGAATA ATGAATGGTT AAAATGACCA CCGCCATTAT TACGGACTGA CATCCTCATC	720

GCTTCCGGTA CCTTGTCTAA GTnAGCAATC ATATCCGCTA GTGATTGATG CTCTAACTCT	780
GTTCCCTTCAA CTGTTGCGTT TAATTTTCGTC ACGTACGTAT TGTGATGTTT GTCGTGATGA	840
AACTCCATTG TTCTTTGATC TATATATGGT TCCAATGCAT CATATGCATA TGGTAAATTT	900
GGTAATTTAA ATGCCATAAG TATATTCCTC CTTTTATGAA TATACTTTTA TAATAATTAA	960
TTTTGGGTGT GTTTTGCAAT AATTATTAT TATTTGTTAT ATCCAATTAT ATAAAATTTA	1020
AATATTCGAA ATTGATATAA TATTTAATAT TGAATGCAAA AAGGCATTTA ACTGCTTTTG	1080
TTTCCCGCTT TTAAAGAGAA TTAAAAAGA CAACTTCCAT TTTTCAATAA GAAATTGCCT	1140
TTTCT	1145

(2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 902 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

AAAAGAGGnC CAATATTATC AATATACGGC CGGAAGATTC CCTTTTTCTT CTCCACTTAC	60
TAAGCCCATC AATGGTGTAT GTTATCaATT GGTGCTATCC GCATTAAATA ATTATCTTCA	120
ATTGTGGTAT CAAAGCTATT CGCTTTTTCT CCAATAATGT CTTTACCATA TTTATTGAAT	180
GCACCTACTA AAATCAACAT AAATGGAATT AACAAGGTTA CTACAATTGC CATTCTTATA	240
AATTGTGGTA TATAAGAAGG TCGCCAATTT AAAGCTTTAA TACCTTCTTw TCTAAATGGA	300
GTTTCTATAA AGCGATATGA TAGCTCTGCA AATATAATTG TTAAACTTAT ATCTATAAAG	360
TACACATATA CAGGTATCTG TCCGTCTACA AGTAACTAT GTACGAAACT AATTACTGCA	420
AAATGCCATA AATATAAACT ATAAGACCTT TTCCCGATAA ATACTAACAC TGGATTTGAA	480
AATATCTTCG CtATCCATGT AGATGGATGA ACGACACTAG CAATAATAAA TAACGTTAAT	540
ATGGATATTA AATAGAAACC ACCATCATAT ATCCAATTCTG TCTCATCATT AATAATGAA	600
AATAATAATA TAAGTACTAT AAATGATAAA CTACCTATGC TATCAATAAC ATATTTTACA	660
ACTTTAGGTG GATCATTTTT CAATTTAAAC GGTGGCCATA AAAAAGCTAA AATAACACCC	720
AGTAACAATG TCTGTAATCT AGTATCTGTA CCAAATACA CTCGTGaATG ATCCCCATTA	780
ATACTATAGA TAAACATCAT TAACCCTAAA GAAATTATTG ATACTCCCCA AAAAATAAAT	840
CCTATTTTGT ATCGCTTTTT AATTGTAAAC AATAATGTAA CCAAATAAC TGGGAAAAAT	900
AT	902

(2) INFORMATION FOR SEQ ID NO: 779:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

GGAATTAGTT TCCTAATGAT CAAACCATAA CCATAGCTT TTAATGATGT TACGCCTTTA	60
AAGATTAGAG GATGATGACT AATAATAGTA TTATAACCTT TTTCGATTGC TTCATTTACT	120
ACTTCCAACG TACAGTCTAA TGCTGTTAAA ACACCAGTAA CTTCAACATC TTCATCACCT	180
ATTAACAATC CTACATTATC CCAAGATTCA GCAGTACTAA ATGGCACATG ATGATCTAAC	240
AATGTCATTA AATCAGCTAT TTTCATaCTA TAACACCCTT TCAATTACaG CAATTTTCGTC	300
aTTAATTTGa GCTAAAcGTT GakGakGTTG TTCAGTawTG AGtTTCGaTT TAAtATGATA	360
AAgTGCyTCt AACTCtCTTT GcCATTTtTT TATAAAATAT	400

(2) INFORMATION FOR SEQ ID NO: 780:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

GTTCTGTTT TAACATCAAT ATCTATCTTT TTAATATCTT GAACATAAAG CAGATTCAGT	60
TGGCTAATAT TTGAATTTAT GTTAATCACT TTTTTCGTTT CATTTTTAAA ATGTACTGTG	120
TAAGTnGCTT TTTTTCGATA TTTTAATTCA CGTTCCTCGA TACCTCTATC ATGCTTCAAT	180
ACTGaTTTAA CTTTTTTAGA GATATCTTTG TAGCCTACÆ GTGGGTCACC TGTAATTTT	240
AAATCTGaTA AAATTGGTGT TGATGTGCCA TTTACTGCAA TTGTGTATGG TACATATCTG	300
TCTGCTTTTCG CTTTAGTTCC TGTTTTAACA GTAATTTCAA TTCTCTTAAC ATCTTTTCGA	360
TGAACTAAGT TTGCTGTGTA ATTTTTTGAA TTCAACTGTA AGATTCTTTT ACCACCATTT	420
TTAAAATAAA CAGTATAATA AGCTTTCTTA GCATATTTTA AATCTTGTTT ACTAATACCT	480
CTATCATGCT TCAGTACTGA TTTTATTTGA CTAGTTAAAT TTTTGTAATT TGTCCAAGGT	540
TTATnTGAAA ATGAAAG	557

(2) INFORMATION FOR SEQ ID NO: 781:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

TTCTGATAAC ACAACTTTCT TGGACCAAGT GACAATGGTA AAGTTGATAT TCTCAAAAAA	60
TATATTTTAT TGAAAAGGTA ACTATATCGA CCGCTCTGTG CGACTTGCTG TGTAGAAACA	120
TCAAGCCCAG CTTGAAACTT CATATAAACT AATAACTTTT GATAAATGCT ATTCCCAATT	180
TGTTCATACT GCTCCAAGTT ATCATTAATT CTAAATTTAA TETTACTTC ATTTTAACT	240
GGAATAAAAT GTACATCACT CGCTTTCATT TCTATCGCTT TATTAATTAT TTCTTGAAAT	300
AGAATCTTCA AAAAAACACC TCCTACATAT AATCACGTAG GAGGTGTTTT TATTACTTCA	360
ATTTAACCGT GTAAAAATGG ATTTAATTGT TCATCATCAA CCGTCGTATA TGGACCATGT	420
CCAGGGAATA AAGGTAAATC GCCTTCTAAT TCAAATATTT TATCTTGAAT AGAAT	475

(2) INFORMATION FOR SEQ ID NO: 782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

ATGAATATCG GTGCAGGACG TATCGTTTAT CAAAGTTTAA CTCGAATCAA TAAATCAATT	60
GAAGACGGTG ATTTCTTTGA AAATGATGTT TTAAATAATG CAATTGCACA CGTGAATTCA	120
CATGATTCAG CGTTACACAT CTTTGGTTTA TTGTCTGACG GTGGTGTACA CAGTCATTAC	180
AAACATTTAT TTGCTTTGTT AGAACTTGCT AAAAAACAAG GnGTTGAAAA AGTTTACGTA	240
CACGCATTTT TAGATGGCCG TGACGTAGAT CAAAATCCG CTTTGAAATA CATCGAAGAG	300
ACTGAAGCTA AATCCATGAA TnAGGGCATn GGCCATTTGC ACCGGGCCT GGCCGTAATA	360
AGCCAAAnGGA CCGGGCCAAC CGTTGGGACC GGGAAGAAAA	400

(2) INFORMATION FOR SEQ ID NO: 783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

GATTAATGTA CTCGTGTACA TAACGTTTGA AGTATGATAA ATAGATATAG AAATAAAGTC	60
ATATGTGACA TCAATTAAAT GATGTTCAAA TGACAAGATA CAATAGAGGA ATGTTTGTAA	120
TAnAAACGCT TCATATAAAG GTCGAGTCAA TATATGATAC GACTTTATAT GAAGCGTTTT	180
ATTTGCTATG AGCTAGTATA TTTTATAATA ATTTTCTAT TTCTCTTTCG ATTTGAACAG	240
GTTTTTTTTG AGGTGCAAAT CGTTTAACAA CGTTACCyTC GCGATCCACT AAAAAGTTAG	300
TGAAATTCCA TTTGATTTTC TCATAAAGA ATCCGTGTTG TGCCGCAGTC AAATATCTAA	360
ATAAAGGTAA TTGATGTTCC CCTTTTACGT CTATTTTTTG ATGCATAGGG AAGGTAACAC	420
CATAGTTTAA TTTACAGTTT TGAGCTGCTT CTTCGCCTGA ACCAGGTTCT TGGCCACCAA	480
ATTGATTACA AGGGAAACCT AGAATTACAA ACCCTTGATC TTTGTATTTCTCGTATAATG	540
ATTGCAAACC TTCAAATTGT GAAGTAAAGC CACATTCGCT AGCTGTATTA ACAATTAGCA	600
TAACGTCACC CTTATATGCA TCTAATTTGT AAGTAACACC TTTATTTGTT TCTACTACAA	660
AATCATAAAT TGTCTCCATT GTATCATCCT TTCGATTTAC TTAAaATGTA CCACAAAATC	720
GTGTAAAtAGT CTkTACTArA ACTCTATGAT AGAATACTTT GAGTAGGATT TTATTAAGGA	780
GATGTATAAC ATGGnTCAGC AACAAATTCA	810

(2) INFORMATION FOR SEQ ID NO: 784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

AAATTCATTG CAGAAAACAT AGATAAATAA ACAAATTGAC TTAAACGAG CGTTGCAACA	60
TATCTCGAAT TGTAAGGAG CTTGAAATG AATAAAAATA TAGTCATTAA AAGCATGGCA	120
GCATTAGCCA TTCTAACCTC AGTAACTGGA ATAAATGCTG CAGTCGTTGA AGAGACACAA	180
CAAATAGCAA ATGCAGAGAA GAATGTTACG CAAGTTAAAG ATACAAATAT TTTTCCATAT	240
AATGGCGTCG TTTCATTTAA AGATGCGACA GGTTTTGTA TTTGGAAAAA TAAATTATC	300
ACCAATAAAC ATGTATCAAA AGATTATAAA GTTGGCGATA GAATTACTGC CCATCCAAAC	360
GGTGACAAAG GAAATGGTGG TATATATAAA ATTAAAAGCA TTTCTGATTA TCCGGGTGAT	420
GAAGACATCT CTGTCATGAA TATTGAAGAA CAAGCAGTCG AACGTGGACC AAAAGGCTTT	480
AATTTTAATG AAAATGTCCA AGCATTCAAT TTTGCGAAAG ATGCTAAAGT TGATGACAAA	540
ATTAAAGTTA TTGGTTACCC ATTACCTGCT CAAAATAGTT TTAAACAGTT TGAATCTACA	600

GGAACATAAA AAAGAATsAA AGACAATATT TTAAATTTTG GATGCCATAC ATTGGAACCC	660
GGGGAATTCA GGGATCACCA GTTCTAAATT CTAAaATGA GGTCATAGGT GTGGTGGTAT	720
GGGCGGGTAT TGGGAAAAAT TGGGTTCTGG AATAATAATG GGTGGCCGTA TACTTTACGC	780
CTCCAnAT	788

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1023 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

CAATATTTTAA GAAACAaTAA TTAACCTGCG ATGAACAAAC TATTAACAAT AATCTTAGT	60
ATTATATTTA TCTTAATTAA TAATATATTT ATTTAAGATT ATGTTACTTC CAACTTTCAA	120
AGTAGAAAAA CGGTATAATT TGTTGATGGG TGTTTATTGA TAAACTGCAA AAAATACAGC	180
CTACAACCAC ATAGATTGTA GACTATATTT AAAATAATAG GTATTTATCA TATCTCGTAA	240
ACTTAGTGCC AATTTTTATA CTCGTGGTGC TGGTAAGCTA CCCTTAAATT CAGGAACGTA	300
GTGTGTaGGG CTATAACTTG GAACAGCATA TTGATAATTT ACATTTTGA TATTTAATGA	360
TGGTTTCCCA ATTTTATAAC CATTTGATTG TGAAAATGAG AAATAkTTCT TCACACCTTT	420
AACTACTTTA TAAGAATAGA AGTATTTATA GTCATATCT TTATTTACTT TAGCATTTTG	480
ATGTGTTGCT GTTGTGTTAT TTTGGAAACT TGGTACATGC ATACGATGTG AATTGTGACC	540
ATATGGTGGA ATTACCTTGA AACTATTTAT TTGTGGCACA ACACAAAAGT GATTAATTTT	600
AATGCTAGCA TGCCCTGGTG TAACAAATTT ATGCGCGTGA TATCCAGGAA CTGCAAAATG	660
ATGCTTGATA ATTAAAGATT gAGATGGATG TGTATATCTA GGCGATTCTG ATGGTTTAAC	720
AATAAAGTGT TTATTAATAG AATCCTTTGC ATGATTTACA TGTTTATGTA CATGTGTTGA	780
TTTGTATGAA GTAATAACTT TCTTGTAGTG GGTTCGTA GTAATGAAGT GGTGGTTTAC	840
TTTGTTTTGC GTAATAAATC TATTTACTTC TGGGCCTTTA GCAACAAAAT GCTTATCAAC	900
TTGTTGTGAA GCTGGATTGT TTGTTGCTAC ATTCACGCGA TTATTGATTT CTTTGTACTC	960
TGGCACAATG TTTCTAACT TTGATTCTGG nACGACAAAG TTTTATCTA CAATTTTACT	1020
AGC	1023

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

TCAAGTTTAT TCGCTTGTTG GAAAGCTTTA ACTTGATTTT CTAAAGCTTT ATCAAATTGC	60
GTTGATTCAT TATCAACTTT ATAACCTAAA GCTGATAAAC CAATTTTAAT AGTTTTAATA	120
TTTTTATCAT CGTCTCCAAC TTTAAATGTT TTCGTATTAG GAATGACATT TAAAGATTGA	180
TATTTAGGTG TGTCAATAGT AACGTCTGGT TTAATGCCTT TACCGTGAAT ATAATGACCA	240
TCTGGCGTTA ACCATTTTAT TTCAGTATAT TTTAACAATG AACCATCCTT AAACCTCTCTT	300
GTAGTTTGTA CGACACCTTT GCCGAATGTT TTTGACCCAT AAACCTTAGC TTTATTATAG	360
TCTTTTAGCG CACCAGTAAA CACTTCAGAA GCGCTAGcTG AACCTTCATT CACTAAGATG	420
GATATATCCA TGTCTTTCGC TTCTTTTAAC GCATCATTAG AAGTtGAATT GCTCAGTACT	480
TTACCTT	487

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

GnAAACnATA TTTAnAATTA AGTGTTTCGAT TTGCAGTAAA TTCAACAGAA AAAGCTAAAA	60
TTAAAATGAT ACaGTGGAAT AATGTCACAT TCTCCATAAA TAATTGACCG AAGAAGCATA	120
AAACATAGAA TAGTACAGTA AACTTACCG GCTGCTTTTC TTTATATATA ATTGCATTAA	180
TACAATAATA AATAATAAAG AGTGAAATTA GTGTTGATGT CGCATAATTA TAAATCCTG	240
CAAACCAGCC ATATGTATCT GCATAAATAG CACTTGGTAA AATTAACATT AAAGAAAATG	300
CTAACAAATA ATAGCTTGTC CACGCTTTAC AACGTGTAAT GTGCATAATC ATCCAAATGA	360
TGCCCATACT AATGAGGCCA TATGAAAGCC AACGTAACCA GCTTACATGT ACAGCTATAA	420
TTTCAAAGAT ATTTCCGATA TAGCGACAT TAAGTGATGC AAATCCTACT TTTAAAATAT	480
CAGTATTATA ATTGCTAAAC CATTGTAAAT CATCGTGCAT GAGTGGTAGT AAGATACCCA	540
TAAAAGTATA AAACAATAAT ATCGCAATTA ATATCAAAGT TGTCTTGTGT AATTGAATTG	600
TTTTCACTTT GCTAATCCTC AAATCTAGTT AAATTTTCCT CAACCTGTAG GTGAAAAAT	660
TAATTCAATA TTTTAAATGT ATTTCTAATT TTCACCTATG CATGTTTCCT CAATCAAATT	720

AGATAAACAA GGTATTTAAT ATTACTTTCA ACAATTTATC TAAATCGCCC CTCGTCTTTT 780
TCTATGaCGA ATGATTACAC TTG 803

(2) INFORMATION FOR SEQ ID NO: 788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

GAAAAGTTGT ATTATGAATA AAGTTAATCA AGGTGCTCAG GAAGAGGCAA TGGAAGAGTT 60
ATTAGTGACT TTTCAAAAAT TGATTAAAGA CTAAAGGAGT TTAAGATGAT ACATCAAAAT 120
ACGATTTACA CAGCGGGAAT TGAAACAGAA GAACAAGTAA GTCAATTGAC AGAACGCATT 180
TCAAATATGA TAGGTGTTCA TCAAGTGAATATTAATATAA TAGATGGTCA AGTAACTGTA 240
TCGTATGAGA CACCAGCAA TTTGAATAGT ATTGAAAAAG AAATCTATGA TGAAGGATAC 300
AAAATTGTAT TTTAGGGTAT AATGTAGAGT GCGCTATAGA TTTTAATTTT GAAAATAAAT 360
TAAAAATTTT GTAAATGATG TAGTAAAGGT ATGTCGAATA 400

(2) INFORMATION FOR SEQ ID NO: 789:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

GTTTAAAGAT GGAGAGATTA TTGATTTTTTC AGCTGGAAAA GGTGAAGCGG TATTGAAAGA 60
TTTAATCAAT ACTGATGAAG GTTCAAGAAG ATTAGGTGAA GTAGCATTAG TACCTGATGA 120
TTCACCGATA TCAAATCGTA ATACCATTTT TTACAATACT TTATTTGATG AAAATGCAGC 180
ATGTCATTTA GCGATTGGAT CTGCTTACGC CTTTAATATT CAAGGTGGAA CGGAAATGAC 240
TGTTGAGGAA AAGATTGCAA GCGGATTAAA TGATTCAAAT GTACATGTCG ATTTTCATGAT 300
TGGTAGTAGT GATTTGACTA TTTATGGCAT ATTCGAAGAT GGTTCAAAAAG AACTAGTATT 360
TGAAAATGGA AATTGGGCAT CAACATTTTA ATAATGTTA TTTTGAGGTG CTGAGTAGGA 420
AATGAAACAT GTATTTAAAG GTCAAATACG TGATTAAAGT ATAGATTGGG AGATAAAATA 480
ATGACAAATC AGGACAGACC AATGAAATCT ATGTCAGAAT CAAAATGTTA TAAAAATAGA 540

CAAGTTTTCC CTCAAGATAC GAATCACCAT CATACAATGT TTGGTGGTAC ATTGATGGCT	600
AATATTGATG AAATTGCAGC AATCACAGCT ATGAAACATG CTGGTGCGCA AGTAGTTACC	660
GCATCTACAG ACTCAGTAGA TTTCTTAAAG CCGATTAAAA CAGGGGACAT ATTACAATAC	720
GTAGCGATGG TTTCATACGC TGGGACTAGT TCAATGGAAG TG	762

(2) INFORMATION FOR SEQ ID NO: 790:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

TTTAATTTTA TCITTTGGAT ATCACATAGA TGCTACTTTT CTATACTGTT CTAAATCTAT	60
TATTTGTCAT CATTGATTTG CAATAGCCAT ATCATGTGTT GCTAAAATCA GCACTTTATT	120
TTCATCGACC AAACCAAATA ATGATTGAAT AATCATCTGT CCTGTTTTAG GATCTAACGC	180
ACCCGTTGGT TCATCAGCTA ACATAACAAT CGGATCTTT AACATCATTC TAATTAAAGC	240
GACACGTTGT TGTTACCTC CACTTAGCGT ATGAACTTTT CTTTTTAAAC TGTTTGACAG	300
ACCAAATGT TCtATATAAC GtATCTttAT TTGTnCTTTT TCTTTCTTAC TTATTTTTTT	360
ATATGCTAAT CCAATATCTA AATTTTCATT TACTGnCAAA	400

(2) INFORMATION FOR SEQ ID NO: 791:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 791:

TTATACCTTG GGAGATGATT CCAAGATGTC CAAAATGTGA TGCCCCAATG GAAGTGAnTA	60
AACGTAAAGC GGAAGTTGGG ATGGTTGAAG ATGCTGAATT TCATGCGCAA CTACATCGTT	120
ATAATGCTTT TCTAGAGCAA CATCAAGATG ATAAAGTGTT GTATTTnGAA ATTGGAATTG	180
GTTATACTAC ACCACAATTT GTGAAGCATC CTTTTCAGCG TTGACACGTA AAAATGAAAA	240
TGCCCTTTAT ATGACGATGA ATAAAAAGGC TTCGCATTCC GAATTCAATT CAGGACGTAC	300
CATACTTTAA CTGAGATTCT CAACTTGTTT AGCAGACTCC GGACGCAGCA CACGAAATAC	360
ACATGGGGGC AGAGTnACTT ATGGACCGTT GAATGnGATA	400

(2) INFORMATION FOR SEQ ID NO: 792:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

```

GTTCCGTTTG ATACAGAGAA GCGAATGTAA GCATAATCTT TAACAGTATC GTATGATAtA      60
AtTTAATTGG CAACTTTTTG TCACCTTCAT AACTTTCAA TTTTCTCCAA AATTGACCTG      120
ATTGTAATCC TAATTCAATT TCTGGTTTTG AATCAGTGAA AATAACTCTA GCAGGTTTAA      180
CAGAACTTGC ATAATGATAA AACTGTTGAG TTCCATCTTT CTTTTTCATT TCAAATCAA      240
TTGGACGAGA GTTTGGTGCG CTATGATCTT TGTCTTTTAT TGCAGGGTTT TTAATCGCTT      300
CTCTAAGTTC CTGaTTCAA ATAGGATATG TATTGTTAgT GGCyTTTGCT GCTGGTTTAA      360
CTTCTTTTGT TTCCTTAGGG GcTTTAACTT CTTTAACTTC TTTAGCTTCT TTTGTTTCAG      420
AAGTAGGGGC CTCAACTTCT TTATTAGATA CTGAGACAGC ATTAGCTACT GGTTTAGTTT      480
CTGGAGCTTT TTCAGATGTT GTTGTTGGAC TTGCAACTGC TTCAGTTTTT GGTGTGCTT      540
CTGTATTTGT ACCACCTGTT TCTTCAGCTG CTGCTTGTGT TCGCøTTTG ACATTAATAA      600
TAAAGTGTA CTAATTGCTA CAGATGCAAC GCCTAGTGAT GACTTTCTAA TTGAATAAAA      660
TGATTTAAAT TCTTTTTG                                     678
  
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(2) INFORMATION FOR SEQ ID NO: 793:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793:

```

ACTGGCGGAT CCACGATGGC ATGTGTTAGT GAAGCAATTC ATTTATTACC ATATAATGTA      06
TTCTTCGTAC CAGCCAGAGG TGGACTAGGC GAAAnTGTTG TCTTTCAGGC AAACACAATT      120
GCAGCCAGTA TGGCACAACA AGCTGGCGGT TATTATACGA CGATGTATGT ACCTGGATAA      180
TGTCAGTGAA ACAACATATA ATACATTGTT GTTAnGAGCC ATCAGTCATT AAACACTTTA      240
GGACAAAATT AAACCAAGCA AAGTTAATA TTACACGGGC CTTTGGTGAT GCGCTGGAAG      300
ATnGGCGCCT CGGACGTCCA ATCACCTGGA AAAGGTCCTT GGAACCACTT C              351
  
```

(2) INFORMATION FOR SEQ ID NO: 794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

```
GGGCGAGGCG TTCGCGCACC GGCCGAGCAG CAAATAGGCC GGGATGTCGC GTCTTGCTGC      60
AGGTCCGAAA AATATCAACT TGAAGAGGTA ACACCGnTAG ATATtTTCC ACAAACAACA      120
CATGTTGAGA CAGTGGCATT ATTCAATTG AAATAGCGCA CATGATTGA GATAAAATTT      180
CGCCTTAATA AGTGAAGAAA GAAGTCGTAT ATTAAAATTT TATTACAGCC AATTTACTTT      240
CTTGATATGA ACTTTTTTAAA TTAAATGTGA CATTGTATAC TATATTTAAA GAAGAATAAG      300
AATGTCATGA TCGGGAGGGT TGGTAATGCA TAAAATTGAT TTAACGACAA ATAATTTTCA      360
AATGCGAGGT TTATTATCCT GGCAACCTGG TTATTGCGTT      400
```

(2) INFORMATION FOR SEQ ID NO: 795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

```
ATGTTCCAGG AACGTATTTT TACAACCGAC AATTAGCATA TGTCATAATG AGTTTTATAA      60
TTGTATTTTT TATTGCATTT TTtATGAATG TTAAATTACT GAGTAATATT AAAGTGCAAA      120
AAGGTATGAT TATAACTATC GTCTCACTAT TATTACTGAC GTTAGTAATA GGTAAAGATA      180
TTAATGGTTC TAAAAGTTGG ATAAACTTAG GATTTATGAA CTTACAGGCA TCTGAGTTAT      240
TAAAAATTGC AATCATATTA TATATCCCAT TTATGATCAG TAAAAAAAt CCTAGAGTAT      300
TAAGTAAACC AAAATTAATt TTAAGTCCTA TTGTATTAGC ATTAGGTTGT ACGTTTTTtAG      360
TTTTCTTACA AAAAGACGTG GGCAACATTA CTAATATTAA TnATnTT      407
```

(2) INFORMATION FOR SEQ ID NO: 796:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1053 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

CAGTAGGTAC ACTTGCAGCA TTTGTTGGAT ACTTAGAGTT ATTGTTCTGGG CCTTTACGTC	60
GTTTAGTCGC ATCATTTACA ACTTTAACGC AAAGTTTTGC TTCAATGGAC CGTGTATTCC	120
AATTAATTGA TGAAGATTAT GACATCAAAA ATGGTGTGG TGCTCAACCT ATTGAAATTA	180
AACAAGGTCG TATTGATATT GATCATGTTA GTTTTCAATA TAACGATAAC GAAGCTCCAA	240
TTTTAAAAGA TATTAATTTG AGTATGAAA AAGGAGAAAC AGTTGCTTTC GTAGGTATGA	300
GTGGTGGTGG TAAATCAACA TTAATTAAC TAAATACGAG ATTTTACGAT GTAACCTCTG	360
GGCAAATTTT AATAGaTGGT CACAACmTTA AAGaTTTTTT AACGGGAAGT TTAAGAAATC	420
AAATAGGATT GGTGCAaCAG GATAATATTT TATTCTCTGA TACAGTTAAG SA AATATTT	480
TaCTTGGTCg TCCaACAGCa ACAGATGAAG AAGTAGTTGA AGCGGCgAAA ATGGCTAATG	540
CACATGACTT TATTATGAAC TTGCCACAGG GATATGACAC TGAAGTAGGT GAACGAGGTG	600
TTAAATTATC AAGTGGTCAA AAACAAAGAT TATCGATTGC TAGAATATTT TTAAATAATC	660
CGCCAATTCT TATCTTGGAT GAAGCAACAA GTGCACTTGA TTTAGAAAGT GAATCCATTA	720
TTCAAGAAGC ATTAGATGTG TTGAGTAAAG ATCGAACGAC ACTTATCGTA GCGCATCGCT	780
TGTCCACTAT TACACATGCT GACAAAATTG TCGTAATTGA AAATGGACAT ATTGTTGAAA	840
CAGGTACGCA TCGTGAATTG ATTGCAAAAC AAGTGTCTTA CGAGCATTTA TATAGCATTC	900
AAAACCTATA AAGTATTAGT TGTTTGACTT CAGTACAATC TTGAAGAGAA AATTTGTAAC	960
AGGATGGTGG GGTCAATAACA TAGAAAAAGC AGTAAGAGAT TTTCTTAGTT GAAATAATC	1020
TTnCTGCTTT TTAAATTTA ATTTCGnGAT TCA	1053

(2) INFORMATION FOR SEQ ID NO: 797:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

AAGAGTGACT CCTGAAGTGA AAGAAGGGGA CCGTGTCGTG TTCCAACAAT ATGCTGGTAC	60
AGAAGTTAAA CGAGATAATG AAACATATCT GGTATTAAAT GAAGAAGATA TTTTAGCAGT	120
TATTGAATAA TACAGAACTT AATTCATAAA TAAATTAAAT AGAACGAAAA TGAAACACAA	180
CTAAACAAAT GGAGGTTTAT CATTTATGGT TAAACAATTG AAATTCTCTG AAGATGCACG	240
TCAAGCAATG TTACGTGGTG TTGACCAACT TGCAATGCA GTTAAAGTAA CGATTGGTCC	300
TAAAGGACGT AATGTTGTAT TAGATAAAGA GTTTACAGCA CCTTTAATTA CGAATGATGG	360

TGTGACGATT GCyAAAGAAA TCGAATTAGA AGATCCAT GAAAATATGG GGGCTAAACT	420
AGTTCAAGAA GTCGCAaATA AGACAAATGA AATTGCTGGT GACGGTACGA CAACTGCAAC	480
AGTATTAGCT CAAGCAATGA TTCAAGAAGG CTTGAAAAAT GTTACAAGTG GTGCGAACCC	540
AGTT	544

(2) INFORMATION FOR SEQ ID NO: 798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ D NO: 798:

CAATTGCATA GATATTGCTG ATAGACGTAC GGCTTTGTTT ATCAACTTCT AATAATCCAC	60
GGTCAGCGAA TTTAACACCT AATTTCGTCT GTGTTTGGAC GACGACCTAC AGTTACTAAT	120
ACATAATCAG CTTGATTGT TTTCTCTTCG CCTTTAGCTT CATAAGTAAC TTTAACTCCG	180
TTATCTGTTT CTTGCTGA TTTAGCCATA GCTTCAGTAA CGATTTCAAC ACCTTTTCT	240
TTCATACCTT TTTAACAGG TTGTGTGCAT TTGnTTTTTC GAGGCCACCT AAGATATCTT	300
TAGCACCTTC AAGGGATGGG GtACTTTCTG nAACCAAAGT TAGCAAATGC TGTACCTAAT	360
nCTGGTCCAA TG	372

(2) INFORMATION FOR SEQ ID NO: 799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

AAACGACATT TGTTTAATTG GAAGAATTaG CACCATTTTT TGAGGCGGGT ATAGAtTCAT	60
TTAAAATCGA TGGTATTCTA CAAACGGAAG AATATATTAA TGTGGTAACG GAACAGTATC	120
GTCAAGCGAT AGATTTGTAC AATGAAGATC CTGAAATCTA TGAAGATGAG AAATTTATGT	180
TGATGGATCC AATTGAAGAA ATTCAACCTg ATCATCGACC ATTTGACGAA GGTTCCTTAT	240
ATAAACAAAC AGTATATTAA GGAGGTTAAT CATGAAGACA ATAGAAGAGA TTAAATCAAC	300
TCCTAAAACA GTTATGAAGA AACCAGAATT ATTAGCACCT GCTGGAACT TAGAAAAGTT	360
AAAAATAGCA GTACATTATG GCGCTGATGC CGTATTTTTA GGTGGTCAAG AATATGGATT	420
ACgTTCaAAT GCTGaTaATT TCaCGATGGA AGAAATAGCT GAAGGTGTTG AATTTGCGAA	480

CCGTTACGGT GCCAAAATTT ATGTTACGAC AAATATTATT GCACATGATG AGAATATTGA	540
AGGTCTAGAA TCATATTTGC GTAATTTGGA AAAGACTGGT GCACAGGTA TCATTGTTGC	600
AGATCCTTTA ATTATCGAAA CATGTAAAGA AGTTGCGCCA AAAGTTGAAA TTCATTTATC	660
TACTCAACAA TCACTTTCTA ATTACAAAGC TGTAAGATAT TGGAAAGAAG AAGGATTGGA	720
TCGTGTTGTA TTAGCACGTG AGACCGGCGC GATGGAAATG CGTGAAATGA AGGAAAAAGT	780
AGATATTGAA ATCGAAGCAT TTATTCATGG TGCTATGTGT ATCGCCTATT CAGGTAGATG	840
TACATTAAGT AATCATATGA CTGCAAGGGA TTCCAACAGA GCGGTTGCT GTCAAAGTTG	900
CCGTTGGGAT TATGAATTAT TAGAAGTTGA TGATAATGGT GAACTTGATG TTTTTTATAA	960
TCAA _g GTGAA GTTACACCGT TTGCATGAG TCCTAAAGAT TTA _g AATTAA TCGAATCAAT	1020
TCCTCAAATG ATGGATATTG GTGTGGACTC ATTAAAAATT GAAGGACGTA TGAAGTCAAT	1080
TCATTATATT GCAACAGTTG TCTCAGTATA TCGTAAAGTC ATTGATGCGT ATGCGGCAGA	1140
TCCTGACACT TTAAGATTAA TCCGGAATGG TTAATAGAGT TA	1182

(2) INFORMATION FOR SEQ ID NO: 800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

GTATTCTTCC AATAACACCT TTCATTTGGA AACCGTTTAG AAAGAATACA GTTACTTCAG	60
TTTGGTTTGC TTAAAAATTC TCTaGTGCTT TGTCTTGGAT GTTTTCGtTG cAATCATCTG	120
TCGGACTCCT TTTACTTAAT CTGGGTTGTA ATCTCATCTA ACATCATTTG AAGTGACATA	180
TTTTCTTTAT CTAACCAATG AACACTCATT TTATTCTTGA ACCATGTCAT TTGTCGTTTT	240
GCATATTGGC GTGAATGTTG CTTTAAATCA TTGACAGCAT CTTCATAAAT CATTTGTCCG	300
TTAATCACAG GTATTAATTC TTTATATCCA ATAGCTTGCA TACTTTGGCA AGATTCATAG	360
CCTTGTTCAA CAAGTTGTTG CACTTCTC _A AATAATCCGT GATCCAACAT AATATCAACA	420
CGTTTATTTA TTCTTGAATA TAATGTTTTA CGCGACATTT CAATCCCTAA TAATAATGTA	480
TCATAATTTT CAGTAAATTG TTGCACTTTC TTGCGATTAC TCAAAAGTTT TTTTGTTTTT	540
AAATAATATT CAATAGCGCG CAACACTCTT TGGcGGTTGT TAGGGTGAAT ATTTCTGaC	600
AGAAACCGaC ATCAAATTGA GCTAAATAAT CGTGTAGTTG CTGATTATCT AAATGTTCTA	660
ATGCAGATAA CTTTGTGTTA ACTATGGATA ATTGTGCAGG TGTA _c TGTTT CATCTTCTAA	720

TTCATAATTA TATATTAATG ATTGAATATA TAAGCCTGTT CCACCTGCTA TGATTGGaAC	780
TTTACCTCTA TTCGtAtATAT CAGTAATTAA ATCTTCTGCT AATCGCTTGA ATTCATATGC	840
TGAAAATGTA TCATCAGGAT TCAAGATATC AATTAAATGA TGTGGAATAC CATCCATTTT	900
TTCAGGTGTn ACTTTTGCAG TTCCAATATT CATATGTCTG TAGACTTGCA TAGAGTCACC	960
GCTTATGATT TCACCATTGA TACGCTTCG	989

(2) INFORMATION FOR SEQ ID NO: 801:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801:

CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGACTGCAG	60
AAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAG CGACTTGGTC AAATATTCAT	120
TACCAATATC ATCAATTACC GCTAAAGGTC AAAAAGTAC AATTAAAACC AACTCCGTT	180
ACCCTGaACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAGATGCTA	240
AATCAGATGT TAATCAAACCT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTATAAGC	300
AATCTCGAAA AATATCATTG TCGAATTTTA AGGACTATTG GCAAGGTAAA CCGAAACTTG	360
ATCATATTAC TGTGACGTAC CAAGAAGACG GCAATAATCG CGTCAGAAAT TTAGAATCTC	420
AAAAAGATGA TTTAATAACT GATGTCCCAG TTAATAAAGT TCAAGACATA GAAAATAATC	480
AAAATTTAAA AGTGTCAAAA GAATCTGGAT TTAGAAGTTC TTTACTTATG TATAATCATA	540
CTA	543

(2) INFORMATION FOR SEQ ID NO: 802:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

GCGAATTCGT ACACACATAT ACACAAAGAT AATCATAGTT TTACATTGAA GCACATGAAA	60
GATAATTCAT TTAAAGGAAG GTATTATCAA TGAATAAAA AATGGGATTA TTAGTTATGG	120
CTTATGGCAC ACCTTATAAA GAAAGTGACA TAGAGCCATA TTATACAGAT ATTAGACATG	180
GTAAACGTCC ATCTGAAGAA GAACTTCAAG ATTTGAAAGA TAGATATGAA TTTATAGGTG	240

GTTTATCACC	ATTAGCAGGT	ACAACAGATG	ACCAGGCTGA	TGCGCTAGTT	TCAGCATTAA	300
ATAAAGCATA	TGCAGATGTT	GAATTTAAAC	TATACTTAGG	ATTAAAACAC	ATTTACCCAT	360
TTATCGAAGA	TGCGGTTGAA	CAAATGCACA	ATGATGGCAT	TACTGAAGCA	ATCACGGTAG	420
TACTAGCACC	ACATTATTCT	TCATTTTCAG	TAGGATCATA	TGACAAACGT	GCTGATGAAG	480
AAGCTGCAAA	ATATGGTATT	CAACTTACAC	ATGTGAAACA	TTATTATGAA	CAACCTAAAT	540
TTATTGAATA	TTGGACGAAT	AAAGTCAACG	AAACATTAGC	TAAATACCG	GAAGAGGAAC	600
ATAAAGACAC	GGTATTAGTT	GTTTCGGCAC	ATAGTTTGCC	AAAAGGTTTA	ATCGAAAAGA	660
ATAATGATCC	ATATCCACAA	GAAC TAGAAC	ATACTGCGCT	TTTAATTAAA	GAACAATCTA	720
ATATTGAACA	TATCGCGATT	GGTTGGCAAT	CTGAAGGTAA	TACAGGTACA	CCTTGGTTAG	780
GGCCAGATGT	ACAAGATTTA	ACACGTGATT	TATATGAAAA	ACATCAGTAT	AAAAACTTTA	840
TATATACGCC	AGTAGGTTTT	GTATGTGAGC	ATTTAGAGGT	GCTTTATGAC	AATGATTATG	900
AATGTAAAGT	AGTTTGCGAT	GATATTGGTG	CGAATTATTA	TCGTCCAAAA	ATGCCGAATA	960
CACATCCATT	ATTTATCGGT	GCAATTATTG	ATGAAATCAA	GTCTATATTT	TAATGACGAA	1020
AGAAGCGTGA	AACGTTGTGA	CTAAATCAGT	GGCTATTATA	GGAGCGGGGA	TAACAGGTTT	1080
ATCAAGTGCA	TATTTTTTAA	AACAGCAAGA	TCCTAATATT	GATGTAACCA	TCTTTGAAG	1139

(2) INFORMATION FOR SEQ ID NO: 803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803:

TATCCnAAAT	AnAAATGTGC	GCATTTATCA	AAACCTTACA	TACAAAGAG	TTTTCCCTAA	60
CAGTAAATTA	GATATTATTA	CACCTGTTGA	TATGTCTTCT	AATGCCAAAC	TGCCAGTTAT	120
TTTTTGGATG	CACGGTGGTG	GTTATATTGC	GGGTGATAAG	CAGTATAAAA	ACCCATTATT	180
AGCGAAAATT	GCTGAACAAG	GGTACATTGT	TGTGAATGTA	AATTATGCAT	TGGcGCCACA	240
ATATAAATAT	CCCACACCAT	TAATTCAAAT	GAATCAAGcA	ACTCAATTCA	TTAAAGAAAA	300
TAAATGAAT	TTACCTATTG	ATTTTAATCA	AGTAATTATT	GGCGGTGAyT	CTGCAGGTGC	360
TCAATTAGCT	AGCCAATTTA	CGGCAATACA	GACGAATGAT	CGCTTAAGAG	AAGCCATGAA	420
ATTTGATCAG	TCATTCAAAC	CATCGCAAT	TAAAGGTGCT	ATACTATTTG	GTGGTTTTTA	480
TAATATGCAA	ACAGTTAGAG	AAACTGAGTT	TCCAAGAATA	CAGTTATTTA	TGAAAAGTTA	540

TACTGGCGAA GAAGATTGGG AAAAGAGTTT TAAAAACATT TCACAAATGT CGACAGTAAA	600
ACAATCGACA AAAAATTATC CaCCAACATT TTTATCTGTT GGAGATAGCG ATCATTCTGA	660
AAGTCAAAAT ATAGAATTCA GTAAGAAATT ACAAGAATTG AATGTACCAG TAGATACTTT	720
GTTTTATGAT GGTACGCATC ATTTACATCA TCAGTATCAA TTTCACCTTA ATAAACCTGA	780
ATCGATAGAT AATATCAAAA AAGTGTTACT TTTCTTAAGT CGTAATACAT CCTCTAGTGG	840
TATTCAAACCT GAAGAGAAAC CACAAATAGA AAATCCGAGT AATGAATTAC CGTTAAATCC	900
TTTAAACTAA TGATAAACAG TAGTAATTTA TTAAGTAAAG AACATTTAAG ATTTTCAAAT	960
TAAAAACGAG AATTTAAAAC ATGTGGTGTC	989

(2) INFORMATION FOR SEQ ID NO: 804:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804:

TAA _n CCCTGG TTTAATGATT TTGATTACGT TTTTTATAA TAAAAACATA TCGAACATTG	60
ACTACGTTAT TAAGCTGCTT TTTTGTACAC TTTATAACCA ATAGCTTAAG ATTTAAACT	120
AATCGGAAAG AACAATGATT CACCA _n AAAA ATATTTATGT TGCTATTAAA AATCAGTTAA	180
TACGAATGTT AAAATACGTT TGATTTTCAT TAATAATGAT TCAAGTTTAT TTAATAGC	240
GTTAATGTCA GTCTGTTTTG ATGCACCTTA TAATAAAGAC AGATAGTTCA AATTACGTAA	300
TAATAACAAT CCAATACATT AAGATTGGAG CAAAAAATA TGAAATTAAC AACGATAGCT	360
AAAGCAACAT TAGCATTAGG AATATTAACT ACAGGTGTGT TTACAGCAGA AAGTCAAACT	420
GGTCACGCGA AAGTAGAACT TGATGAGACA CAACGCAAAT ATTATATCAA TATGCTACAT	480
CAATACTATT CTGAAGAAAG TTTTGAACCA ACAAACATTA GTGTTAAAAG TGAAGATTAC	540
TATGGCTCTA ACGTTTTAAA CTTTAAACAA CGAAATAAAG CTTTTAAAGT ATTTTACTT	600
GGTGACGATA AAAATAAATA TAAAGAAAAA ACACATGGC TTGATGTCTT TGCAGTACCT	660
GAATTAATAG ATATAAAAGG TGGCATATAT AGCGTTGGCG GTATAACAAA G	711

(2) INFORMATION FOR SEQ ID NO: 805:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805:

ATCAGGAAAA ACAGaATAAT GTAAATCAAG CTGTTTCAGCC TCAAAATAAT ACTAATGAAA	60
CATCAAAAGT ACCGGCTAAT TTTGTCAAAT TGAATGATAT TAAACCAGGT GATACTTCTA	120
TACAAGGAAC AACTTTACCA AATCAATTTA TACTATTAAC TATTGATAAA AAAGATGTGA	180
GCTCAGTTGA AGATTCTGAC AGCAGCTTTG TTATGTCTGA TAAAGATGGG AATTTTAAGT	240
ATGACTTAAA TGGTCGCAAA ATTGTTTCATA ATCAAGAAAT TGAAGTGTCT TCATCAGATC	300
CCTATTTAGG TGACGATGAA GAAGATGAAG AAGTAGAAGA AACTTCAACT GAAGAAGTTG	360
GTGCTGAGGA AGAAAGTACA GAAGCTAAAG CTACATATAC AACACCGCGA TATGAAAAAG	420
CGTATGAAAT ACCGAAAGAA CAGCTAAAAG AAAAAGATGG ACATCACCAA GTTTTTATCG	480
AACCTATTAC TGAAGGTTCA GGTATTATTA AAGGCCATAC CTTGTAAAA GGTAAAGTTG	540
CTCTATCTAT TAATaATAAA TTWATTAACT TTGAGaCAAA TGCTAtGGTG GtCCaAATaA	600
AGAAGaAGCG AAATCTGGAT CAGAAGGAAT CTGGATGCCT ATTGATGACC AAGGATACTT	660
TAATTTTGAC TTCCAAACGA	680

(2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806:

GTATTTTCATT AGCCATTGGC AATTGACATC TGACAATGAG GAATGGCTTT TGCATTGGAA	60
TTCACAGTTG GAGTGCATTT ACTGGTTATT TTGGAGGTCA TTGTTGATAC ATTATTAATG	120
GAGAATAACC GAATTTGTTA TGTTATTTCC ATTTTAAATA TTTGCAATTG TATTAAATGC	180
TGCACTTGGA GATAAAATTA AAAATCCTTA TGGATCTGCC ATAATTCTTG TTCTAGTTAT	240
TATCGTATTA AGTTGGGGAG GTATTGACAA GACTTGTTCTG TGGTAAAGTA CTTCAAGAAA	300
AAGAAAATGA ATACTTTTTG GCAGCAAAAT CAATTGGTAC ACCCACATAT AAAATTATTT	360
TGAAACATCT TTTGCCGAAT ATATTAAGTG TAGTTATCGT ACAAGaACA TTGTTATTTG	420
CCGGTATGAT TGTAGTGGAA TCAGGrTTGA GCTTTTTAGG ATTCGGAATT AGTAAAGCAA	480
TACCATCTTG GGGTAATATG TTGAGTGATG CTCAAGAAGG GGATGTTATA AGTGGTAAAC	540
CGTGGATATG GATGCCACCT GCTATAATGA TTACATTAAC TATATTAAGT ATAACTTTG	600
TAGGGGAAGG GATTAAAGAT GCTTTTAATC CTAGAGGTAG ACGTTAAATA ATAAAAGAGG	660

CACTAGTTAA TTCTAGTACC TCTTTATTTT ATCTCTTACG TCCTAAACCC ATCGCTTTTT	720
CCATTTTTTTT GACAGTTTTA AATGAACTT TGTGTGCTyT ATCTCTACCT TGATCTAAAA	780
TATCAyCAAG TTTATcTGAG TTATAGAAc TTTCTGATTTT TTCTTGAAT TCTACTAAAA	840
ATGCTTTAAC TATTTcAGCA AGGTCACCTT TAAATTTACC ATAACCTTCG CCCTCATATT	900
TTGCCTCAAT ATCTTTAATT GGCATGTCTG TTAATCCAGC GTATATTGAA	950

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807:

GTTACCAGTC GAAGCTTTAC GACCTGTTAC GAAACATTGT TTACCCATATGAGTACCTCC	60
TTTAATAAAT ATAAATACAC ATAACACTT ATATACTTAA TTAAGATAGC ATAGTTTCAT	120
TTGAAAAACA ATGAATAATT TTCACATAAA AGTCAAAAAT ACTGAGTTTT GTGATATAAT	180
TGTAGACTGT GAAGTTATGT AGTATGATAT TTTAGAGAAA TAAGTGAATG AAACATTTAA	240
AATTTTTATT TrATGATACT ACATCTATTA AAAGAAAACG CCTATAGATA ATCGTCaTGA	300
GTGTAAATTC AGTTtACTCa AcAtATAaTA GGkGaTTTTAA gCgTAAGtCa TTCTGATAAG	360
TTGTACCATT GATATTTTAT GAAATAnTCn ATGAACTTAA AGCGTTTATG CTACACTA	418

(2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808:

AATGGCnATT AATCTTTAAT ACGATGCTG AGGATTTTTTC CTAATAAAAC CTTGATTTCm	60
AAAAGGGTTT AAATCmAATG AAACAATAAT AAaAAAATGw CGCAATATAA TAATAAGTAC	120
AAATTTAATT AAGAAATTAA ATTGATTGTA TATGTATATT TTGGTAACGT AAAAGAGAnA	180
TATACAAAAT AATTAATTAT TTATATGAAA AGAGAATATA AATGAAGTAT AAACAGAGA	240
GACGTGAAGC GATGGGATAT TTAaMAAGGT TTGCATTGTA CATAAGCGTT ATGAyTTTAA	300
TATTTGCGAT AGCAGGTTGT GGCAAAGGTA ATGAAACAAA AGAAGATTCA AAGGAAGAAC	360
AAATCAAAAA GAGCTTTGCG AAAACATTAG ATATGTATCC AATTAAGAAT CTCGAGGACT	420

TATACGACAA AGAAGGATAC CGAGATGGCG AATTTAAAAA GGGTGATAAA GGGATGTGGA	480
CGATATATAC AGATTTTCGCC AAAAGTAATA AACAGGTGG ATTGAGTAAT GAAGGTATGG	540
TCTTATACTT AGATAGAAAT ACACGGACTG CAAAGGGACA TTATTTTGTT AAGACATTCT	600
ATAATAAGGG CAAATTCCCA GATAGAAAAA ATTA A AAGT TGAAATGAAA AATAATAAAA	660
TTATCTTATT AGATAAAGTA GAAGATACAA ATCTAAAAAA GAGAATAGAA AACTTTAA A T	720
TTTTTGGACA ATATGCAAAC CT T AAGAAT TGAAAACTA CAACAATGGT GaTGTCyCAA	780
TTAATGAGAA TGTTCCAAGT TATGACGCAA AATTTAAAAT GAGCAATAAA GATGAAAATG	840
TT	842

(2) INFORMATION FOR SEQ ID NO: 809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:

TAAGACTATG CCATCTTGGC AACGCGTTGT CGCATATTCA TTATTAGTAA GTATATGCAA	60
GCATGATTTT GCCATAACtT TACCTCtTTC TATATTTAAG TACCACTTTT ATCATTCCCT	120
ATAATATTTA ACTTATTTAA TTAAACGTAA ATTTAACACA ATACGAATAC CAAATCAAAA	180
ATAAATAAAA CTATATAATG GTTAATTTTT AACTTATAT ATCAATCATT TAAATATTAC	240
AAAAATAGAT GTAGTCAGTT TAATTAAACT ATCCAATTGA AAACACACTA CTTTTTAGTA	300
TTTTCAAAAAT AATTTTAAAT GACCACATCT ACAACGTAT ACTATTATCT TTTGTTAGTT	360
ATATATTCAT TTTCAATTTA rAAATAAACA CTTAtTTAAA TCACATTCTA CTTTTGAGAT	420
GAGCTCAAAC TAACATTAAA TTGTTTATAT T	451

(2) INFORMATION FOR SEQ ID NO: 810:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

ACATTTTGTG CTTGTTGTCC AATCCAATTT CTA C TTTGTT GAACAGTATG AGTTGCTTGA	60
CCACGCATGT TACTCAGCAT TTGTCCAACA TGAGTATTTT GAGCAAAGTT ACGAGATTGA	120

TTCAACACAC TGTTTTTCAT CATThCCATT TTAGGTGAAA TACGACTAAC TGCTTGTTC	180
ATTGTCTTTT GCAATCCTGT TTAACTGCA AATTTTTCTC CGCCTTTGAA GCCTAATTC	240
ATTAACTTT TCCCAGCACC TTGAGGAAG CCCATACCTG GCAATGGAAT AAGCGAAAGT	300
CCTTCCATGA TTCGTTCTTC TTTAGATAGC TTTCTTCCAG TTACAATATT TTTTCCTGTG	360
GCTGCATTTG CTGCTGAATA AGCGGAATAA GCACCAATAG CTACTGCTCC AGCAACAGGA	420
TTAATACAAG ATAAAACTAC CATACCAGCT AGTGCTGCAA TCTATAGC TTCTTCTTTT	480
TTCTTTTGCT CCTCTAGcTC TTCCGCTTCA GCTACTGTCA TGTAATCACA AGAAGCGCCC	540
TGAGTCATCA TTTTTTCAA ATCACTTTTA GATAATTTCT TATCTTCTTT TTTCAATTTCT	600
TTGTAATGCT GATCAATTAC TTTTACAAAT TCTTGATCCG ATTTTAATAT TTCATCGATG	660
CTATAACAT CGCTGTCACT TTTCTTGGCA TCTCCCTTTG CAATTTTCCC AGAAGCCCCA	720
TAGGTATCTC TACCATGTCC ACCACCATTT TTAATTAGTA TATTTTCCAA TTTAACATTC	780
GTTATACCTT TGAATGCTTT ATCTATATCT TCTATAATG GCGTGCAAT AATTTCTTTC	840
ATTTTCGAAT CTAATTGAGA TGQATAATCA TATAACTCaT TTTGÀTAATA CCCCATTAAT	900
TTAGATCCTT GTGGAcCTAC TACACTACTT GTTAATGATA TTGCGCCATC TTCGTCTAAA	960
GAAGTACAT CGCTTACCGC ATCATCCATT GTTGATCTA CATCTAAGAA GTCTTGACCC	1020
TcTATTGCAT CTATTACACT TTGGATAGAT GACTTTTCAT TGTCATAAT AGCTGTTAGA	1080
TATTCAATAT CTTTTGTCAT GTCATGCACC TATCCCTCAA TATTATAGTA AAGCTTGGCA	1140
AATTcCGTAC CCCAATGTTT ATCTGCTTCA AAGAACTTTT GTGCTGAATT cATGACGCCA	1200
CCACCGAGTG TACTCAATGG ACCTTTGAGA CCACTAATGA CTGTTGCAGC ACTACTATAG	1260
CCATTTTCCA TAGAATGTGC AGCTTTTTTCA CTACTGTAGT AATTTAATTG CGCTATTTTT	1320
CCAAAGTTTT GAGCTATTTT ATCATACTTT TGAATTATGC TTTCCAATTC TTTTACAACA	1380
TGTGCAATCG TTTcAGCTTT AACACTAATT TTTCCACTCA ACGTCATTAC TCCTCtGcTt	1440
TATtAATATG ATTTTcATCA GTATCGAATC CAAATAATTC TCGTGATAAA nGTATTGAA	1499

(2) INFORMATION FOR SEQ ID NO: 811:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811:

CnCGCTGCAC CGAAGAATGC TTTTGGTTTG TGTAAGATG CAGGATCTAA ACCACCTGAT	60
AATGTACGAC CACTTGGTGG AATAACyAAG TTATAAGCGC GTGCTAATCT CGTTATAGAA	120

TCCATTAAAA TAATGACATC TTCCCCAATT TCTACTAAAC GCTTTGCACG TTAAGTAAT	180
AATTCAGCTA CTTTAACATG GTGTTCTGGT GGTTCGTCAA ACGTTGAATG AACGACTTCA	240
GCAGCTTCTA CTGAGCGTTC TAAATCTGTT ACCTCTTCAG GACGCTCGCC AACTAACAAA	300
ATAAATAGCT TTGCATCTGG TTTGTTCGTA CTGATTGCAT TCGCTATTTT TTTAATAAC	360
GATGTTTTAC CTGCTTTAGG TGGCGCCACT ATTAAACCAC GTTGACCTAA ACCAATCGGT	420
GTTACTAAAT CCATGATGCG CGTTGAATAA TTTTGTATTT CTGTCTCTAA TTTAATACGC	480
TCATCTGGAT AAAGTGGTGT CAAAGCTTGG AAATGCGGAC GTTTCTTCAC TTCTTCTGCG	540
TTATGGTCAT GACAAAGTCA ACTTGTAATA AGCATAATA TTTTTCGTTA TCTTTAGGTT	600
TTCTAACTTT CCCAGTTACT	620

(2) INFORMATION FOR SEQ ID NO: 812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812:

CCGGCTGAAA TTAAGTTCTT GTTATATTTT GCAAAAATGA CAAAGAAAGA TAAAAATAAA	60
CTATATCATT TTCTTAAGGA GGATTAATAT GTATTATCCT TATTTGCGTG GGAAAGAAAA	120
TGAACTATTT GCAATTAGAG AATTGTTAGA GAAAGGTTTG ATTGGTGATT GTATTCAACC	180
TATAATTGAA CCAATTAAAT ATACAACCAC ATTTAAAAAT ACTTTGCAAT ACTGTGGTGA	240
AAAAGCATT CTTATAAATT TAGTAGTAAA TTCAAAGTTA ACTGAAGAAG AGATTAGTAA	300
CGAAaCTGTt GCACATTTAA CTGAAATAAT AACAAAAAAC AAAAGTGTTA TTCAAAAAGC	360
TTACTTGGGT CCTTCTGATG AAGGCAATGA TAGGTTGAAA CAGCAATTTT CAAGTAATAG	420
TTTAGCTATT TTAACAAGTG TAGATGATTG GGAAATGTTT GGAGATAAAA ATAACTTGA	480
AATGGTTTTT GTACCAGATG ATAGACACAT TAAACGAAA TTGCGTAATA TTCCAAACAA	540
AGGCATsATT ATGGATCCTT TTAATAAACT AAGTCGTAAT GTTGATTATT TAGATAATGA	600
TGACGAGTTT TATAGCGACG ATCACCTTTA TTATAAGGAA GATGGATACG TAGCATTTTC	660
AGACTATTCT GTTATAGGTG GAGAATATGT AGACGGTGGC TTTTCGCCAT TAGCtATTGc	720
GrTACATATT GTCTATTTTG ATGAGGCTAA TGAGCTAAGA GTTAAGCATT TtGTCTCTGa	780
TTCTAATAAT GATAGATCAA ATCCAGGTAA AAnGTTTTTT GAGGCTGTAG ATAAATTAGT	840
AACATGGTCA AAAAaCTTAG ATATTAAAAA TAGATCTTAT GCGCTTGGAC AATTTGAAGA	900

ATTAAATGAA AATAATAAGT ATCCAGGATT AGGTTTAATT AAA _n GTTATC TATCAGCATC	960
ACCTAGAAAT TATGAATAGA TACTGGGTCT CAAAGAAATA GGAAAAGTTT ATATCGAACT	1020
GAACTGCAAG AATGCATTGA CATGGATGAA CACACGGGTA AAATGATCGC AGCTGAAATG	1080
ACTATGGTAT TAGC	1094

(2) INFORMATION FOR SEQ ID NO: 813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

CACCTATCAT CGTCTCTTTA ATTCTATCTA TCTATTTACC CCAATCGTAA ATATGATGGA	60
CGTTATAGAA TACCAAGAGT TGCAGGTAT _n TCTATTATTT ATCTAGCTGT AGTAGGTGTT	120
ATTACGTTAA TTGT _T TAATTT ATTGATACCT ATTATTGGTT CGCAAGTAGA TAGTTTAGTT	80
AAAAATTCAC CGCAATATCT AGAAAAATTA ATTAATTCTA TTGATAAAAT AGCAAATAAT	240
ACGTTTTTCT CTTCGTATTA TAGTCAAATT AATGATTGGT TAAATTCTTT ACCTAAGAAA	300
ATACCATCTA TGTTAAGTGA ATTTACAGAT GGCTTTGGGT CTAAAATTGC AACGTTTGCA	360
GAAACGATTG CTAATATTGG C _g TTGTGATT GTCACAACAC CaTTTGtACT ATTCTTTATG	420
CTTAAAGATG GACATCACTT CAAAGAATTT TCAACGAATA TTATGCCACC GAAATTCCGA	480
AAAGATTTTC ATGATCTACT TGAAAAAATG AGTGTTCAAG TTGGTTCATA CATTCAAGGA	540
CAAATTATCG TTTCATTCTG TATCGGTATA CTGTTGTTTA TCGGTTATC GGTTATCGGG	600
TTGAAATATA GCTTAGTATT AGCTAGTATT GCGGCAGTTA CAAGTGTTGT ACCATATTTA	660
GGGCCTACTA TAGCGATTTT T _c CAGCTATT GTAAT _n GCTG CTATAACa _y C GCCGTGGATG	720
CTCTTAAAT TAGCAGTAGT ATGGACTTTA GTACAATTTG TTGAAGGGCA CTTCATTTCA	780
CCAAATATCA TGGGTAAAC ACTTAAGATT CATCCACTTA CAATCATTTT CATTTTACTG	840
TGTGCAGGCA AATTGCTTGG TATTGTAGGC GTTATTTTAG GTATTCCGGG ATATGCTATT	900
TTAAAAGTAT TtAGTTACTC ATTTATTCCA	930

(2) INFORMATION FOR SEQ ID NO: 814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814:

GTATGATTGC TGTTTTAATA CCAGATGATG GCAGTGGCAA ATCTTATGAC TATATGCTTG	60
TGAACCCAAA AATTGTAAGT CATAGCGTTC AAGAAGCTTA TTTACCAACT GGTGAAGGTT	120
GCCTTAGTGT CGATGATAAT GTTGCTGGTC TAGTTCACCG TCATAATAGA ATTACAATTA	180
AAGCCAAAGA CATCGAAGGT AATGATATAC AATTACGACT AAmAGGATAT CAGCAATTG	240
TTTTCCAACA TGAAATTGAC CATTTAAATG GTGTAATGTT CTATGATCAC ATTGACAAAG	300
ATCACCCATT ACAACCACAT ACAGATGCAG TAGAAGTTaA aACACATTTT cTAATTATCA	360
AAgCTTAGGA TAAtATGATG tCCTAAGCTT TcCTTTACAA CTTTTCGGAT AACCAACAGT	420
TAATATATCA CCTTCTAACC AAACTTTTAA TCCCTCATTA A	461

(2) INFORMATION FOR SEQ ID NO: 815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

AATAAATTTT AGAATTGTCG CATAATTCAT CATGACAACA TAATGACATG TATTGTTATT	60
AACGATATAA TAGAATTGAA TAAAGTGGGT GATAATGTGA CTAAAAATGA GATTAGAAAA	120
TACATTTTAC ATAAAATGAA GAATTTTAAT AAAGCTGAAA AGCGAAAAGC AGACACATGG	180
TTAAGAAATC AATTTTTTGC AACTGAAGAA TACAAAGAAG CAAACGCAAT TGCGCTAGTT	240
CTTTCTTTTA ATCATGAAGT AGATACTTTT TCTATTATTG AACAAGCCTT AATGGATCAT	300
AAACGTATTT TTGTACCGAA AATGGATTAT TTAAATCATC AAATGACTTT TAAAGGATA	360
TTTAATCTCA AAGATATTGA TGTCGATAAT AAGGGGATTT ACTATCCAAC TTCAAAGGT	420
GAAACAACGA ATAACCTAGA TTTAATTGTT GTTCCTGGTG TTGGATTTCA AGACGATGGA	480
TATAGAATTG GGTATGGTGG TGGCTATTAC GACAGGTTTT TAGCTAATTA TCAGACAAAG	540
ACAATAAGCT TATTATACGA TTTTCAAATA ACA	573

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

{xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816:

TAGTTTAACA ATGTCTATTC TCATAGAATT TGTCCAATA AATGTAGACG ATTCACTAAA	60
CTTCTAAAAA AATAAACCCC AAATTATAAT AGTCTCAATA TTAATATATT ACAATTTATT	120
CATAGGATTT TTATCATTTT AATTAATAGG TTTTATCAG GGTAAATAA ACATTTTTTG	180
TAATAGTCCT TTTTACGTT CTTTAAATAA CTCAATTCTA TTCATTTGAT TATTCATTTT	240
ATTGTCTATA GATTTTAACA ATGCACTTAC TTTATC _y TGT TCAGTGAGAC AAGGTATTTT	300
AAGATTTATA TTGCATAAGT TCGCATGAGT TAATTTAGCT GGTGCATTAC CTGTGACAA	360
TGCTCGTAGT TCTTTAAAT TTAAATAATA ATTCATAAAA AACAAATTAT GATCATTACT	420
TTTAACTACA TCGCATGAT TATTTACCCA GTATTGCCA TTAGCAATAA AGCTACTCGT	480
CTCAAACGTC CCCCATTTTG CACCATCTTC TCCTATTAGT AATCGTTCTT CATTATTGAA	540
TAAATAATCT TTTACGTAAT CAATAATTCC AGTTGCACCA TAGTAAGGGT ATAACCCCTT	600
TTCTCTTAAT GAAGAAGTAA TTGGTTTTCT TCTATTATTT TCAAAGATAA AGATGTCTTT	660
TATGAATTTG TTTTCCCACT CTGGATATTC TTCACCATTC TCATCTTTGA ATCGCAATTC	720
TTGTGTGAAG ATTTTCTGCA TATAGCCTTT TTTCTGTTGT TGAAGCAATT CAAGTTTTTG	780
TTCTTCTAAT TCAATTTGTC GGTGAGTTT GCTGAAGAAC TTGCCTATTT TTTGCTGTTC	840
TTCAAATATA GTTGGGGTGA AGATTTTTTAA ATTAGCAATT TCTTTGAAGT TTAGACCTTC	900
TCGACTACCT CCACTTTGTG CAAGGAAAAT TTTCTTTTA CCTTTTCTTG ATAATAGATA	960
CTGTCCAAAA AAATTATAAT AATACTCTTT TTTCAATCTA ATAATACATA CATGTTGATT	1020
TAAATTAGCA TCGGTTTCAA CTATCGAATT AATGGCTGTT CTACCTATTG ATGCTCCTGT	1080
AATATTTAAA AGAACATCAC CATAGTACGT TCTACTATTT TTCATCTCAT CATCTATATC	1140
TTTACTAATA TAACTAAGT GATTAAGATT TAATTTACCA TTTCTAATAT TTTGACTCCT	1200
TAAAAATGGT ATGCCTTTGT TTGTATAGTT TTCACTTCCA CCTTTGGGAG TCTTTCCACT	1260
ACCTATTTTG GTAGTAAGAT TCCCTAACTT CTTCTCTTCC CATTCGCCTT CAAATCCTGG	1320
GAATCTCAAC TCTGGCACAT TTTTCGTTTG TGTATTACTC ATCTTTTAC ACCCCAAGTT	1380
CTTTCAGGTA TGCATTGATT TCTTGTTCAA TTTCTGCGAT TTCTTTGTCTG ATATTTTTC	1440
AATCTTGTTG GACTTGATCT AAATCAATTG GTGCTTCTTC TTCGAATGTA TCAACATATC	1500
GCGGTATGTT TAAGTTGTAA TCGTTATCGG CGATCTCTTG TAATGTCGCG CTGTAGCTAT	1560
ATTTATCAAT CGTTGCTTTA CGCTTATATG TGTCTATAAT ACGTTCGACT TGGGCATCGC	1620
TTAAATGGTT TTGATTTTTT CCTTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT	1680
TGTCGTCTTG TTGGCGACAT TTTTAAATA CTAATAACA TGTTGGAATA CTTGTCCCAT	1740
AGAAAATATT GGCTGGTAAC CCAATCACG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT	1800

AGCGACGAAT CACACCTTCT GCGGCACCAC GGAATAATAC ACCATGTGGG aGTACGACTG	1860
CCATGGTACC TTCATCGTCT AGGTAATGTA CCATGTGTTG AATAAAGGCA AAGTCTGCTT	1920
TGGaTTTTGG CGCAAgCTTG CCGTAACCAC TGAATCGTTC ATCATTTCa AATTTGAAT	1980
CTGCTGTCCA TTTCGCACTG TATGGTGGGT TCGCAATAAC CGCATCAAAT GTATTGCCTA	2040
AAAAGGCTGG ATTTTCCAAT GTGTCATCAT TACGGATCTC GAAGTTCTCA TAACGCACAT	2100
CATGTAATAA CATATTCATG CGTGCTAAGT TGTATGTAGT ATTGTTACGT TCTTGTCCGA	2160
AATAACGATA CACTTGCGTT TCTTTACCAA CACGTAACAA CAATGAACCG GAACCACATG	2220
TTGGGTCGTA CACGTGACGT AATTTATCTT TACCGTCTGT GACAATCTTC GCCAGTATCT	2280
TAGATACTTG TTGTGGTGTA TAGAACTCGC CTGCTTTTTT ACCCGcTGTC GCCGCAAAGC	2340
GCCCGATTAG GAATTCATAT GCATCACCTA ACATAaAAT TTCCATGTCA CTGTGAACGA	2400
ATGGTAAGTC GTCAAGATTA ACCATGACTT TAGAGATTAA AGCAGTACGT TCTTTGACAT	2460
TGTTACCTAG TCGCGTTGAA CTCAAATCCA TATCGCTGAA CAGCCCGATA AAGTCATTTT	2520
CACTTTCTTC ACCTAATGTA GATGTTTCAA CTTTGCGAAT CGCCGTCGCT AGATGTTCTA	2580
TATCGAAATC TTGCGTTTCA ATTTACGAA TCATCGCACT GAATAAATCT TGTGGCTCAA	2640
TGAAGTAACC GACTTGATCA ATTAATTCTG CTTTTAAGTC TTCACGATAT TCTTCATCTG	2700
CCCATGCTTC TTGATACGTG ATGTCTTCAC CTGACAAGGC ATCTGCATAT TCTTGTTGCG	2760
CTTTTTCAGA TAAGAAGCGA TAGAAAATCA AGCCTAAAAT GTAATTACGG AATTCACTCG	2820
CATCCATGTT CCCTCTTAA TCATTCGCAA TCGACCATAA TTTTTTATGT AATTCAGCTT	2880
GTTGCTGACG TTGTTTTTCA GTAATAGACA TGTGATTCTT CCGCCTTTGC ATAAGTAATT	2940
TATCTCTTTG TGTAATAGAT TTATTATAAC ATTTGGTTAT GTcCGATGT TGATAATTTG	3000
GATGTTGGTG GTGGAAATTT TGAGTTTTAG TGGCGCAATT GTTATTGAAA AATTTTATAG	3060
AAATGTTGTA GCTTTCAAAT GCTTTCAAAA TCATTTATAT TCTTAATGAT GTCAAAAAGT	3120
TGTTCAATCA TACATAAATA AAACCAATCA ACAATTGAGT TGGTGAAAAT CAATCGTTGA	3180
TTGGCTTTGA TGCATATTAA ATAATGCAAT ATATATTAAT AAATGTTAGT TATAGTATAT	3240
TTTGTcAGGA TTGGGTGAAT GTCTAAGTTT TAATTATTTA TCTAAATTAT CTGCAATGAA	3300
TTTCTTAATT TCAGGAGAGA AATAAACAGC AAATCCTCTT GTGCTTTTAC CTGATGGCTT	3360
ATTACCGGCA TAGATTACAC CAATAGCTTC GTGTTTACTA TTTAATATAG GTGAACCAGA	3420
GCTACCAGGC TGAATAATTG CATCCGATGA CACTATATTC CCATTCACTG ATAATACTTT	3480
ACCAGTTGAT TCATACATTT GTAGTTTATT TCCATTAGGA TTTGGATAAC CAATGACTGA	3540
TATAGGTTCA TTTTCTTTAG CTTCTGATGC TATATTAAAT TTACTAGTGAAATCTTTGAA	3600

TTTTCTACCT TTTGGTTGTG TTGATTTTTC TTCAACTTGT ACAACCGCAA TATCTTCTTT	3660
ACCAGGATAA TCTACAATCT TAGTAACTTT ATAAAGTCCA CCACCGTTAT TATAAAAACC	3720
ATTAGGATGT GCTTTGATTT CATCACCGAC TTTCATGTGA TAGGTAACAT GTTTATTGGT	3780
AATGATTGTA TGATTTCCAA CTACAAATCC TGTTCAGCG CCCATCCATG TAACACCACT	3840
GTATGGTGCA ACATTTGTAT TTGTAATTTG TTTAACAGTA TTTTCGGCTT TGGCTGTTTG	3900
TTGAATACCT TCAACCATTG TTGTGCCGAC ACCAGTTATT GATGTTAAAA TCGTCAATGC	3960
TGCAATACTT TTGATGATTA TATTTTTTAT	3989

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

CGTTGAGCAC AGTTTtagat AATAGATAAT CTTGctCTAG TTGTTGCAAT GTCTGCGATT	60
TATTGTGCAT TAGCAGTTGA TACGCCATAG ATAATAATAG TTTTtCTTTA TATGATTGAA	120
TATGCGTGTA ACGTTCAGTT ATCGTTTCTA AGGTATACTG AGATGTATTT AATtATATC	180
CTTTAGATTT AATACTTACG ATGATATCAT CCATAAAATT GCTATTGATA ACATGGATAT	240
CATTGCGAAC TGTGCGGTTT GAAACATTGA CATGTTTAGC AATTTcATTA GAACTAATGT	300
GCTTTGATGG ATTTTtAATA AAAAACTGGA GTAGTTTTAA GTGTCTATCA AGCATTtAAC	360
ATGTACCTCC TTTCTAAATT TTTCGTGTAA GCGTTTTTAA GGGTGTATTA ATATTATTAA	420
ACATGAGAGC TTATACATAC GTCAATGACA TTAAAGCGAA CTTTTATATG ATTTTAAACAG	480
AGTGCGAATT ATGCAAATAA AGAACAGCAG TAAGATATTT CAAATAGAAA AATATCTCAC	540
TGCTGTTTTT CTGAATTTAT GCATCTGGTA CTTGTtGACG TATCAGGCAA ATGATTAATT	600
TTTAGGTGAT TGTGCTTGAG GTGTTTGTTT AGAAGGCGTA TTGGTATTAT TTGATTTATT	660
AGCAGGTGGT GTGTTCTGTT GTTGATTATT TTGGTTGTTT GTTGACGATT GACTGCCACC	720
ACCGTGAGTA TTATTTTTAT TTGAATTTGA GTCTTTTGGC TGAGCTGGTT GCGTATTtCGA	780
TGGTACTGTT GAATGGTTGT TAGGAACATT TGACGGTGAA GATGGTTGAT TGTCATTAGT	840
AACGTTATTG CCATTATTTT GATTtTTATC TGTTTTGTCT GCACTATCAT CTTGTTGATC	900
ATTT	904

(2) INFORMATION FOR SEQ ID NO: 818:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

TTTAACatGa TAATAAAAAA TCTTTTGTGA TATCATTAGG AATATTTGAT GAACTTGATA	60
TTAAGGTTAC ATTTTGAGAA ATGGACTTAG GGATATTTCC ACTATTATTT AGTAAGAAAT	120
CTTTAGCTAA TAAAGATTTT CCTACACCAT TTTTACCAAC AATGTGATTG ATCTGACCAA	180
GATAGAAATT TAAATCACAA TTGTCAACTA GTTGTTTGT TTTAACTTTT AAAGAATAGT	240
TATTTAGTTT CATGTATACA ACTCCTATGT ATAAAGGGAT TTATTACACC GATATTTAAT	300
TGTATTTTTA AAAATTCTtTT CACATTATGT ATAGAwGTTA TAAATTAGTA TATCaCACTA	360
TATTTtGkCT AAATGATAAA TATATCGTTA TATTTTTACA ATATTCTGAA ATTTATGTTC	420
GCCTCTGAAT GCTATATCCA GTGTAATGTG TTTTGCATAT ATGAAAGCAA TTTCAAATG	480
TGAATATAGG TTCATTGTGG TATGACAAAC TTCATTGCTT GTCATGAGAT GGATATAATG	540
AAGACGACTA AAAGAGCAAT GAGGAGGATA ATCATGGTTA AGGCTATTGC GGTAGATATG	600
GACGGGACGT TTTTAGATT CAAAAAGACA TATGATAAAC TTAGATTTGA AGCGATTTTT	660
ACTGAACTTA GAAATAGAGA TATTACATTT ATTGCTGCGA GTGGCAATCA ATATGCGAAG	720
TTGAAGTCTA TTTTCGGGGA TAGAGATATG TATTTTATTT CTGAAAATGG TGCAGTTATT	780
TATAATGGCA ATGAGTTATA TAATTATAAA AGCTTTAATC GTCAGtGTT TCAACAGGTT	840
GTCGATTACT TAAATATGAA GCAAAGTATT GATCAACTCG TCATCTGTGG TTTGAAAAGC	900
GCGTATATTT TAAAACATAC TTCTGAAGCG TTTAAAGAAG ATACGAGATT TTATTATCAT	960
CAGTTAAAAG AAATTGACAG TCTACAGCAA TTACCTGAGG ATGATTATGT CAAAATAGCA	1020
TTTAATATTA ATCGTGAGAC GCATCCGAAT GTTGACGAAG AAGTAGCAAC GCAATTCAGC	1080
AATGATATTA AACTTGCTCTC AAGT	1104

(2) INFORMATION FOR SEQ ID NO: 819:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

CCCNtTTTAC GGATTAAngG CTTTTTCCTA TTAAAACCT ACGGCATTTT CTTTTCAACC	60
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ACGGCGGCTC CCATATGGAT GGTATnGGGA TTGGGGTTTA TAAATGGGG ATTGGAAATG	120
GTCCATCCTA AATACTCAGT TTAGTGCTTA TTTCCTTTAG TGCTGACGAA TAAATATGAT	180
CTAACTCTAC GAAACCTAAT AACGTATCAA ATGCTTCATC ACCATTTTCA AATTTACTTA	240
AACTATTTTT AAAATCATGT CGCAAATCCT CTAAATATAG TGATGGTTT CGATCTACAT	300
ACATTTTTTAT ACTAACCTCC GATATATAAT CATCTTTATT GTACCTAACA TTTTATTAAG	360
ATAATACTAA TACACTATCG AACTTTGGGC TGATACTGAA ACAGCACAAA GAAACTCAAA	420
CAATTCGAAT TATGTATCAA AACCTTCAAT TACAGGAAGT GATTTTAAAA TGATTTAACG	480
CAAAAAAACA CCTGTTACCG TTATATAGGT ACAAGTGCTT AATTGATAGA GATGTTATAC	540
GTCTTTAAAT GATTCCACAA CTTTTGGATG TGGACCATCC ATAAGCGGT CTCTTTGTCG	600
AACGCCACCA CTTTGGTTGC CAATTGATTC GCTATCAAAG TACGATTTAT CTTGATTTGA	660
TTGTTCTTGA ATATGTTCTT CATTATCAGT TGTTGCATAT TCACTATCCA CCTCTGTTTT	720
TTCCATTGTT GCTGTATGGA ATTGTACGAA GTTCTCTTCT TCTAATGCTT TGATTTCTTC	780
TTTCGATAAC GCTCGATACC AATCTTTCGC TTTTTCGCC GCAaTAGGAa CAaCAtCTTT	840
TyCaAGATAT CCTtCTTTTA ACATTGCATt CGCAATTTCT ATCGCTTTTT GCCGtTAAT	900
TACTTCAAAT TCTTTCCATT TTTCGGGGTA ACCTTTCATT GTAAAGGGCA TTCCCTTAAC	960
CTCCAATATG TTATAATTCA TGTTATATAC CACCATAATT ATAAAATGAA ACATATTAA	1020
CACAATTTTT TAGACTCCCG TCATAATAAC TTCAGACAAA CGTTAGTCTG ACCTGATAAA	1080
TATTTAATTT TAAACGTTCT TGTCTCTCTC ACGAAAACCA TTGTGTTGAA TATTCATCAT	1140
TGCTGATTGA ATATAATTAT ACTGTGGTAA ATCTGGTAAT ATCTTTATTT CTAATTCTGT	1200
ATTTAATTCG AAATGCTTAG CGATGTTTTT AAATATTGCT AAATACTCGC CCATTAATTG	1260
TTCATTTATT GTAAGTCTAT CTTCATTAGC CATGGCTGA TTTAACATAA AGCTAATTTT	1320
TTCTAATGCG AATAAGCTAG GATAATAATT TTGAATCAAT GTCTTATCAC TAAATAATTC	1380
ACCATTAGCT GCATTATAAA CTTGCGTGCA TGTTATTTAA TTTGC	1425

(2) INFORMATION FOR SEQ ID NO: 820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:

nCGnCCTTAT ATATGTTTTT CATGTCCTAC AAAAAACGAA ATATTCCAAT TGCCTATAT	60
CAGATATTCA TTAATGACAC ACTCAATAGC AACCAtnACA ATATTATGTT ACCTATTTAA	120

ATGAAATAGT TCTTTTAAAG AAATACATTT TTCACATATT AATCTATAAT CAAAATCAAC	180
TGACCGATAT TCTATAATTT ATGATTAAAA TAAGTTATAA TATAATAGTA AAGATAAAGA	240
TAGAGGTGGC TATAATGTGT GGAATTAGAA GTATAACATT AGGTACaACA AATATAGAAC	300
AGACaAAACa TTTCATGGTT GACATATTAG GATTAAATTA TGAAGAACTT CTTGAAAAC	360
CAATTCGTTT CGGCGATGCA GATATAAGCC CAGGAACAAG ACTTCAATTT ATACAAGTTC	420
CAAGTGAGCA ATTAGAAGAA TCTCACTTTG TGGGTATTGGATTACGTACA CCAACTGACT	480
CAGGTTTAGA GGAGTATGCG GAAATATTAT CGAATAAGGA TATTCCATTT ACAACAGTTA	540
AAGAATTAAA TGGCAATAAA TATTTTCAGTC TCGAAGATAA CAATGGTCAT ATTTTCTCAA	600
TATATTCAAA CGAGAATAAT TATGGCGTTG GTTTAGGTAT GCCTTCTTyT GAGAGTGC	660
TCAATCCGTT ACATCAAGTG CAAGGTTTAG GACCAGTGAT TCTTAAAGTG AATCATGTAG	720
ATATTACAGG TCAAATTTTA ACAAATATAT TCGGACTTGA AGTATTTGCA GAATACCAAC	780
CCTTCGACAA TGCTGACTAT CATGTCCAAG TATTCAAAGT TGGAACGGGT GGTCTAGGTG	840
GCGAAATACA TTTAATGCCT GTAGAAACCG AAATGACAAT GCCGGAATAT GGCGCAGTCG	900
ATCAAGTTGA GTTTGAAACG AAAGATGCAG ATTTCTTTAA TCAAGCGAAA TCGCGCTTAG	960
ATGAAGTGGA AATACCATAT CAAACGCTTG AGCAAGATGA TATTGAATCA ATTAGAaTTA	1020
CTGAAAACAG TGGATTATCG TTTATATTCA CTTTACAAAA ATAATTTTT TACGATAGCG	1080
AGGACAAAAT TTATGTTACA TGAACTTGG AAAGAACGTA CACCAATCAA GAAAGTAGAA	1140
GTCATTAATA CAGATGCAAA GAAAT	1165

(2) INFORMATION FOR SEQ ID NO: 821:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821:

TCGCCAATT ATTATGAAAT ATTCAATACA GTTTATTGAT CAAAAACAA AAATCCATTA	60
TGAACCTTGT CATCACGAAT ATTAAGTGAC GTTAGATGGA CCTCTTTAAT GATAGAACAA	120
TTAATAAATA ATGCACTTAA GTATGCGAGA GGTAAAGATA TATGGATTGA ATTTGATGAG	180
CAATCCAATC AATTACACGT AAAAGATAAT GGTATCGGTA TTAGTGAAGG nACTTGCCTA	240
AAATATTTGA TAAGGGCTAT TCAGGTATA ATGGCCAGCG CCAAAGTAAC TCAAGTGGGA	300
TTGGTTTATT TATCGTAAAA CCAATTTTCA ACACACACAA ACCATCCGTT TCCGTCGTAT	360

CTAAACAAAT GAGGGTACAA CCnTTACGAn TnCCATTTCC

400

(2) INFORMATION FOR SEQ ID NO: 822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822:

TGATATAATA CTTTTGTAAA GAAAAGCATG TGTGGGAGGT ATGACCTEA TGTCGAACGA	60
AATACTTATC GTAGATGATG AGGATAGAAT CAGAAGATTA CTTAAATGT ATTTAGAAAG	120
AGAATCTTTT GAAATCCATG AAGCAAGTAA TGGCCAAGAG GCTTATGAAC TTGCAATGGA	180
GAATAATTAT GCTTGCATAC TACTAGATTT AATGTTGCCT GAAATGGATG GTATCCAGGT	240
GGCAACTAAA TTGCGTGAAC ATAAACAAAC ACCGATTATT ATGTTGACTG CTAAAGGTGA	300
AGAAACAAAC CGTGTGAAG GTTTTGAATC TGGTGCAGAT GATTATATCG TCAAACCATT	360
TTCACCAAGA GAAGTAGTCT TAAGAGTTAA AGCACTTCTA AGAAGAACGC AATCTACAAC	420
TGTAGAACAA AGCGAACCTC ACGCACGTGA TGTGATTGAA TTAAACATT TAGAAATAGA	480
TAATGATGCA CATCGCGTAC TTGCTGATAA TCAAGAAGTT AATTTGACTC CTAAAGAGTA	540
CGAATTATTA ATATATTTAG CTAAACACC AAATAAAGTA TTTGACCGTG AACAAATTATT	600
AAAAGAAGTT TGGCATTATG AATTCTATGG TGATTTAAGA ACAGTTGATA CTCAGTTAA	660
ACGcTTAGAG AAAAGTTAAA TCGTGTGTCT AGTGAAGCTG CGCATATGAT TCAAACAGTC	720
TGGGGCGTTG GGTATAAATT TGAGGTTAAA TCTAATGATG	760

(2) INFORMATION FOR SEQ ID NO: 823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823:

CAAAGGAAAT TGCACAATTA GAAGACCGAT TACGTTACG CTTTGAATGG GGGCTAATTG	60
TTGATATTAC GCCACCAGAT TATGAACTC GAATGGCAAT TTTGCAGAAG AAAATTGAAG	120
AAGAAAAATT AGATATTCCA CCAGAAGCTT TAAATTATAT AGCAAATCAA ATTCAATCTA	180
ATATTCGTGA ATTAGAAGGT GCATTAACAC GTTACTTGC ATATTCACAA TTATTAGGAA	240
AACCAATTAC AACTGAATTA ACTGCTGAAG CTTAAAAGA TATCATTCAA GCACCAAAT	300

CTAAAAAGAT TACCATCCAA GATATtCAAA AAATTGTAGG CCAGTACTAT aATGTTAGAA	360
TTGAAgATTT CAGTGcAAAA mAACGTACAA AGTCAATTGC ATATCCGCGT CAAATAGCTA	420
TGTcTTGTCy AGaGAGCTTA CAGATTTCTC ATTACCTAAA AATTG	465

(2) INFORMATION FOR SEQ ID NO: 824:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824:

CACCGCGGTG GCGGACGCTC TAGAACTAGT GGATCCCCCG GGCTGCAGGA ATTCGGCAGC	60
AGGTAAGGAG GTCTCTGTAC CATGGCTCGT ACAAAGCAGA CTGCCCCGAA ATCGACCGGT	120
GGTAAAGCAC CCAGGAAGCA ACTGGCTACA AAAGCCGCTC GCAAGAGTGC GCCCTCTACT	180
GGAGGGGTGA AGAAACCTCA TCGTTACAGG CCTGGTACTG TGGCGCTCCG TGAAATTAGA	240
CGTTATCAGA AGTCCACTGA ACTTCTGATT CGCAAACCTC CCTTCCArCG TCTnGTGCGA	300
GAAATTGCTC AgGACTTTaa AACAGATCTG CGCTTCCAnA GCGCACTATC GGTGG	355

(2) INFORMATION FOR SEQ ID NO: 825:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1099 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825:

TTCACTTGGC TTGTTGAcTG ACTTGTAAtAT GAtGATGTGC TTTGTGAATC GGATTGCTC	60
GTGCTTGTAC TTGTTGAGTT TGAGGCACTT TGGCTTGCTG AGTTTGAGTC TACTCCGCTT	120
TGATTCATTG AGGCACTTAG TGACAATGAT GTACTCGTTG AGTCAGACAA ACTTGTA	180
GTTGACGTAC TTGTACTTCC TGATGTTGAT TGAGACATAC TTATGCTCAT TGATGTTA	240
TCGGATTTAC TTTCACTTGA TGATGTTGAG TCGGATTCAC TTTCACTTGT AGAACCACTT	300
AATGATGTGG ATGTACTAAT GGAATCAGAT TTACTTGTA	360
ATTGATGTAC TTAATGAATC AGACTTACTA TCACTTGTTG AATCACTTAA TGATGTTGAC	420
AAACTTGTAG AGTCAGACAA ACTTGTA	480
TCGCTCTTAA ACGTTGACGT TGATTCACTG ATACTTGTCG ATGTTGAAAT GGACGTACTA	540

CCACTTGTTG AATTACTTAA TGATGTTGAT GTGCTACCAG ATTCTGATGT ACTGTCTGAT	600
AATGACGTAC TCTCACTTGT CGAACTACTC ACTGACTCTGATGTTGATTC AGACGTACTT	660
TCACTTAATG ATTCACTTAA AAAGGCAGAT GCACTTTGTG ATTCTGAATC GCTAGTACTA	720
TTTGATTCAC TTAATGATAT AAACGTGCTC TCTGAAGCAG ATATTGCTTC ACTTATAGAG	780
TCGCTCGTTG ACGTTGATTC ACTTATTGAA TCAGACTCTG ATGTACTTAA GCTTGTGGAA	840
TCACTCaTAG ATGTTGaTGT ACGTTCTGAA TTAAGGATGT CGAAGTACTT	900
ACCGAACCAG ATGTGCTCGT AGAAGCACTT TgTGATATTG ATTCACTTGA TGCAGTTGAT	960
GCTGATTTGC TATCACTCGT TGAATCACTA AACGACGTTG ATATGCTCaT TGAATCGGAT	1020
TGACTTGCAC TCAnTGAACC AGACGTACTT TGTGATTCCG AAGTACGTAC TGAAGCACTT	1080
GTCGACGTTG ATGTACTTG	1099

(2) INFORMATION FOR SEQ ID NO: 826:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826:

TATGCGTATC CTGATAGTCA CTTTGATTTT GATATGGAAT TAGCGAAAGA GCAATCTCAA	60
GACAATCCAG TTTACTATGC TCAATATGCA CATGCGCGTA TTtTTCAAT TTTAAAACAA	120
GCGAAAGAGC AAGGTATTGA AGTGACTGCT GCGAATGATT TTACAACGAT TACTAATGAA	180
AAAGCGATTG AnTTGTTGAA AAAAGTAGCT GATTCGGAnC CTACAATTGA AAGTGCTGCT	240
GAGCATAGAT CGGCACATAG AATTACTAAT TATATCCAAG ATTTAGCCTT CTCATTCCAT	300
AAATTCnATA ATGCTGAAAA GTGTACCAGT TGGTATTG	338

(2) INFORMATION FOR SEQ ID NO: 827:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827:

GTATTTTCTT TCGCGAATGA TTTTATTACT TGAATACCAC GAATAACCTC CAATACCTTT	60
TCCACTAATT GGTTTTGTAC ATTATGATAC GcTGCGCAT TTTGTGACT CTTTCTTTCT	120
AATAATTGAA TCGCAAAAAA TGATAGTAAT ACGCCAATGC ATGCTAATAA TGATACTTGC	180

CACGAACTA CAAGTAGAGA CAATATGAGT ACTGTAATTA ATATGTATCC ATTAACAACA	240
ACGTCCACCA TTTTCATAGC AAAGTTTCT AAAAAGGTTA AATCTGTTGT TACTATTGTT	300
GTAACTCAT TTGAATGATG CGAATTAAAA TAACCTAACC TTACATTTT CAATTTATCC	360
CCTATATCTA AACGTTCTTT CGCACTCATT TCATAAGCGA TGCTCTCATG GCTTTTGCTT	420
TTGAAATATG CTGTAATAAA TCGTCCAATC ACTAATAAAA CCATGATAAT TACAACATTC	480
AATATATCTT TCATATAAAT AGGTTTATGA GATAGCACAT TATTAAATAT TTTTGCAGCT	540
AAAAAGATAG GTAACGCAAT AAAAATAGCA TTTAAAAATG ACATGCTAAA TCCTAAAATC	600
ATTCTTGCTT TATATGGTCT TATCCAGTTT AAAATTTTAA ATGTAATTTG AAACATATTT	660
GACCTCCTTT TCTCATTAGT TTAATTATGT CCAGTATTGA TTCCCCAATC TTTTGTATGC	720
ATGTGCGTAT CCCACATTTT CTTATAATTA CCGTTTAATT TTAGCAATAA GTGATGTGAC	780
CCTTTTTCTA AAATTTGTTG TTTACCTAAA ACAATAATTT GGATCTGCAT GTGGAAnC	838

(2) INFORMATION FOR SEQ ID NO: 828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828:

TCCnAAAGAA GAAATAaCAT TATCATaAAA TCCATTGAAT ATAAATTCAG TCATCCCCTC	60
TGAACTtCTC CATAAATATA ATGGTGAATA AGTATTTGTA ATGCAATTAGTAGTTGTTTG	120
ACTTATTAAA TAAGCTTTTA TAATTAAATT TTTAAATCCA TCAGTCTTAT AACCATTTAA	180
TCGAACTCTA TCTCTAATTA TTTCCATATT GTAATCACTA GGCAACTTAA CATGATATTG	240
CATTGCATGC ATTTAGCATA CCCCTTTTAA TAAAAAGGAT AGCAATAATA AGTAAATCT	300
CATATTATCC AATTGTGATA TAGTTATCAT AAAAAGTGAT AGGTGATTAA ATTGAACTTT	360
AATGATTTGG AAATTTTTAT AACTGTATGT GAAGAAGCAT CTATCAATAA AGCTGCAATT	420
AAACTTAGAT ATGCACAATC TAATATATCT CAAAGAATTA GCAAGCTTGA AAATGAATTA	480
GGTGTAGTTT TGCTTTTTAG AAATCAAAAA GTGCTAAGG CAACTAAAGC AGGCGAAGAA	540
TTCTTAGCGT ATAGCAAAAA AGTATTAAGA GATACAGAGA CTATAAAAAA TAAATGAAA	600
AATAATACTA TGTCTATTTT ATGCTCAGAA CTGTTATTTA ATTATTTATC TGAGAGCGAA	660
GAAATTATGA TGTCGAATAA CTCAATTAAT TTTATTTCTA GTGGAAATAT TAGAAAAGT	720
ATAGAAAAAA ATAATTATGA TAAGGTTATT TCATTCATAA AAaTTAACGA CTCAAATTAT	780

AGACTTAGTA ATGTTGATAC TATGaaAGTA ACGCTTTACA GTAATGGAAG TAATTATGAT 840
 AAAGAGGCTT TACTAATAAA TAAAGATGAG TTTGGTCCTT TAAGGnAAAT AACTTTAG 898

(2) INFORMATION FOR SEQ ID NO: 829:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829:

AGTAGGAGTC ATAAAATCGn ATTTCAAAAG CAATTAATGC AAAATACTGA GTCTACAGTG 60
 CTATTTGCGA AAGCGTCcAT ACGAAgTTGA GcAATGCTAA TAATAATGGT CTATCAAAAA 120
 GAGACGTGAT TAATCaATTT aATGaTTTgA AAAAAATGAA AAAATyCCCT TCtAATCTTG 180
 AATATGTTGA TAGTTACACT GATTCTCTTA CTGGAGAAC AACTTCTGCT TTTTAAATA 240
 AAGATACAGG CAAAGTAACT CTCGGGATGA CTGGGACTAA TTTACAAGAC GAAGCCTTTA 300
 AAAAGTTAAA AGAAGGTGAA TTTTCAAGAC AAAATGTTAC CAATGCTTTG GAAACAGTTA 360
 AAGATGGATA TGCAGATCTT AAAATATTAT ATTCTCCTGC ATCTGATCAA AACTATAGAT 420
 ATGCGAATAC ACAAGAATTT ATAAATAAAA TAAAAAGTAA GTATGACATT GATTTTATTA 480
 CTGGACATTC ACTAGGTGGA AGAGATGCGG TAGTTCTAGG AATGAGTAAT GGTATTCCGA 540
 ACATTGTGGT TTATAATCCA GCTCCTATTT CTATAACTAG TTTGAATCCT AATTCCCCAG 600
 ATGGAAAACG TTTATTAGAA TTATATAAAA ATTATAAAGG TAATATTACT AGGTTTGTG 660
 CAGAAAATGA TGCATTGACA GAAAATCTGA AGAAATATAA GCATTATGTT TTTTTCGGTA 720
 ATGATAAAGT CTTTAAAAAT GGTAAAGGTC ATGAAATGka AGGctTTCTG ACCGAAGAAG 780
 AACAAAAAGC tATAAAAn 798

(2) INFORMATION FOR SEQ ID NO: 830:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830:

AATATCAATC TCTTCATAAG CTGAATTATT TTCATGCACT TCTTGATGTG ATGATTTGTC 60
 ACGAACnGCT ACAACTAACA TTTTATCGTC TAAAATAAGT TGTTTATATT TTTCTAATTC 120
 ATCAGGCGCT AAGTTGTAGC GTGATAAAAC TGCATGTTCA CCATCTTCTC CTGTTAACAG 180

TTTAGTCATT CTATCACTAA ATGTTCCACT TGTGAGATA AGGGGAGATT TCAGAGTCGT	240
GTAAGTCATT AGGTGTAATT TACTTTTACT AATAATTGTT AGCCTGATCT AAATAACTTC	300
AGATTCTTTG ATTGATAnGT GnATAATCGC AGTGCATTAC ACAGAATACT GCCAAGTGCG	360
CCCTTAAAAT TGTTATTAnC TTACCTCTAT ATAAGAACCC	400

(2) INFORMATION FOR SEQ ID NO: 831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831:

AAGTCTGCAT GACTTTTATT TGCAAGTTCG ACTGCTTGAT CAAAAGCGCG ATGATCTTCA	60
GGATtAGCAC TTTGAACTGA GCTGAAATTC GGATCAGGTT TACATTGTGC TTCTACAAGA	120
TTAAATTGAT TGAAATTCAA AGATTGTAAT AACTCAGGTA CAÆCGGAAC ACTTGtACCA	180
TGCAAACTAG TGAACACAAC TTGTAAATCA GATTTAGGAA TATAGCCAAT CATATTTTGA	240
ATGTGTTTCA TATAGTCATC AGTTACAGAT TTCGAAAAG GCTTGaTATA AGATGTATTT	300
TGTTTAGAAA tAGGTATATC AATCTGTAAT GGATCGCCAA CTTCTTCGAT ATAACGACTT	360
GCAAGCTCAG ATGCATCAGT CGATAATTGC GCACCATCAG AACCATATAC TTTGATGCCG	420
TTATAGTCTT TCGGATTATG ACTTGCTGTA ATCATAATGC CAGCAGTAGT ATTAA	475

(2) INFORMATION FOR SEQ ID NO: 832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832:

CTTGAATTGA AGGATACGCA AATGATGCAT AATCAGCTTC TGTATAAAGC TGTAATGTAA	60
TGTCATCAAG GTCACCTTTT CTAACAAGCA CCTTATTAAT AGAAGTATGA TTCGCTTGCC	120
AAGTACCTTG ATTATTTTGT TCTAAATGAA TGAÇTTCGCC TAACGATTTC AACGTAATAT	180
CTGCACGCTC GTCTTCGCTA ATAGTATATG TCTTACCATC TCGCAAATTG AGCATCTTCA	240
ATTGTTTGTT ATATTTTATA ATCAATTTAT GCATTGTCTT TGCCTCÆTC CTATACTATT	300
TTTTTCTTTC AGCTTCTTGG CGTTTTTCTT TATCTTTTTG TGCTTGTTCT TTTTGTTTCT	360

TTTCGTTCTC TTCTTGTTCG TTTAATTTCT CATCTTTCGC TTTTGCTTTC TCTTCTTCAG	420
ATTTTCGCTTT TTCATCTTTA ACTTGTTTTT CTTTGTCTAA AATATCTTGC AATTTATCGT	480
TATACTTTTT CGTTTCTTCA GAACGTTTAT CATTCGATAA ATCTCCGTTA TTTTTAATCT	540
CATTTAATTT ATTAATCAAC GCTAACTTTG TAATATCGTT ATCATCTAAA TAAGTGGCAA	600
TATTAATCGC TTCATCAAGA TGTCTTGTC CTAATCCAT CCAATATAAT AAGTAGTCTT	660
TGTTTGAATT TGGTGTCA n TTATTAAGT AATTTTCTTT CGTATCTGTn TCTAAAC n T	720
GTTn	724

(2) INFORMATION FOR SEQ ID NO: 833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:

AGCAGTTTGG CTCGTAGAAA TCTCCCGTCT CTATTCTATG TATTAAC TTT TATTATATTT	60
GTTATGATAC TATCGATATG AAAGCGTTGT CAATGGTTTT TGTAAAAATTTTGTCAAATT	120
TAATTTTTCA AGTCTTTATA AAAGTAGTTT AATTTGAAAA CTAGAAATAC CAATCCTAAC	180
TAATTTATTT ATGACGCTCT TTTGTTTAAT TGACATTCTT CAGCCATATT TTTTATGACT	240
AGTTGCATTT TTTACTAATA AACACCTCTA AAAC TTTAAT GATTTTAAATC GTTTTAGAGG	300
TGCTAATTAT TTTATTTGAT TATTTTTTGT TTGATACCTA CTGCATATCC CATATGAAAA	360
CGGCTTTTTT ATTATGTTAT ATGACTAAAT CTCGTGAAAA ATGAAATTTT TGCAGACTTA	420
TGATTTACCA AAGTTTATCA TAACTAGTAG TTACATATTT CGCTCCATTT TTAACAGCTT	480
CATTGACTTC ATCTATTGTA TTAATTAGGC CACTGCAAT GACTTGTGTG TTTGTTTCTT	540
TCTGAATATG ATGAATCGCT TTA CTGCAA CACCTGGAAG TACTTCAACA AAATCAGGT	600
CAACTTTTTT TATCAAATCT ATACTGCGTT TCAATGCTTG ACTATCAATA ATAAATACTC	660
TAAAAATCGT TAAAGTATTT AATGATTTAG CTTTTTTTAT TACTTTAGAT TTAGTCGAA	720
CGATACCTTT TGGCTTGAT TGCTGAATAA TAAATTCACT TGCAAATTCA TCGTGGCTTA	780
AACCTTTTAT CAAATCTATA TGAATAAAAC ACTCTATATG ATTTTGCTTC AGCAATTCCA	840
TAATACTTTT TATATGTCCT ATATGCATAT CTAGAAGCAC ACACATTTTA TAGTCTGTnT	900
TAATCCAGTT TCTCTAAAATC nTTAATGTTT CCTATAAGCA GGCAATATGT TGTTAATTCA	960
CTnGATCCAT CCTCTCTACA TCACACGCTT AAAT	994

(2) INFORMATION FOR SEQ ID NO: 834:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:

TCnACAAAGT CGGTATTAGG CTATGGGCCA TTTnACTATT ATAACTAATC GGAAATATAC	60
CACATAACAT CATTATTGAG TTGATTCTAT CATTTCCTT ATTAGGGTTT TTTATCATAA	120
TGATTTGCAT TTTGCTACTA GTTTATAAAA TGATTAGGAA CTATGATCCA AACACTATAG	180
ATTTACTCGT TATGTTTATA GCAATCTATC CAATCACATT ATTAATGTTT AGTTCAAATT	240
ATTTAGTTGT AAGTGAATTT TGGTTTGTGT TGTTCATTTT TATTACAAAA GGACGGCGTC	300
ATCATGGCTA AGAAAGTTTT TATTATGGAT AGCGTAAAGA CAATAATTGG TACGTTGCTT	360
ATAGCTTTAG GATTACAATT TTTAGCTTAT CCAATTATTA ATCAACGAGT AGGTAATGAA	420
GCGTTCGGTT CTATTTTAAC GATTTATACA ATAATAACAA TCACGAGTGT TGTATTAGGC	480
AATACGCTTA ACAATATACG mTTGATTAAT ATGAATCTAT ACAAATCCAA TCATTACTAC	540
TGGAAATTTG CATCGATACT TTTAATCTCA ATTCTGATTG AGAGTATAGC TTTAATTATT	600
GTATTTCTTT ACTTTTTTAA TTTGAACATC ATCGATATTA TCTTTTAAAT TCTACTTAAT	660
ATTTTAATGT GTTTAAGGAT TTATCTGAAT GTATTTTTTA GGAGACTTT AAAATATAAT	720
CAGATTTTGT ATATTGCTCT TATTCAATTT TTAGGTTTGC TGATAGGACT ATTTCTATAT	780
nAT	783

(2) INFORMATION FOR SEQ ID NO: 835:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

TTACCTAATT TTTCAATCaT AAGATTCCCC CTATTGTTTA AACaTAAAAA TATTATaCGA	60
TTAAGCACGA GmCACTTCAA TATATTTTTC AGAATATTCT TATAAATATT AATATGATCA	120
TTTCACTATT TAAACACGTT TAATATTAAA ATAAGTTATT CATATAAACT GGTGCTGTTT	180
GATCCAATTG CAGACTTACG AGTCATTGAA AAGTCTCACA AACTATTGmA AGTAAAtATC	240
TTAAAATAGA AAGTGAATGG TTAATTTAAG TATATTTmAA AAATATTAAC CTTTTTAAGC	300

ACTGCTATTT AGGATATACT AAATAATAAC TAAGTTTAGA AAAATAGGAG GAACATCGTT	360
TATGTTAAAC AAGGTTTGGT TCCGAAC TGG CATCGCTCTG ATTATGCTGT TCATTCTCAT	420
CAAACTATTT ATGGAAGTGC ACGAAGTATT TACTCCAATA GCTACAACA TCGGTTCTGT	480
ATTTCTTCCA TTTTAAATTA GTGGTTTTTT ATTTTATATC TGTCTACCTT TTCAAAACTT	540
ACTTGAAAAA GTCGGTTTTT CAAGATGGGC TAGTATAACA ACAATCATGT TAGCTTTGTT	600
TGCTATTATC GGCTTAATTG TTGCGTTTGT TGCACCAATC ATCATTTCAA ATATCAACAA	660
TTTAATTAGT CAGACACCTG gCCCTACAAA AAGGAAGCAG AGCAAATTAT TAAATTGCGA	720
CTGGCTCAAA TGGnTAAATT ACCTGGAGGA TGTAAACCAng TGGATTACCA ATATGGTAAA	780
TCAATGGGTG ATGG	794

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:

TGTTTATACT GTGCCTGAAT TAGAAGAGGT TTTAACACCT ATGAGACAAG ATGGAAC TCG	60
TGATATTTAT GTTAATTTAG AAAATGTGAG TtATATGGAT TCGACAGGTT TAGGTTTATT	120
CGTAGGTACA TTAAAAGCAT TAAACCAAAA TGATAAAGAA CTATACATTT TAGGTGTGTC	180
AGATCGTATC GGTAGACTAT TTGAAATTAC TGGTCTTAAG GATTTAATGCATGTTAATGA	240
AGGAACGGAG GTCGAATAAC ATGCAATCTA AAGAAGATTT TATCGAAATG CGCGTGCCaG	300
CATCGGCAGA GTATGTAAGT TtAATTCsTT TAACACTTTC tGGCGTTTTT TCGAGACTGG	360
TGCCACATAT GATGATATTG AAGATGCCAA GATTGCAGnT	400

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:

ATTGATCCAT TTTGCGGTTT GGGTACAATA GCTATAGAAG CTTGTTTAAAT TGCTCAAAAT	60
ATCGCACCTG GTTTAATCG CGAGTTCGTA TCAGAGCAAT GGAACATCAT GCCAGCAAAT	120
ATTTATGATG ATTACCGTGA TGAAGCGGAT AAGATGGCTG ATTATGATAA AGAAATCGAA	180

GTATATGCTT CTGATATCGA TCCAGAAAT G GTAGAGATTG CTAAGCGTAA CGCTGAAGAA	240
GTTGGGTTGT CTGATATTAT TAAATTTAGT GTAAAAGATG TCAATACATT AACAAATTGAT	300
ACAGAAGAAC CGGTGGCGTT AATTGGAAAT CCTCCATATG GTGAACGTAT TGGTGaTCGT	360
GAAGAA G TtG AAGAA A TGTA CCGTTATATT GGTAAACTAA TGAAACAACA TCCATTTTA	420
TCTACATACA TTT	433

(2) INFORMATION FOR SEQ ID NO: 838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838:

ATTGGGCCAA CTAATCCTGT ATATCCAAAT CCAGCAGACA ATGGTGTTCC TTTAACCTGA	60
AGAACGTAAG CAATGATTCC AGTAATTATT CCATTTATAG TCAATGGTAT CGAAATAATT	120
AAATTTTTCa AGTAAACTGG GATCATCATT TTTGCAGCTC CTATGAGTAA AACTGCATTT	180
ACACCAATAG AATTGACACG CAATGAGCCA AATAAGAAAG TAACACAGGC AGCCACTATA	240
CCTAGGTTTG CTGCTCCACT TCCTAGTCCG TTAAACTAA TCGCAGTTGC AATCGCTACT	300
AACGATATTG GTGTTACCAT TAATAATGAA A T GCCACAC TAATAAGTAT AGACATTAAC	360
AACGGATTTA AGTCTGTAAA AGAATGAATT ACATTTCCAA TTGCTTGAGT AATTTTTCGA	420
ATGTAAGGTA ATGTGATTAG ACCGATACCC CCACTAACGA TAGGTACTAA AACTGGTAAT	480
ATAATTAATT CAAAAGATCC AAGTTTGTTT TGTAATACCA TATATATAAG ACATGC AA	540
ATAACAACCA AACTCGTATT TATAATGtCa CCTATACCTT TTAACATAAA ACTATTATTG	600
CTATATACAA CAGCACCTGA ACCAATCATA GCTGATGTAC CTACTATAGC AGCACCTGCA	660
CCATTAAATT TAAATTGATG AGCAGCTAAA ACCCCAATAA TAAATGCCAT AAATGATTGA	720
ATTAGTATCA CTA A CTGATA CGTTAATTCT AAAATTT C AT TACCACTTTT AAATATTTTt	780
AATACTTCAC CTAATAAAGC ATTCGGAACA AGTGCAATAA CAACACCAGC ACCAATAGAA	840
TTTAA A ATCT TACTGAAAAA CTGTTTATTA TCAGCATTAT TTGCGTTACT CATAAACGAC	900
CTCCAATTTG AACATTAnAC TCATCA	926

(2) INFORMATION FOR SEQ ID NO: 839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839:

CTTCGAAACG TACTTGGTCA TTCCCTTTAC CAGTACAACC ATGTGCAATA CCTACTGAAT	60
TTGTTTTCTC AGCAATCTCT ACTAATTTTT TAGCGATTAA TGGTCTTGAT AAAGCTGAAA	120
CTAATGGATA TGCATTTTCA TACATTAAAT TTCCTTTGAT TGCATAACTT ACATACTCAT	180
CACTAAATTC TTTTGTGCA TCAATAATAT GACATTCAAC TGCTCCCATA TCTAAAGCTT	240
TTTTATAAAC GATGTCTAAA TCTTTACCTT CACCAACATC TAGGCAACAA GCTACAACGT	300
CGTATCCtTT GTCGATAAGC CATTGAACGG CCACACTTGT aTCTAGtCCt CckGAATATG	360
CTAAAACAAT TTTCTCTTC ATAAAATTCA CCTCATTGTA	400

(2) INFORMATION FOR SEQ ID NO: 840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840:

GGATCGCGGT GTTGTGCTTG ATATACTTTG TAGCGATAAC GTTTACCTAC ACAATCATAA	60
CGACAATGAA AATCGTCATC GACTGTAACT ACATTGTTGA CATAAATATC ATCAGGTAAC	120
GTTTCGGTTCA TTGCATATTG CCATTGTGAC ATAGGTAT A TCAGCTCTGT GTCGAAATGA	180
AAGTATTGCT GTATCGCATG TACACCTCTA TCAGTCCTAC TTGAAGGATG GATTCTCACA	240
TGTCTTTTAT GCATGCGTTG TAATAGCTTT TCAAATTGTT GCTGTACCGT TCGACCATTT	300
TGTTGAATTT GAAAACCTAG AAAATTATTT CCTTGATACG CAATTTCTAC TAATATACGC	360
ATGAATTTAC ACTCCTGAAT ATTTTAATAC GAATAAAATA ATTGCAATTG GGATAATCAT	420
GGTTAAAGAT ATCGTATCTC TCAATTGCCA TTTAAGCTGT CTGTAGCTCG TTCTCTTAAC	480
ATTGGCATCA TAACCCCTAA CTTCCATTGC GACCGCTAAT TCTTCGGCGC GTTGGAAGC	540
TGAGATGAAT AGTGGCACTA GTAATGGAAT AAATGATTTA ATACGTGTTG CAATGTTCCC	600
TGAACTTATT TCAGAACCAC GCGACTTTTG CGCCAAATG ATTTTATCTA ACTCATCCAT	660
TAACGTCGGG ATGAATCGTA ACGCAATGGA CATTATCATA CTTAATTGAT GAACTGGTAA	720
TTTAAACATC tTTAGTGGTG CAAGTAATCT TTCAAACGCA TCTGT A AAT CAATTGGACT	780
TGTAGATaGT GTCaTAATTG TTGCAATCAT TaCaATCCCA ATTAAACGCA GTGrTATATA	840
TAGCCCTTCT AAAATACCAT TAGTTTCAAT CGTGATGCCA TGCCATTCAA CTAATACATA	900

TCCACCTTTA GTTAAAAATA TATGCATCAT TAATGTGAAG ATTAAAAAGA AAAATATTGG	960
TGTTAAACCT TTGATTAGGA ACCATAATTG AATTTTTGCT AATCTCATAA TGAAnAnGAT	1020
AAGTGCAAAC ACCCAAAGAT ATG	1043

(2) INFORMATION FOR SEQ ID NO: 841:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841:

TCGAAATCAA ATTATAATAG ACAATTTTAG GAGGTGGACT TTCGATGACC AAAGGAATCT	60
TAGGAAGAAA AATTGGGATG ACAAGATAT TCGGAGAAAA CGGTGAATTA ATCCCTGTAA	120
CAGTAGTAGA AGCTAAAGAA AATGTTGTAT TACAAAAGAA AACTGTAGAA GTTGATGGAT	180
ACAACGCAAT CCAAGTTGGA TTTGAAGACA AAAAAGCATA CAAAAAAGAT GCAAATCTA	240
ATAAATATGC TAATAAACCA GCTGAAGGTC ACGCTAAAAA AGCTGACGCnGCACTGAGAG	300
nTCCCCTCAT AATTTCCTCCA AnCGTAACCA TGTGTGAATA AAT	343

(2) INFORMATION FOR SEQ ID NO: 842:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:

ATGAGTATTT TAATGATGCG CTACGAGCGT ATGGTCTTAC TGTGAnAACA GGTGAATTTG	60
GAACACACAT GAATGTTAGC ATAAATAATG wtGGwCagTC TCTGGTAGTT TAGAATTAGA	120
AGAATTAAAG CAATTTAGAC AATGGGGTTC TAAAACACCA GGTCATCCTG AATACAGACA	180
TACAGATGGT GTAGAAGTTA CTACCGGACC ACTTGGACAA GGTTTTGCTA TGTCmGTAGG	240
ATTmGCTTTA GCAGrAGATC ACCTAGCAGG GAAATTTAAT AAAGAAGGAT ATAATGTTGT	300
AGATCATTAC ACATATGTAT TAGCTTCTGA CGGTGATTTA ATGGAAGGTA TATCGCATGA	360
AGCAGCTTCA TTTGCTGGAC ATAATAAATT AAGTAAATTA GTTGTTTTAT ACGATTCAAA	420
TGGATATTTT	430

(2) INFORMATION FOR SEQ ID NO: 843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843:

```
GGACTGCCCCG ATGATTTGAC AAATGAATTG CTGATTTGAT TTATATATTATCTGnAATTA      60
ATACTCAATA CAAACTAAAA CGGTACTATT AAATTGTGCA AAGCTAAAAC AAATTTATAT      120
TCATCTATCC AACAAATATGT CTTATCAATG GTATAGTCTT TGCACACCAA TGGAGGnAAA      180
TAAATCTCAA CCTTACTATA TTAATATATA ATCAAATCTT AGATTAACTA GTGTAATGAT      240
ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAACC      300
TCAGGGnTTA TTTGATTTTT ATATAATGA      329
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(2) INFORMATION FOR SEQ ID NO: 844:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844:

```
AGATGAAGAA AGTGTTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACAnTTCT      60
TCCTAGATCT TGTACCGTTG AAAAGAGAC TGGTTGTAAA ATCTTAATTG ACATTTTCAA      120
TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTTCG ATTTGTATAA      180
ATTTCTGTTC ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG      240
GTTACGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCGCCAG      300
GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTCGCAA TACCTACAGA ACCTGGCATG      360
AATTTTTTAA CCTTGGGChG ATTACGTCTA nGGnGTATGT      400
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(2) INFORMATION FOR SEQ ID NO: 845:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845:

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CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT      60
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TATTTCTTAA CTGATTAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT	120
ACCAAACCCA CGTTTGCAAT GTTGCATGAA TGCTACCATT GGGCTTTTGC CATAACCATT	180
TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT	240
CGTTTTCACT GATATTATAG GCTTTTGCTT AGATGAAAA ACTGATTGGT GTTTTAGGAA	300
GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAAACTAAT TTATTCATGA	360
TGTTCTTTTT CATATGAAAA TCTCCTTTGC GTGAATTACC CAAAGTATAT AAGCTATTAC	420
ACCGATTCGG AATTAAATAA AAGCTAAAAC TATGTTAAAT AAAGTTAAAC AGTTAGTGT	480
GTTATTTAAG CAAAAGTTAT CATTTTAAAG TTGGACAGAA CAGATCAATA AGAGC	535

(2) INFORMATION FOR SEQ ID NO: 846:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846:

TCAATCGATC AAATGGTGAT TGACCTTTTA AATTTGTATG ATCAAAATAA TGATTGTTGG	60
CCATATCTTT ACTATGCTTA CGTGCGATTT CAGAATTCTG TTTAGAATAC TTCAATGTAG	120
ATAATTGATG TTGTTTTCTT TCAGCATTAA CTAAATCAAA ATTTTGTAGT TCAAACTAT	180
CTGCAAGCGA TTTCGATGGT GCTCCATATT GTTCTTTTAA TCTATTTTCC ATAGCATCAC	240
TTACTTGTA AAGAGCTGTT ACATTATTAC GTCGATGCTT ATCATAAAAT ACCGTCGTAT	300
AAATGTGATT TTTATGGAAA ACATCATATT CTTTATATT TTGTTTCGTAA CGCACTCTAC	360
CTTTAACAAT CTCTGTTTCT GGTTGCGCTA ATCTTTGCCT TACAACCGAT TTAGGTGTAT	420
TGTATTTAAT TTTTGATTTT GAAGTGATTA TATTTTGATT TGTATATAAC GCATTAAGTT	480
TATCTTTCAT GTAAGTTATC ATTATAAAA	509

(2) INFORMATION FOR SEQ ID NO: 847:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847:

CGTATTGATC TATAAATAGT GTTTAGATGC TATAGTCGGA TGCTTAAGTA ATTTAAAGAA	60
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AGTATCTTTA ACATCGATGT GTGTATAATC ATTTTITAGAA GTATTATAAT CTTTTTCTTC	120
TCCCTTCTAA AATATATACA GGTGCTTCAT CAGCTAGTGG TTCAACTGGA ATGTCAGCAT	180
AAACTTCGCA TCATATGTTA AACAAAAACG ATTGTATCTG TACTTCACCT ATAACAGCAC	240
TATCCAATTC GTGCTTATCA AATAAACTAA GATTTTTGTC AGTACCTTTT CACAAC TAGT	300
ACATACGTCT TGAGTTCTGA AGCATCATTT CATAAGGAGA ATACTGGCCA CGTGTGGACT	360
GTCTATCTCA ATGAACCACT ACACTTTGCG GCATT CAGC	400

(2) INFORMATION FOR SEQ ID NO: 848:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848:

TACCACTTGA ATACATTGCA TATAAAATAC GACGTTGTAC TGGTTTTAAA CCATCACGAA	60
CATCTGGCAA TGCACGCTCT TGAATAATAT ATTTACTATA TCTTCCAAAG CGATCACCTA	120
AAACATCTTC AAGTGATAAA TCTTGAATTA TTTCAC TCAC TAGATTTTCCT CCTCATCAAA	180
TTGATCATTT TCAAGCACTT GTACTTCAGA ATTATCTAAA ATACTTTGGT CCTCTTGCAT	240
ACCAAAC TCA ACATGCTTTT CAATCCATTC ACGTCTAGGT TGTACTTTGT GCACCCATTG	300
AATGTTGTTA CACGTTT TAGA TGGAAACGCAC TTGCATCTTG CAACTTGTGA CACGnATTGA	360
AAGTTnCGTG TTTGCGGGG Tn CAGCGTC GTTTGCCCAT	400

(2) INFORMATION FOR SEQ ID NO: 849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849:

TTTATATGAT TTATTTGAGG AGTTAAGAGA TTTATTTAAA GAAGAAGATT TAGAACCATG	60
GACATCATGC GAATTTGATT TTACAAGAGA AGGTGAATTA AAAGTTTCAT TTGATTATAT	120
TGATTGGATA AATTCAGAAT TTGGTCAAAT AGGTCGACA AATTACTATA AGTATAGAAA	180
ATTTGGAATT TTACCAGAAA CGGAATATGA AATTAATAAA GTTAAAGAAA TCGAGCAATA	240
TATTAAAGAG CTAGAAGAAT AAAC TATCTT AATGTAAGAC TAAACAATAA AGCTTTGTTT	300
AGTCTTTTTTA GCGTTTAAGT AAAAAGCaAT AGATACCGTA AAGTTGATGC TCATCAAATA	360

ATAATATAaA GATAATTTTA GGTTTTTAAA CTTTTAATCG

400

(2) INFORMATION FOR SEQ ID NO: 850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850:

CAGGCCATAC TTACAATTTT GGCCATCGTC CGGATGTATT nGGAATCGTT GGATAATAAG	60
CATCAAGGTC GTGACTATTT CGTAAAATTC CAACTGTCCC AGAATTTACA TCATTATGTC	120
CAATTACTGG GCAACCAGAT TTTGCCAACT ATCTATATtT CaTATATTCC aAATGTTAAA	180
ATGGTTGAAT CAAAATCTTT GAAATTATAC TTATTTAGTT TCAGAAATCa CGGTGATTTT	240
CACGAAGATT GTATGAATAT TATTATGAAT GATTTGATAG AGCTTATGGA CCCACATTAT	300
ATTGAAGTCT GGGGCAAGTT CACACACGTG GTGGAATTTT TGTGATCCT TATACAAACT	360
ATGGACGTCC AAATtCTAAA TATGAAAAAA TGGCTGAGCA TCGTTTGATG AATCATGATT	420
TATATCCCGA AAAAATAGAT AATCGTTAAA TGTATCATTT AATAAACACA CCAATAAGTT	480
GATTTTCCTA ACTTATTGGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT ACATTAAAT	540
AACATTTTAT ACCAAAGTAC ACCAAAAGAA TATTAGTACA CGAATTAAAC AACATTTTTA	600
TAGAAACCTA TTGCACTTTA ACGTCAATAA GTATATTTTT ATATTATCTC TAATTAATTG	660
TGCGCGCTTA ATAACAGAAT ATTCTCAATA TTTTATTTT TTTGTGATT GTTGAATAT	720
TTAGTTGATA AGGCACAATC AAATTACTT AAATATTGT ATTAGGGGAA GAAAGGATGG	780
GATGTATACA TGACACAACA AAATCCCAT GGAAATCAAA TTCAAGACAT ACCTCAAACA	840
GGATTTTTTCG GGcATCCTCG AGGACTAGGC GTACTCTTCT TTGtAGAGTT CTGGGrAAGG	900
kTTAGTTATT ATGGGCATGC GTG	923

(2) INFORMATION FOR SEQ ID NO: 851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851:

TTAnTTGCAT CTATTTCACT TGGTGTAAG AAAGCGGAAT TTGATTTTAT TGAAAAGTTA	60
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Gc t CAAGAAA AATTAATCCC CgAATATATT ACAATAGATA TTGCGCATGG TcACTcAGAT	120
TCaGTGATAA ACATGATTAA ACATATAAAA ACCCATATAC CTGATAGTTT TGTTATTGCT	180
GGTAATGTTG GTACGCCAGA AGGTGTTAGA GAATTAGAAA ATGCTGGTGC TGATGCTACC	240
AAAGTCGGTA TAGGTCCTGG TAGAGTTTGT ATTACAAAGA TTAAAACAGG TTTTGGTACT	300
GGTGGTTGGC AGTTAGCGGC ATTAAACATA TGTAAGTAAAG CAGCTCGTAA ACCTTTGATT	360
GCCGATGGTG GTATAAGAAC GCATGGGAC ATTGCTAAAT CAATTAGATT TGGTGCATCA	420
ATGGTCATGA TTGGTTCATt wTTTGCGGCA CACGAAGAAT CACCTGGTGA AACTGTAGAA	480
CTTGATGGTA AACAGTATAA AGAATATTTT GGTAAGTGCAT CTGAATTTCA AAAAGGCGAA	540
CATAAAAATG TAGAAGGTAA AAAAATGTTT GTAGAACATA AGGGTTCATT AAGGATACC	600
TTAAAAGAAA TGCAACAAGA TTTACAAAGC TCAATTTTCAT ATGCCGGTGG AAAAGACTTG	660
AAATCATTAC GTAGTGTAGA TTATGTTATT GTTAGAACT CTATTTTCAA CGGTGATAGA	720
GATTAATATT TATAGTAGGT GAKGTAAATT AAAAAATTCA TAGTAACTGT TGTTGCGTTT	780
TTATCAATTA TTATCATTGC GCCAnTAACA GAATTTAAAC CATTTCATTCA TTTACAAAAT	840
GAAGTAAGAC AATATATTGA CATTACATC AATAAAGAAA CAATTTCTGC GGAAAATAAA	900
TTGGATACAC CGAAGAAACA ACAATTTGCC TTTAATAATA TACAAATGAA CATGTCGAAA	960
TCAGATGTTG AGAAAACATT AAATAAACCA AAAAGTGA CATn	1004

(2) INFORMATION FOR SEQ ID NO: 852:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852:

GTTCGCTCCA ATGTACGCAG TTGTATATGC ATAGACACCA AAATCGAACC ATTCCATTGC	60
ATTACCGATA CCGGTTGCAA CAACGGTTTT TTTAGCTTTC TTTGCATCCA CCATGTTAAT	120
ATTCTCTTTA TTAAAATCCA TGAATTCATA CACTCCCTCT TGTATGTTTC ATAATATAC	180
GGAGTTAATT AGTTTTGTCA AATTTATAAG AATTTAACT TTTATATAAA TACCAAAGTA	240
TGTTTGTTCA AAAATTTTCGC TTTATCGnAT TAAATTCATG GTTTTATACC TCATACATTG	300
ATTAGACATA ATAATCTAAA CACGACGTTA CTTTGGATAT ACTnAATGGT nnCACACTCA	360
GTAGGAAGCA CcATTTCGCT CGATAATGTA ACCATACTCA	400

(2) INFORMATION FOR SEQ ID NO: 853:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853:

GGTGAAATTG TAACTATATA ATCGATATTA CCTTCAGTGT TCAAAACTGG AAAATAATAA	60
TTACCATCAC TCTTTTTGTT GAATTTATAA ATTTTAAAAG GTTCACCAAG TGTATACGAG	120
GCTTTCTCTT TATTATAGAT TTTATCAAGT GAAGTAACAT AAGAAAGATA GTCTTTTTGC	180
GCTAAATTAC GTACGTCAGT AGGAACACTC TTGTCCTCGA CATTAAGTTG CACATGCTTC	240
TTATCTTTTG CTTTGATATT TGAATTGCTC TCAGCGTTTG CAATAGGGGT AACACTTAAA	300
GAAATATTA AACTTAAAGC TATTAATTTT GGAAAGTTTC TTTTCATATA AAAACTCCTT	360
T	361

(2) INFORMATION FOR SEQ ID NO: 854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854:

ACnTTATACT AGAnAAAGnT ATTAAAGTAT ATCTGCTTTA CACCATTAAA AAGCGGCAAA	60
TGCTATAGAT AATCTAAAGC ATCTGCCGTA TGAGnATTTA TTTATTTTTG ATTGTCATAA	120
TCGTGTGGTT TTAAATTAAT TGTTTCTAGC TTTACAAATT TTGTTTTGTG AATGATTTTA	180
TGAATAAAGT AAATCAACGC TAGAATGATT AAAGGTAAAA AGTTTTTAAA AGCATTTAAC	240
CATTGATCTT TTAAAATATA TTCAACTGAG CCACCAAATA GCAAGAATAA TAGTGTAGTG	300
ATGACAATGA TTGGTCCTAA TGGATAAAAA GGTGCTTAT ATGGTAGGAC CTTATTAGGG	360
TCTTGACCTT GTTTTTTAAT AGCTTGTCGC AATCGTATTT GTGACCAAAT GCTTGATCCC	420
CAAACAATA TAATCATTGA ACCAATAATT TCAAGTAAAT TAAAAACGGC ATTTGAATTA	480
AAGTTTGCAT AAATAATAAC AATAACAACG ACTGCATAAG TAGTTAATAA TGCTCTTAAA	540
GGTAACTTAG TTGTCTTGTT TAATTTACTT AAAAATTGGG GTGCTTTTTT GTCTGAACTT	600
AAGGA	605

(2) INFORMATION FOR SEQ ID NO: 855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855:

TTGAACAAGC ATTTTAAAT AGTCAACAAC ATCAmGCAAT TAGTGAAGAG GCACAAC	60
TAAATAATCC AGATGAATTA ATGGCATT	120
ATGCATACAT TATGCCGCAT AATATGAGAG AAATGTTACG AAGTTATTTG GAAAGTATGT	180
CTCAAGACTT TAATGTTGGC GGATTTT	240
AACAGCGATT ATTAACAGCG ACAGATGCGT TACAAGAACA TTAATCAA CAAATTCGTC	300
AACCAATGCG AGAAGATATG TCATTTGTTA CGCGTTTTAT CAATAAAAAA GmAGCTTCAG	360
aTAmAGTATT AAATCAGCAT TATGACGTTA AGCCAGAAAT GATTGAAGGT TTATATCAAC	420
CACAAACATC AATCAGCAAT ACTTATGTAC TTACATTTTC AGACGAAGTG GTTAAAGCCA	480
TTAAGAAATA TGTGAACAA CAATCAACAC CAATT	515

(2) INFORMATION FOR SEQ ID NO: 856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1607 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856:

GTCATTTTTA AAATTTGCA TTCGCGTTA ATTTTTCTC TTTTCTTT TTCTTCTAGT	60
GACATACTTT CTTTAGGTGT TTCAACCAAT TCAGATGTAT CTACATCATC AATTTTAGTG	120
ATTTTGTCTA CATCTTTCTT TAAATCTTCT GGGACGTTCT CGAAACGCTT ATATTGCTCT	180
TTAGAGATAC TAGCAGCTAT TTCATTAGCT CCTAAAATTT CATCTATCAA GCCGAAAGAC	240
AAGGCTTCTT CTGCAGTAAG CCAAGTTTCT GCATCTAACA TCTGTTTTAA GTGTTCTTGA	300
TCTAAATCTT TTGCTTTATC TAAATAAGCT GAATTACTAA CAGATCTGT TTTTCAAGT	360
AAATCCGCTG TCTTCTTAA TTCTTCTGCA TTACCTACAG TCATAACCCA TGAATTATGA	420
ATCATTAATA AACTATTTTT GTGCATAAAA ATAGTGTCAC CACTCATAGC GATAACACTA	480
GCAATTGATG CCGCTAAGGC ATCGACATAG ATATTAATTT TTGCAGGATG CATTTTTAGC	540
ATATTGTATA TTGCATGTCC TTCAAATACA CTGCCTCCAG ATGAATTTAT ATGAACATCT	600
ATTTCACTGA TGTCTCCTAG TTCATCTAGT TTATTTTGA AATCTGTAGC AGTTACATCA	660
CTTTCAAACC ATTTATCACT TACAATATCA CCATAAATGa ATATTTACACC TTTACTTTTT	720

GATTTTCTTT TCATTTGAAA ATACTAGCT TTCATTGACA TTTTATCAC CACCTTTCaA	780
AGATTTTCTT AATTCAAGTG GCGTGTCAAT TGGGTATAAA TCACCGCTTA ATTAGCGGCT	840
TATCTCCACC TTCAACTGGT GGTAAATCTT CCCACTCTCT AATGTCATTT ATAGTGTAGT	900
AACCACTACG AACTGCTTTA AAGTACACTT CTGCTTGTGT TGCACATCA GCCTTAAAT	960
AAGATTTAAC GTTAAATTTA AAATACCTAT TTTTCTCT GTCTGTTTTA GTAAGTAGTT	1020
TCCGATTAA _n TTCTTCTTCA TACTGTTTGA CGATTGGCAA TAAGGTATGC TGCAAGTAAA	1080
ATCTGTTTAA CTCTTCATTT TTCGCGAAAT TTGTATTTGA TCTTGCATTT AAGAATATTG	1140
AGGGCAATTG AAAAACGTTA GCTACTCTTT CTCTTGTTAA ATTCTCGCTT GCCACTATAT	1200
CTTCAGAGAC ATATTTTTTA GGTAAAGGTT CGATTTC AAC ACCAGGCTCT TGGAATAATA	1260
TTCCACCGTT TTCTTCATAG TACTGTTTGA AATCTTCTAA CACTTGTTGC CTTTTTCTG	1320
TACTTACATT GGAACCATAT TTAAGCATAA AA _Q ATCTGG TTTTGCATT TCTGTAAGAT	1380
TAAAGGTTCT TACTGCATTG TCAAAATCAG TTGTATTCTT CAACACATCA ATCGGACTAA	1440
TACCTTGAAC CATATTAGAT GCCACGATGT GTTTAAATG CAACATGTCC aTATTATGAA	1500
CAATCAATTT ATTTCCAGTT GCAGCATGAA TGGAATAATA AAGTTCAC _c G TGATTGGTT	1560
TCAATTAACA TTTCAACAAC ATCTGGATTT AATAAGAAAA GCTTTGA	1607

(2) INFORMATION FOR SEQ ID NO: 857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857:

ATGCGCATTT AACCGCATTT AGAGATGCTG AAGATCAGTA TAAAGCTTTG TTAGAAATTA	60
CAACATTACC AGAAGGTAGA ATTTATGTTG CTCGCCAAGA TCAACTCATT GTGGGTATG	120
TCACTTTCCA CTATCCTGAT GAAATTGAGC GCTGGTCTAC AGGTAAGCTT CCATATTTAA	180
TCGAATTGGG GGCAATTGAA GTCAGCATCA ATTTTAGGCA ATTACAACCT GCAGAAAAGC	240
TGATACAACT TAGCCTTCTA CACCAGAATT CGAGAATTAT ATCGG _n ATAA CTACAGGATA	300
TTACCGGCAT TGGGGGTTTA AAAAATTCCC AGT _n AG _Q GT ATT _n CC	346

(2) INFORMATION FOR SEQ ID NO: 858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858:

ATTACTATAA TGAATCTTGC GAGATATTTA GAAGTAATGA TACAAnATAA TGGACTTTAG	60
AATTTmAATT TACAATAAAT AGTTCTATGA TTAAATGTCA GTTTTATGAC ATTTATTTAT	120
TGAAAATACG AACGAATGaG CGATaTGATA ATATAGATAA GAATGATTTT AATTTAGG	180
GCCTTTATGG TGCATAATAA AAACAATACA ATTTTAAAAA TGATCAAAGG TGAAGAAACA	240
TCACATACAC CTGTTTGGTT TATGCGACAA GCTGGCCGTT CGCAACCAGA ATATCGAAAA	300
TTGAAAGAAA AATATTCCTT ATTCGATATT ACACATCAGC CGGAGTTGTG CGCTTATGTA	360
ACACATTTAC CAGTTGATAA TTATCATACA GATGCAGCA TTTTATACAA AGATATTATG	420
ACACCATTAA AGCCAATTGG TGTCGATGTA GAAATTAAAT CGGGTATTGG TCCAGTGATT	480
CATAATCCAA TCAAAACAAT TCAAGATGTT GAGAACTTT CTCAAATAGA CCCCGAACGA	540
GATGTACCAT ATGTATTAGA TACAATTAAA CTTTAAACAGAAGAAAAGTT AAATGTGCCG	600
CTAATAGGAT TTAAGGGGC ACCATTTACA TTAGCGTCAT ATATGATTGA aGGCGGACCA	660
TCGAAAAATT ACAATTTTAC AAAAGCGATG ATGTATAGAG ATGAAGCAAC ATGGTTTGCT	720
TTAATGAATC ATTTAGTTGA TGTATCTGTT AAATATGTAA CAGCTCAAGT CGAAGCAGGT	780
GCCGAATTGA TTCAAATTTT CGATTCATGG GTAGGTGCAT TAAATGTCGA GGATTACAGA	840
CGTTACATTA AACCACATAT GATTCGATTA ATCAGTGAGG TTAAAGAAAA ACATGATGTG	900
CCGGTAATTT TATTCGGTGT AGGTGCCAGT CATTTAATCA ATGAATGGAA TGATTTACCG	960
ATTGATGTAT TAGGCCTAGA TTGGAGAACG TCTATTAATC AGGCTCAACA ATTAGGCGTT	1020
ACTAAACAT TACAAGGGAA TTTAGATCCA TCAATTTTAT TAGCACCATG GAATGTCATT	1080
GAAGAGAGAT TGAAACCAAT ATTAGATcAA GGTATGGAGA ACGGTAAACA CATCTTTAAT	1140
TTAGGACACG GTGTATTCCC AGAAGTGCAC CAGAGA	1176

(2) INFORMATION FOR SEQ ID NO: 859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

ATTTGGTGCA TTGGTAnAAT TGACCTGAAA GnAAAAAGTG GTTTAGTTGC ACATTGAGTG	60
nAAGTGCGCA GATGAATTAT GTTGAAAACG TGAGGAAGAG CACCTTTGCT GTTGGTGATG	120

AAGTAGACGT AAAAGTATTA TCTATTGCTG ATGATGGAAA AATTAGTCTT TcAATTAAGA	180
AAGCTAAAGA CCGTcCACGT AGaCAACATA CGAGTAAACC AAGTCATCAA AAACCAGTGc	240
AAAAAGCCGA AGATTTTGAA AAGAAATTAA GCAATTTCTT AAAAGATAGT GAAGATAAAT	300
TAACTTCAAT CAAACGTCAA ACAGAATCTA GACGCGGTGG CAAAGGTTCA AGACGTTAAT	360
TAAAATAAAT AAAGACTGTT TCGATAAGGA ATATATTTAG AATGATGCGT ATCGAATAAT	420
CGATTGCAGC GTTAGACAAT CTAAGACTGT TTCTTAAATA AGGAGCAGTC TCTTTTATTT	480
GTAATGATAT AACTAAGACT TATACCATTT TTGAAAATTG TAAAAGTGAG GTGATGTTAT	540
GCAGTTAAAT AGTAATGGTT GGCATGTTGA TGACCATATT GTTGTGCTGTTTCTACAGG	600
TATTGATAGT ATGTGTTTnn T	621

(2) INFORMATION FOR SEQ ID NO: 860:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:

TATATTAGGT ACTTGTTGTTG GTATTGTGCC AGCTTTGCTG TCTACTATAA TTTCTAAAAG	60
GTTTGAACAT ATAAAAGGGA AAGTGCTAGG TGTATTTAAT TTTGTGAGAT ATATTGGAAT	120
GA CTGTCGGT GCATTATTAA TTGGTATCAT TTCTCAGCCG TTGGTAGCCT TTTACTTCAC	180
AACTATAACT ATCATGTTAA TAGTAATATT TCTTTATATA AAGATAGTTG ACTTTCAGCT	240
AAAGTATGCC AAATAAACTT AAAAAAGCAG TGAATCATTT CAATAGATGG AATGATTCAC	300
TGCTTTTTGT TTATAGAAAT TTAAAATTa TGCCTTTATG CTAACAACAA TATTATTTTA	360
CTCTCTTACG TTTGCCAATG TAACcGTATA GCAAAGTAAA TGACTGCGAT AATGATGACA	420
ACATACATAt ACGTGAATAG GAAGGAAGAC CAGTCATCAA CATACCAAAG CTATCGCTCA	480
AAGTGCGnCT GGTAATTAA ACCGAATTCC AnGATTGTAG GAACCCnATT AATGAAATA	540
ACGG	544

(2) INFORMATION FOR SEQ ID NO: 861:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

TACGTCCGCC AACATTTCGTC GCTTTAGTTT CATAATGTAT TGCCATACTT ATAACCTCCT	60
AATTTTAAAT ACATTTTATGC TTTACCCATT CGAAAATACC TTAATCATT TCATTTATAG	120
CATTGTTTGA TTGAAGGATA AAAAGTTGTT GTTTACAATA AAAATAATGA GTATCTGAAA	180
TGAGGGATTTC AnTATGACAC ATGTGGAAGT AGTAGCGACT ATCGCGCCAC AATTATCTAT	240
CGAAGAACT TTAATTCAAnA AnATTAATCA TCGTATTGAT GCAATAGACG TATTAGAATT	300
ACGAATTGAT CAAATTGAAA ATGTCACAGT T&TCAAGTG GCAGAAmTGA TTACAAAGCT	360
GaAGGTTATG CAAGATTCAT TCAAATTATT AGTTACGTAT CGTACAAAGT TACAAGGTGG	420
CTATGGGCAA TTTACAAATG ACTCGTATCT TAATTTAATA TCAGACTTAG CAAATATCAA	480
TGGCATAGAT ATGATTGATA TAGAATGGCA AGCAGATATT GACATTGAAA AACATCAAG	540
AATCATTACA CATTTGCAAC AGTATAATAA AGAGGTGGTT ATATCACATC ATAATtTCGA	600
AAGTACGCCT CCATTAGATG AATTGCaATT TATATTTTTn nAAATGCAAA A	651

(2) INFORMATION FOR SEQ ID NO: 862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:

TGTGAGTGGT AATGACACAC AAGCAGATTT AATAGGTAT AGTTTTAAGT TTGACGGTGC	60
GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT	120
ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA	180
TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG	240
TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATAAAA AGATTGGAmC AATAACaTAA	300
AATAATAAAa GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTkGAATA	360
GaaAGaGAT ACTGGcAATT TTAATAACCA GtATCTCTTT T	401

(2) INFORMATION FOR SEQ ID NO: 863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

TnTTGTGTTT GTAGAAATAA TTTATAGTAC AAACGTAAAA TGATATAAAA CAAAATAAA	60
ACAAAGTAAT CAATATGTAA TATAAAATAC ACTGGTACTC AATATATAAT GATGATAAAA	120
TTAATTTTAA TTAGATAGAG TTGCTTTGTG TTTTAAACGC nGATGCTACT ACTTATCTTA	180
ACAGTTGATT AAGTAAATCA TTTAACAGCG AGATTATnCA ACCAGGGGGA TGA CTTAATG	240
AATTTATTCA GACACCAAAA TTTAGTATCA GAAATTTAAT GTCGGTATTT TTTCAGCTTT	300
AATGCCAC	308

(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

TTCTACATCT TAAACGATGA CCTAACTATG ACGTTAATCT GGAAAGATGG GGAGTTGCTA	60
GTATGATGTT GAAATTTAAA GCTTGGGATA AAGATAAAAA AGTTATGAGT ATTATTGACG	120
AAATCGATTT TAATAGTGGG TACATTTTGA TTTCAACAGG TTATAAAAGT TTCAATGAAG	180
TAAAACTATT ACAATACACA GGATTTAAAG ATGTGCACGG TGTGGAGATT TATGAAGGGG	240
ATATTGTTCA AGATTGTTAT TCGAGAGAAG TAAGTTTTAT CGAGTTTAAA GAAGGAGCCT	300
TTTATATAAC TTTTAGCAAT GTAAGTGAAT TACTAAGTGA AAATGACGAT ATTATTGAAA	360
TTGTTGGAAA TATTTTTGAA AATGAGATGC TATTGGAGGT TATGAGATGA CGTTCACCTT	420
ATCAGATGAA CAATATAAAA ATCTTTGTAC TAACTCTAAC AAGTTATTAG ATAAACTTCA	480
CAAAGCATTA AAAGATCGTG AAGAGTACAA GAAGCAACGA GATGAGCTTA TTGGGGATAT	540
AGCGAAGTTA CGAGATTGTA ACAAAGAACT GGAGAAGAAA GCAAGCGCAT GGGATAGGTA	600
TTGCAAGAGC GTTGAAAAAG ATTTAATAAA CGAATTCGGT AACGATGATG AAAGAGTTAA	660
ATTCGGAATG GAATTAAACA ATAAAATTTT TATGGAGGAT GÆACAAATG AATAATCGCG	720
AAAAAATCGA ACAGTCCGTT ATTAGTGCTA GTGCGTATAA CGGTAATGAC ACAGAGGGGT	780
TGCTAAAAGA GATTGAGGAC GTGTATAAGA AAGCGCAAgC GTTTGATGAA ATACTTGAGG	840
GAATGACAAA TGCTATTCAA CATTCAGTTA AAGAAGGTAT TGAACCTGAT GAAGCAGTAG	900
GGATTATGGC AGGTCAAGTT GTCTATAAAT ATGAGGAGGA ATAGGAAAAT GACTAACACA	960
TTACAAGTAA AACTATTATC aAAAAATGCT AGAATGCCCG AACGAAATCA TAAGACGGAT	1020
GCAGGTTATG ACATATTCTC AGCTGAAACT GTCGTACTCG AACCACAAGA AAAAGCAGTG	1080

ATCAAAACAG ATGTAGCTGT GAGTATACCA GAGGGCTATG TCGGACTATT AACTAGTCGT	1140
AGTGGTGTAAGTAGTAAAC GTATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT	1200
CATGGCAATT TAGGGATTAA TATCAAGAAT GATGAAGAAC GTGATGGAAT ACCCTTTT	1260
TATGATGATA TAGACGCTGA ATTAGAAGAT GGATTAATAA GCATTTTAGATATAAAAGGT	1320
AACTATGTAC AAGATGGAAG AGGCATAAGA AGAGTTTACC AAATCAACAA AGGCGATAAA	1380
CTAGCTCAAT TGGTTATCGT GCCTATATGG ACACCGGAAC TAAAGCAAGT GGAGGAATTC	1440
GAAAGTGTTT CAGAACGTGG AGCAAAAGGC TTCGGAAGTA GCGGAGTGTA AAGACATCTT	1500
AGATCGAGTT AAGGAGGTTT TGGGGAAGTG ACGCAATACT TAGTCACAAC ATTCAAAGAT	1560
TCAACAGGAC GACCACATGA ACATATTACT GTGGCTAGAG ATAATCAGAC GTTTACAGTT	1620
ATTGAGGCAG AGAGTAAAGA AGAAGCTGAG CGCAAATACG AGGCACAAGT TAAGATAAGG	1680
AGAGATGGAG ATGCCAAAGA AACCGGTAAC ATTGATGTA GATGAAACT TATTAGTAGT	1740
AGCTAGTAAT GAAATATCAG AACTATTATA TGAATATGAC AGTGAGTtAA TGTCAGCTGG	1800
ATGGAAGATG GCGATAATAG GGATATC	1827

(2) INFORMATION FOR SEQ ID NO: 865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

TCAATTGCAT CATCATATGA AATTCTaGGG AATGGTGTCTG CAACTTTTTTC AATTTTGAT	60
GTATCACGCT CTAAAATTTT CAACTCTAGT TTACAATTTT CTAAAACTGA TTTTACAACA	120
TGTGTTACAT ATTGTTCTTG AATTTCTAAA CTTTCAGCAT GATTTGTGAA AGCCATTTCT	180
CCTTCAATCA TCCAGAACTC GATCAAGTGT CTACGTGTTT yTGATTTTTTC AGCTCTGAAA	240
GTTGGACCAA ATGAAAATAC TTTTCCGTGT GCCATTGCTG CAGCTTCTAA GTATAACTGA	300
CCACTTTGAG ATAAAAACGC ATCTTGATCA AAGTATTTAG TATGGAATAA TTCACTTGTA	360
CCTTCTGGCG CACTTGCTGT CAAAATTGGT GGATCAACCT TTGTAAATCC ATCTTTGTTG	420
AAAAATTCAT ACGTTGCACG AATAACTTCA TTTTAATTT TCATTACAGC ATGTTGTTTT	480
TTAGAACGTA ACCATAAATG ACGGTGATCC ATTAAGAATT CTGTACCATG ATTTTtagGT	540
GTAATCGGAT AGTCATGCGC TTCTGAAATA ACTTCAATTG ATTTCACTTG CATTTCTGAT	600
CCTAAGTCAG AACGATTATC TTCTGTAATT GTGCCTGTAA CGTATAGAGA TGATTCTTGA	660
GTAATTTCTT TCGCAAGTTT GAATACCTCT TCATCAACTT CTGATTTAAC TACTACGCCT	720

TGCATAAAGC CTGTTCCATC ACGTAATTGT AAAAAGGCGA TTTTACCACT TGAAcGTTTA	780
TTTGTTAACC AAGCACCAAT TGTAACGTCT TGGTTTAAAT GATCTTTCGC TTGTTTAATC	840
GTTGTTTTCA TAACCATCTCT CCTATTTATT TTTTCGkTAT ACAATACTCA TTCATTTTAA	900
CAAAATCCGC TTTCAAGTTC TAGAACTAGA CTAAAAGATA ACGtGTAAAT GGTAATGATT	960
TACGCACAGA TTTGAACATT AATTTATATT AAGACAATAC AATCATCAGT TTCAGACAAA	1020
ATATATAATA AAGCCTCAAT ATTATTAGTA TGAAGGTCGT TTTTGTnCT AACATTCAAG	1080
TTTAATTATA AAACCTCAAT TTTGACGACC AAACAAAAT TCTTGTAACA GAACATAGCA	1140
CATGTCATGT CACAAGAATT TTACTTTGTA TTTCACTTTT TCTTTTTTTG AATTTGTCTT	1200
AATAATTTTC CAAACTGTTG AATGTCGCCT TTTTCTGAC GATAATTTTC AAGTGTtTG	1260
TCAAAAAAGT TTTTATAATT ACTGTTTATG AGTCGATCAT CAAATGAAAC TATTATGCCG	1320
CGATCATTTT CATTTCTAAT TAATCTTCCA AGTCCTTnGT CTAnAACGTG TAACTGCAT	1379

(2) INFORMATION FOR SEQ ID NO: 866:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866:

TTACAACGAA TAGTTCACCG TTCGAGTCTA ATCTATGTAA TGCTTGCTCG AATATACGAT	60
GCACGGTTTC TTTCCCTGCT CTTATTGGTG GATTGGTTAA AATAAAATCA AAACTTTGT	120
CTTCCACAGC AGACAAAGCA TCACTTTCCT TTACGATCAC ATTATCAATA CCATTTAATT	180
TTTTGTTTTT TTCAACTAAG GCTAGCGCTC TGTGATTAAAC ATCTAGCATT GTAATTGAAT	240
GATGTGGTGA TACTTTAGCA ATCATCAAAC CAATTGGTCC GTAACACAA CCAACATCGG	300
CAATTCGCTT ACTTGACCA GGTGGATGCG CTTTTAAAAA AGTTTGAACA AGAACATCTG	360
aACCATAATC TACTTTAtCt TTCGAAAACA CTCctTATCA GTTATTAAAT CAATTTTATG	420
AnGGTTnTAA TTGGATATTG AGTACGTTGT	450

(2) INFORMATION FOR SEQ ID NO: 867:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867

AATGTTAACA ATATAGCACC AATTAACCCC GACATGATAA TAACGTGTAA TGTTTTATTT	60
CCTATTAATT GTCTCGCAAT ATGAGGTGCA ATTAATCCTA AAAAGCTAAT ACCACCGACA	120
ACTGAAATTG CGGATCCTGC TAATATTACT GCTAAAATTA ACAATAGCAT TTTAATAGTT	180
TTAACTTTTA AACCGAGTGC GGTGCAACA GCATCACCTA GATTCAATAC ATCTAATTGA	240
TAACTCCATA AAATGATGAT GGATCGTTAT TAAAACCAGG GAATATAGAT AATATCCGCA	300
TATCAGGCCA TATAGCTACC TGTACCAAC AGGTTTnTGC TCCAnGGTTC TnTAATAAGA	360
CGCACACGCG ACAATGCGCT TGCTACCATT AGGCAGCTTG	400

(2) INFORMATION FOR SEQ ID NO: 868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868:

AATCCnTnAA GTGCCATAAC ATCATCTCCT AACATCTTTA TTATACATCA ACATTTTATA	60
AAAATAACnT CTTATGATAA AAATGAAAAT ACTAATTTTA ATGAGAGCGT CTTAAGCCGC	120
AATTGATAAA ACATATGCTA CAATATTTTT AAACACTATA CAGGAGGTAC TCTATGACAA	180
AATATACATT TAAACCTAAA GATTTCAAAG CGTTCAACGT AGAAGGCTTA GACGCACGAA	240
TGGAAGCTTT AAACGAATAC ATACGaCCAC AACTCCGTGA ATTAGGAGAA TATTTTAGTG	300
ACTTCTTTAC AAGTCAAAC TGTGAAACAT TTTATCCTCA CGTAGCAAAG CATGCTAGAA	360
GAAGTGTGAA TCCTCCTAAA GATACnGGG TTGCTTTTGC AACAAACAAA AGAGGCTATA	420
AAATGTTACC TCATTTCCAA ATTGGTATGT TTGAAGATCA ACTGTTTGTT ATGTTTGAA	480
TCATGCATGA AGCAAAAGAT AAAGCAACaC GTGCAAAAGT TTTTGAAAGA AAATTTAAAG	540
CTATTCAACA ATTACCTGAT GATTATCGTG TTTGCTTAGA TCATATGAAA CTGATAAAC	600
CATTTATTAA AGATTTAACG GATGATGATT TAATAGAAGC GATACAAAGA GCCATCAATG	660
TGAAAAAAGG TGAATTCTTT ATAGCGCGTG CAATCACACC ACAAGATAAA AGATTAAAAA	720
GTGACAAAGC ATTTATTGCA TTTTLAGAAG AAACCTTCGA TCAGTTCTTA CCATTTTATT	780
CTGCATAAAT AACTTTGTTT AAATAATAGA GCACTTAATC ACATCCaTGA TTTCGTGctC	840
TTtTTTCTTA ATATTAAATC GAACGTtCAA CATAaTAATT CATACTTTTA AAAAAATTAA	900
nATAAATTTA GGTTGGCCTA nACATTTTAT TAGGTTATTA TATTGTCCAT AAGAAGTAGA	960
GGTGAGTCAA AATGAATAAT AAACGACATT CAACAAATGA ACAATTAAGT TTAGACGAAA	1020

TAAACAATAC AATTAAATTC GATCATCGCA GTTCAAATAA ACAGAAATTT TTATCATTTTC 1080
 TTGGACCTGG GTTATTAGTC GCTGTTGGTT ACATGGATCC CGGAAACTGG AT 1132

(2) INFORMATION FOR SEQ ID NO: 869:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869:

CTCAATGTAT TGACTGTGAT TTGGAGTGTA TAATGCTACT GTTTTGTCTA TAGCCTCGC 60
 ATCAAATATT ATATTTGAGT AATCAGTGAT AACGACATCA GACATTAGAA TTAAGTCTTG 120
 AGCACTAAGA TACTTTGGTG CAACAAGCGC CTCTTCTGGT AAGATCGCTT CATCAACACC 180
 CTGAACCACA ACATGATAGG CTTTGAATAA AGCATCTGAT AGTGGTAATT GTTGCGCACT 240
 CACTAATCCA ATAGGTGCGT ATAATAAAAC TGGTTTTTGA TCATTTATTT TAAACGATTT 300
 CTTATACTGT TGTTGAGTAG TACTTTCGTT ACTCTTTTGT AGTAAATATT GGTGTTTAGG 360
 ATTACCATAA GCCAATACAT TGCTTGGTGA CTAGGAAAAG nCGTTTGATA AAAGGGCT 418

(2) INFORMATION FOR SEQ ID NO: 870:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870:

GAGTnTGTTA CAGTAATTGA TTTTATTGGT AATnTAAGA CAAATTATTT AATTCCGATT 60
 GCGCTTTCTG GGGATCAATC GCAAnATAAA GATAATTATA AGAAGTTTTT AACGAATAAC 120
 GATTGATTA ATGGAGTATC TACAATTAAT TTTGAAGAAG TTGCTAAAAA ACAGATTTAC 180
 AATTCATTGG ATGCAGTATC ATTAAATCAA AATAAATTAA TATTAAAAGC TTATGAAGA 240
 GTTGAAAATA GATTGGGACA CATGCCGTTA CTAATGGATT TCATACAACA ACATTCTATA 300
 GATCCAAGCG TTATATTTTC TAAATTTAGT AATTATTACG AGTTCTTAGT GAGATATAAA 360
 AAAATAGATA CATTATTGAC GGAAAATGAA TCTAAAATC TGGTTTTCTT TTCAAGGCAA 420
 ATAGCACCTG GATTGAAAAG AATCGATAGT TTAGTTTTAG AAGAaCTTTT AAAAAATGAA 480
 TTAACATATG ATGAATTAAA AAATAAAATG TTGAACGAAG TTAAGGATAT AACAGAAGAT 540

GATATAGATA CTTCATTAAG AATTTTAGAT TTTTCATTTT ACAACGC

587

(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871:

CTACTAAACC AGGTAATCGG TAGAATCCAA GCAGGAATAA ATAAATTAAT GCnACACCAA	60
TAAACGATGC AAACACAGTn TTATCTAATG CATCTTGACC AAATTGGGCA CCTACTGAGT	120
TTGAATAAAT TTCTTTCAAG TCAACTGGTA AAGAACCTGC ATTTAACAAT kCGGCGATTT	180
GTTTTGCTTT TTTAACGCCT TCTTGTCCTT TAAATCCACC CGAGATTTCT ACGCTATCAG	240
AATTGATTGG TTGATCAACA CTTGCTGCAG AAATAAATTT AGGGTTTTTC TTTTGTGCTT	300
CTTTTTTATA GCTGTCACCT TTTTGTAAAT CTAACCAAAC AACCATGACA TTATCACGTT	360
TCTTAGAGAT TTCTCCGTT ACTTTTTTAA ATTTGTTTTT GTCTTTTACT TTAAAAGTAA	420
CTGTAGGcTG GTTTGTTC tGtTTAAATT CTTGtTTGGC AGATCCCTGT TTaATATCAG	480
AACCGCTTAA TTTtACTTTA TCTTCTGCAT CGCGAATTGT TAAATTAGCT TGAGAAGATA	540
AAATTTTACG TGCTTCATTC TGGTCTGTTA CACCAGCAAG TTGTACTCTA ATTCTATTAG	600
GTTCTTCAAC TTGAATTTTA GGTTCCGAAA CACCTAAAAC GTTACACGA TTTTCTAATG	660
TTTGCGCTGT TGATTGTAAG GCTTTTTTAT CTATTTTGTC GCCTTTATTT AAAGGATCGA	720
CTTGATAAAG CACCTCAAAT CCACCTTGCA AATCAAGTCC TAAATTGmCA TTCTTTATAA	780
CACTTTTATA AGTTGcAGCC ATTCCGGCAA ACAACAATAC GACTAAAAGC AAGAACGCAA	840
TTATTCTACT ACTTTTCTTC ACATGAACAC CTCATTATTT ACGTATGTAT TTAGAATACT	900
TGAATACTAT TTTATAACGC AAGTGAAATC TTTCTTACAA AATTTATTAG CCTTATACAT	960
ATTAACATAC T	971

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872:

CTGGTTAACA ACATCTGGTT CGCATCTCC TTAGCTTCCA CTAAATCTTG GATGTCTTGG	60
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nnATCTTGCG CAAGTnGTGC TTTGGCTTGT TCAATTtCTy CTTTAGTCAT CGCATTGTTA      120
ATGCCGTTAT GACCTTGTTG AAGTATTTGA TTAATACGAT CTTTAAGTGC TTGTTTTTCC      180
TTATCTGTTA GATTTGGATT TCGATCAATT TCGTCAATTA ATGCTTGAC TTGcTTATCA      240
ACGTCTTTAT TGGCATCAAT TTTTGCTTTT GGTATTTTCAT TGGCATGCAC TTGTTCAATC      300
GCGTGGTTGC CTGCTGTTTG AACTTGAGAT ACAGCCTGAT TACTTGTTGC TTTATTAATG      360
TTGTTGATGA TGCTGTTTGC CAATTCTTCT GCTTTATTTT TCGCAATAAG CTTGTCTTGA      420
TCCGTCGCAT TTGAAGCTTC GATTTCTTTT AGCTTATTAG CTAAAGCTTG ATTAATAGAT      480
TGAATTGCCT TGTCTTTAGC ATCTTGTAGT CGTTGATCAC CATTAAGATT ATGGATTGCA      540
TCATTGACtG CTTGGATTGC GCCATTGATA TCATTCACAT tTGTGTaTCA CTATTTAGCA      600
ATGTATTTGC TAGACGTTgG CATCATCGAA GTTTGT      636

```

(2) INFORMATION FOR SEQ ID NO: 873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873:

```

CTCTGAATGC ATTCATTAAA CGCTGGGTCT CTTTATATGA AACGTATTTG TCATTTTTAG      60
AACTCAATCC GTAAAAATTG TCAACTTTCT TTTTAATATT ATCGTAATCA ATGGTTACAT      120
TACTTAAATC AATATCTAAA TCTATATTTT CTGCATCTTC TTTAAAGCCC GTATACTGA      180
AAAAGCCTTC AATCGGCTGA TCAATCATTT CAATATATTT TAAAGCTGTG ATTGAACCTA      240
AACCATGTGT TACAAAATAT GTATCCTTTT TGCGTACATT AATTTGTTTC GTCATAGCTT      300
CAATCCACTG ATCCACTGTC TTCGCTtCAG GGGATTCAAA ATTAAATAAT GTTACGTCAT      360
ATCCTTCTAA AGTTAAGTTA TGCTCCAACC ACTGATACCA ATGATTTCTA CTATTTCCAT      420
GCATAGAATG TACAATAtTA CATCTGTCAT CTCATTCTCT CCTTTCAACT TACTACTTCT      480
TTTCTATTTT TAAAAAATG ACTGATTACC TATAATTGTA AAATAAAAAAC ACCTTAATTA      540
GAAATGTTAT ATCGCAAAGT GACATTTCTA ATtAAGTGT ATTGTCATCA TTTCAATATC      600
ATTCAAAAAC AGCTAAACCT TTGTCTCTGC TTCAATTTCA CAAAAATAAT TCCCGCTGA      659

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(2) INFORMATION FOR SEQ ID NO: 874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874:

```
AAAATAAAAT CCATTTTAGT ATTCTAGAGG AATGAGAGCC CCCTTTACCA CAATATGTAA      60
ATGTATATTG TGAAAAGGGG GCTTTTATTT ATGACATAGT TGTTCAACTC ATACATCAG      120
TTGATAATGC AGTGCATTAT GCAGCTATCC ACTTCATATG TATGGCGCAT ACTTGATATA      180
TGAATATCAT CAAGATTTTA AAAGTATCGC TAATTTTAAA GTCTTAAAC GCAGATTAAT      240
GGTCATGATG TGTTAnTGCG TTTTGGTTTT TAGAGCCACG TAATTCCCAh GGACATATAG      300
GAGGAACCAT TCCAC                                          315
```

(2) INFORMATION FOR SEQ ID NO: 875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875:

```
TACACGACCT TGTAACCTCAG CTGCTTTATA AGCTAGGGCG ATGTTATCAA AGTTGGATGT      60
ACTTTGAGCT TGGCATTTCG TTAATACTTT TAACGAAGGA TTTAATATAT GTCTGATACG      120
TATATATTGA TTATATTCAA TTCTTaATTt GGTAAGATT GCTGATAATT TGAAGCAATC      180
GGAGCTAAAT GGATCGAAAA ATGAATAAAT TTCGATTTTA CTTACAGGTG ATAGaTTGAT      240
ATCTTCACGA CTCTTATTTT CCATTaWTCG TAATTCTCCA GCCATGTTTA TTCACCTACA      300
ATTAATTTTA GGAATTCACC ATATGaTTAG CAGTTAATCT TaAGCGCTCA AATAAATAA      360
CTCCAACACC TTGTGGAAC caGCgCGaTT AATTGCTGTC TGCATATTTT CTAGCCATGC      420
ATCTCTTTCA AATTCAGTGA TTGTAAAATC TATATGTCTT TTTCTTAGCA TAGGATGTCC      480
GT                                          482
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(2) INFORMATION FOR SEQ ID NO: 876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876:

```
ATGCAATTGA ATTCTTAAAA GCAGAAGGCT TTGATGATAT TGAATGGGGC GAAGATTTTG      60
```

GTGCGCCACA TGAAACAGCC ATTGCTAATC ATTATGATTT ACCGGTGTTT ATTACTAATT	120
ATCCAACATA AATTAAGCCT TTCTATATGC AACCAAATCC TGAAAATGAA GAAACTGTAT	180
TATGTGCAGA CTTAATTGCA CCTGAAGGAT ACGGTGAAT TATTGGTGGA TCTGAACGTG	240
TGGATGACTT AGAATTGTTA GAACAACGCG TTAAAGAACA TGGATTAGAC GAAGAAGCAT	300
ATAGTTACTA CTTAGACTTA CGTCGTTATG GTAGTGTGCC AACTGTGGA TTTGGTTTAG	360
GTTTAGAGCG TACAGTAGCA TGGATTTCTG GTGTTGAACA CGTTCGTGAA ACAGCGCCAT	420
TCCCAAGATT ATTAACCGT TTATATCCAT AAGTTTTAGG GTCGTTACTT AAAATATATA	480
TTATGATAAT AAAAAGAATC GTCCAGCCTA TATTAATAGC TGGGCGATTT ATTCTTGGAA	540
AATGAAGATT GATAACGGCT TATATTAATC ATGAACAAAC TTTTGTTTAG TAACTATATT	600
TGGAAAATAA ATAGTTCATC TGATTATCCA TAAAGTTCAT TGTTAAAATC TAGTGTTAAA	660
AAATACTGTT	670

(2) INFORMATION FOR SEQ ID NO: 877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877:

TGCAAAGTAA ACTGGATGGC TnTCTTGCCG CCAAGGATCT GATGGCGCAG GGGATCAAGA	60
TCTGATCAAG AGACAGATCC TAACCTCTCA TTTCCGATAAGTTTAGTATG TATTATAGGT	120
GATGATTnTC TTGTTTTCAA CCTTATACAC AATATTTTTG AnATTTATAT TATATTCATA	180
TAAGGAAGGC GATTAATTAC GATTCATCAT TATATCTCTA CGTGTTAATT TATTAACCTA	240
TACTATATTT ATCaACaCAA CAGTTTTTCC TTTCATTTTC AAACATAACA GAAAAAGCCT	300
GAGACATACT TAGTCCCAGA CTGTTCTATA ATTAATTAAA GATATAACAA GGTTAATCAT	360
TCAAAGCTAA CATCACATTT ATTCACTGTA ATTTTTCATA AAGAATAATA ATGACTGTAA	420
TTCTATACCT AAGTCAATTT GATGTACTTG CACATCTGAA GGCGTATTAA TTCTACCAGG	480
AGTGAAGTTT AAAATACCTT TCACACCAGC TTGGACGAGT TCATCTGCAA CTTTCTGTGC	540
AACTCTTTCT GGTGTAGTTA GAATCACAAC ATCTATTTCT TCCTTCTTCA ATGTTGTTAT	600
TAATTCATCG TTATCTTTAA CAATAACGTT CCCTATTTTC TGGCCAATAA CATCTTCTTT	660
TACGTCAAAC GCTTCTGTAA TCGTCATATC GTCATGTATT GAAAAGTAT ATGTGAGCAA	720
AGCTTTCCCT AGGTTCCCAA CTCCGACAAT TGCGATTTTG ATCATGTCAC TCTCGCTTAG	780

TTCAGATTTA AAGAAATCCA ATAAACTATC TATATTATAT CCGTaCCCTT TTTtACCTAA	840
TTCGCCAAAA TATGAAAAGT CACGACGAAT TGTtGCCGAG TCAATTTGTa ACGCATCGCT	900
AATCGCTTTT GAATTTACAC GATCTATACC TTTAGATTTT AATGAACTGA CAAATCTATA	960
ATATAACGGC AAACGTTTTA AAGTTGCTCG AGGAATTTTA ACTTGGTCAC TCATTCGCTA	1020
TTTCCTCCTT CGTGTTTGAA TGAATTATAT CTATGTATTC AAACGAGTTA GAGCGTAATT	1080
GTTAGATTAT TAAAaACAA ATAATTGaT ACAATGAATA CCTAAATATT ATACATTaWT	1140
GAATTTTAAA AATAAATATC TTAGTTTCAA GACGGCGTTT TATACTGTAA AATGGTTATT	1200
AATGTAATAA TTACGCTTGT TTCATAAGTT AATAAAATTT GAGAAGACGA AGGTGAAG	1258

(2) INFORMATION FOR SEQ ID NO: 878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

AAACAATCCC CnCCAAAGTA ATTCCACCAC TAATTGTAAA TAACTTTGGAAAGGATGTTG	60
TTTGTnATTC CCATGGACAC ATGCCATCTn ATTTAAGTTT TATACTCTAT TTTTCTGATG	120
TCTTGATTAA TTGCAAGCGG TCTTGCGAGC CTTGTTCAAG CTCATATTCT TTATCTACTT	180
GCTTACCGTT TTCryTTATT AATCTTACGG TTGCGGTAAT CTTATCACCA TGTTTTTCAG	240
CATCTATAAT TTGTGGTGAA CTAATCATCA TTAAACTTCC TTTAGATACA CGCTTCTTTA	300
CATCATCATA AAAAGATGAT CCTTTTTTTA TATATGATGA TACAAAATCA AAATCCGACT	360
GATTAAACGC AGCATTATTC GCTAAAGAAT ATCCAGCAAA GAATTCTATC AATTTGTTCT	420
TCAAGCTGTT TTCTTCTTTT TCTTTCTTTT CACATAGTC TTCGATATCT TCACTGTCAA	480
AATTCAAAGT TATCTCTGTA TTGTATTTTA AATCGCTAAG CTTTAATCGT CTTCGTCTGT	540
GATGTA	546

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879:

TTTATGAATT TTTTATGTAA CATTAAATAT TCTTCTGGCA ATCTTCctAC TATrCTkTT	60
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ATATATCCTT CTTCTCCTTC TTAAATACT AACCTGTGG GAGTTAGTGT GTTATACCTA	120
ATTTCTATCT CATTCAAATG ATCATTCAAA AGGTCAAAA ATTCTCTATT AAAATAACCC	180
CATTTCCCAT TTTGTAATAA ATATTTCTTT CCATCTTCCA TTTCAACTTC TGCATGTAGT	240
ATCGTTTTTA GTaGCATATT ATTTGAATGC CCCAAATTAT CkATCACKTc AATTCTGACA	300
TCATTTATAG AATTAACGTC ATATTTTAAT AAGTAATCTC CTATTTTCAGT GATGTAATCA	360
ACTTCAGGAT CAGTCGCATC AAATGTCTCT AATGTATTAT TTTTAAAAGA ATTTATATAT	420
ATATTGACGT CGAGCATATC ATCTAACAAG AGTATATAT TACTTAGTTC TAAAAATCTT	480
GATATATCTA TAGATATATT TTCTGTAGTT GAAGAATTCG ATAGTTTTTT TAGCAATAAA	540
GTATCTAATA CTTCTATTTT ATTCAAGTCT TTAAAGTTA CTATTCTAGG AAATTCACTA	600
ATTTTTTGAG GAAGATTAAT AATAGCGTTT ATTTCTTTGA TTATCACACT AATTTTATCT	660
ATGaATTGCT GcTTTCTATT CGGtACACGC AATGaAATAC TTGTACCACA AGTCCATTGt	720
TTTTCCaAAA ATTTGAGGaT TCTGTGGaTG tCCTTGGaCT GGaTATATAA GATTCTGAAG	780
GTCTAACGTA ATCTACACTA TTCCTTCTAT AATTAACAAT CTCTTTAAGC CTGTTTTGTT	840
GAAAAAATT AACATTTT nTAACTAnGG	870

(2) INFORMATION FOR SEQ ID NO: 880:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880:

GGTTTACATC TTTATCAACT GTAATTTTCAT TGACATCTTC ATTCATATTT AAAACACCAT	60
TAAATGTCCC TGAATATTCA CTTGTTTGTT TAACTGTGGC AGTGACTTGT CGTTACCATA	120
TGTCATCATA TATTGTGCAA ATGTTAAAGT CCCCATGAGTTGACCGACA AAGTTGAATT	180
TATCGAATTG TATTCAGATT GTAACTTAG CAGACATTTT TAACCACGAG CATTCTTATC	240
CAAATAGnCC TTGTCTGTTA TTTTCAAGTC AATTTTCACA ATAGGATCAC TGCATCTTTT	300
CTTAGTTCCC TTTAAATGCA CTGACCATCC TTTGAACGGG AAGCCAGGAT GAATCTTAGT	360
ACCCTCTTTT TCTGCTnCTC ACATAACTTT CAGATGGACT	400

(2) INFORMATION FOR SEQ ID NO: 881:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881:

```
AAGATATTGC GAAAAGAAGT GACAGTAACA GAGGAATTTT AAAATTTATT CAACCATATA      60
TTGAAAATTG ATGAAATGGT GCATGCAAAT GAAGCGCGTA TTGCGTATGA AGCAGACATG      120
CGAAAACCTT TATATAGTAA ACGCATTAT CAAAATTTAA CATTAGACTC TATTGTTTTT      180
AGAAATACAT TGAGATATAC AGCGATTATG ATGATAGCGG ATATTTATTG CGTTAATGTT      240
TGATTTTGAA AAAGCATCCT GGATCCCGTT ATCTGCACAT CCAATATTCC TAGGGCCATC      300
AnCCTATACC ATGCCATCCG AGAGAGGTAT GGn                                     333
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(2) INFORMATION FOR SEQ ID NO: 882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882:

```
ATTGAAAGAA AAAGTACGT ACTTATCCGA TGATAAAATG AAAGAAGTAG ATAATGCACT      60
AATGATTAGT TTAGGGCTGA ATGCAGTAGC TCACCAGAAA AATTAGGCGT CTATTATATG      120
TATTTTTCAG AGATAAATAA AATATTGATA TAAAAGACAA TAACTTTATA ATAATTATAA      180
CTATTTCTAA ATTCTGTACG AAGAATTTTC TTATAAACAA AGATTTTAGC AAATACCAGT      240
TATGATATTC ATATTTTTTA TTATAAAAGG ATGTCTTAAG TTTTITAGGC TTTAGGTATT      300
CCATCCTAAA GTTTTTTTAG CTTAAAAGTA TCATCTACAG CAAAATTGCA AACGACAAAA      360
TTGATAAGTG CAATTAAATA ATGTTAGTA AGTGAATCAT AATTATCCTT GCTTAAGCAT      420
TTGCTTTGTA AGGGAAGTGA GGAGGCAACT AATCGTGGAA GAATTTAAGC AACATTATAA      480
GGGTTTAATT GATGAAAGTT TAACGTGCCA AGATAAAGTA GAATTGATAA AAAAGTGTGA      540
GAAATACACT GACGAAGTGA TTCGTAAGGA CGTCTGCCT GAAGACATG TCGATATTCA      600
CTAAACTAT ATATTGA                                                         617
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(2) INFORMATION FOR SEQ ID NO: 883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

GTTGTATTAA AATTTTTCAA TTAAACAACG AAACAATACG AAGAAAAACA TATTACTGAG	60
CCACTGGAAT TGACGAGCTT ATTAGGTAnT ATTTCTCGTC TAGACAATGG TCATTTTGCA	120
CATTTGCATG CTACTTTCGG TACTCAATCA TATGAACTT TTAGCGGACA TCTCGCTAAA	180
GCAATTGTTT CTGCAACTGC TGAAATCATT CTTACTGTAA CTGATTGGA CATTCAACGT	240
TCATTCAAAG ATGCAGTCGG TTAAATTTA CTTGATCCTC AATAGCACTT TACTTTTTAG	300
TTGAATCAAA TTTTATTACA AGTTATCATA AGTGCTTAAT CATAAATGCA TTCTCGTTTA	360
TTAATATACT TCAACGAGTT AAATTAAATT TTTAATTAGG AATTGAATGC GTTTATAACT	420
ATCACATTTG aATGaATAAC TTTTTCATTA GAAAGTAGTG TktATTATTG aTGCAATCTC	480
GaTACATCGC TAGAATTTAC TTTtaATTTT ATTTATCGTC TCCCTTnTTGAGACTAAAAT	540
TTTTCAATTT ATGACTTTAA ATTTGTTTTT AGCATATATA CCT	583

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

GCAGAGGGCT TACGATAAAA AGAAAAATCT CGCTCGCCCG CTTCAGTCAA ACTCACAAAA	60
GcTAACGCAt GwyTGCTyCA TTCGTGCGAT ACACTTTTGA TACATCTACA CCAATACTTG	120
ATATCGTTTC AATAATGCTA TCTCCAAATG CATCATTACC TAATTGTGTA ATCATAtACG	180
CTTGTTGTCC tAACTTTTGA ACTGTACAAG CTACATTGCA TGGCGCGCCA CCAATTTGCT	240
TCGTAAATGT TTGAACATCT TTAAATTCG CATTTGTAAC ATTTGGAATA AAATCAATTA	300
ACGCTTCTCC TATTGAAAAT AGACGTCTG TTTATGTTCA TCCTTTAAAT CATATTTAGT	360
AAATTGTAAA TATACTTGCC CTGATTCTGT TGATGTTTTA ATACCTAGTG CGTCTTCTGT	420
CGGGAAAATT CGAGATGTCA AAACACGTTC TCCATCATTA CAGAAAATTT CTATACTAGA	480
TGTATCAACA AAAATTTGTA ATTGCTTTAA TGGCGTGTCT AATA	524

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG CGCAAGTACT	60
TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT CATGCTATTC	120
ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCTT TTAAATACGC AGCATCAGCT	180
TTTAAGTAAT GGCCTAATGC GTCACCTCTA TATCTCCGGA TAACATCTTC TGAATAAAGT	240
CATCCTCATA AATATCATAA TGATGGCTTG CAGCTGGGTA CAATTTTGTG AAATTCCATG	300
TAAAAATCCT CCCTAAATAA AAAACTACTT CCAACATGAA GAGTTGAGGC ATGTGCAAAC	360
TAGCCCATCA CTCATAACAC TTCCACGTGG GATACCAAC	400

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

AAGAATTTAA ACAAATGAT ATTTGGAAAC ATTTTAAAGC TGTGAAAAAT AATCATGTTT	60
ATGACTTAGA GGAAGTGCCA TTCGGTATTA CAGCAAATGT TGATGCTGAT AAGGCAATGA	120
CTCAATTATA TGATTTATTT TATAAGGATA AAAAATAGTG AGTTGATATG ATGAAAAA	180
ATAAAAAGAA ACTACTATTT TTATGTTTGT TAGTCATTTT AATCGCAACT GCTTATATTT	240
CGTTTGTAAC CGGTACAATT AAATTGTCAT TTAATGACCT ATTTACAAAA TTTACAAC TG	300
GTAGCAATGA AGCAGTGGAT TCAATCATTG ATTTGCGATT GCCACGTATA TTAATTGCAT	360
TGATGGTTGG CGCAATGTTA GCAGTTTCTG GAGCATTATT ACAAGCAGCA CTACAAAATC	420
CTTTGGCAGG GCGAATATCA TTGGCGTTTC CTCAGGTGCA CTTATAATGA GAGCCTTTGt	480
ATGTTGTTtA TTCCACAATT GTACTTTTAC TTACCATTAT TAAGTTTTAT TGGAGGTTTA	540
ATACCATTTT TAATAATTAT ATTGTTGCAT TCTAAATTA GATTCAATGC TGTAAGTATG	600
ATATTAGTAG GTGTTGCGTT ATTCGTATTA TTAAATGGTG TTTTAGAAAT TTAACTCAA	660
AACCCTTTAA TGAAAATTCC TCAAGGCTTA ACAATGAAAA TATGGAGCGA CGTATACATA	720
TTAGCAGTAT CAGCATTATT GGGATTAATA TTAACATTAC TATTGTCCCC TAAATTGAAT	780
TTACTAAATT TAGACGACAT ACAAGCGCGA AtATCGGTTT TAATATTGAT CGTTACAGAT	840
GGTTAACAGG GTTATTA	857

(2) INFORMATION FOR SEQ ID NO: 887:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

GATTTATTTT AATATTATTG TTAGAAGGAA TTTTACAAA TTCAGCGAGT GCAATCGAAT	60
ATTCAGACTT ACATCATAAA AGTAAGTTTG ATTCAAAGCG TCTAAGTAAT GCTAAGATGT	120
CATTCATCAA TCCAACCTCAG CTTGAAAATA AAAACACAAA CGATAGACTG TTGAAGCATG	180
ATTTGTTATT TCATGACATG TTCGTAAATG ATGATTGGAA AAAGGATTTT AAAGTTGAAT	240
TTGAAAATGA GGCACTTTCA AAGAAATTTA TAAATAAGGATATCGATATA TTTGCTGGAA	300
ATTATGGATA CGGATGTCAT GGGGGAGCAA CCAATAAAAC GCAATGTAGT TATGGTGGTG	360
TTACTTTAAG TGACAATAAT AAATACGATG ATTATAAGAA TATACCTTGT AATTTATGGA	420
TTGACGGACA TCAAACAGAA ATAGAACTAA CTGCAGTAAA AACGAAAAAG AAAATTGTTA	480
CTATTCAAGA ATTAGAGGTT CAATTAAGAA ATTATTTGAA TGAGAAGTAT AAGTTGTACG	540
AACAAGGTGG CGACATTGTT AAAGGGTATG TTAAATATTA TAATGATGAT GAACAAAATG	600
TAGAATATGA TTTTATAAT TTAAATGGTG AGTATGGTCG TGAGGTATTA AAAATGTATG	660
CnGATAATnA AACnA	675

(2) INFORMATION FOR SEQ ID NO: 888:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888:

AAAnAGGATA TAAGGTTAAT AATGGAACAT AGATGATAAG TGTATATCGT CGTAATTTAA	60
AATTCCTAAT TAACAATGCC TTCATTTAAA AACCTTCTTC CATCAATTTG ATGTTTTCAT	120
GATATTTAGG TTTTCTCTTT TCAAGATAAA CCATTAAGTy CTATATAGAA GGTGTAGTGA	180
TATTCACTTT AkGACCTAAA ATTTCTTTAA ATACTTGCGC ATGTTCTGTT AATCCTATAA	240
ATCCCGTACG CTTATGTTCT TCATAAATAA GTAGAGATGC TAATTCATCA TCAAGGTCCT	300
CAATAGCACC ACTCACAAC TGATATCTTT GTAACAGTTG TTCTTTTGAA CCATTTAAGA	360
TAACTTCACC GTCACCTAAG TGAATGATAT AATCAGCTAT TTTTCTAAA TCTGAGATAA	420

TGTGTGTCGA CATGAATATT GTTTTATTTT CATCAATTAA TTCTTGCTGA ATTATCTCCA	480
ATAGCTCATT TCTAGCTAAG GGATCGAGAC CTGAAGTAGG CTCATCAAAA ATATAACAATT	540
CAGCATGATG TGAAAATGCA ACTGCTAGTG ATAATTTTCAT TTTCATCCCA GTCGAAAATG	600
TTTTTATTGA TTTATTGATT GGTAATCGA ACTTTTCAAG ATAAAATTCA AATACTTGAT	660
GGTCCCATT T ACGATAAAAA GGGGcAATCA TTTTTTCAAG TTGCTTCGTA GTCCATCTCT	720
CATTAAAATA ATTTTCAGAG TAAACnAACC CAATTCTATT CTTTAACTCTATCGGATTGA	780
GAGCCATATC CTCTTCTAAT ACTCTAATAA CACCAGTTTG TGGGTGATAC AAATCCATAA	840
TTAACCTAAT n	851

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889:

AATCACCTTC ACGCCAATAT TGATTTTCAT GCGTAAATAC TTGTGCCGTT TCATGATACT	60
TTGTCAATCG TGC GTGTTGC TGGGGGGAAT ATTTTTCAGT AGCCCAATTG GCTGCATGAC	120
CTTCAATGGC TAGTTCAATT GCAGGATTAA TTAAATCTTC CAATGACAAT TTAGCATAAC	180
GCTTGTGAAT ATAATCAAAC AGCTTTGGAA TTGCTGGCAC ACGACAGTTT TACCATGTGT	240
AGTCATATCA AAAAATGATT TATATTCGc TGAATCAnCT AGATAAAATT GGTGGCTAC	300
ATGGTCAGGG TGCTGGCTCA CGGTGCATCA AACGcGnTA ATACTGCCCA GTACCTTTGC	360
TC	362

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890:

TTGGTTTATT CCCAAAAAGT ACGCGAAAAT TAGTAGAGAA GAATTTGAAAGTTTAAATAT	60
TGTCAAACCC GCTAAAAATA ATACTTTCTG GCCTGTTGCA GGATTTGCAG TGTTATTAAAC	120
AACCTTAACA AGAAAATATA TCTATTTGCT TAACATCCAT TTAGAAAAAG AAATAGTTAT	180
ATTAACATGC TGTATGATAC TTCTAGGTGT TTTCGCATTG TTTATATATA TAAATACAAA	240

ATTGAAGTTA CATATTTTGT ATAAAAATAA AAGTAATAAC GAAAAGATCA TATTAATACC	300
TACATTTTAAA AATATTTGTT TATCCTTATT TGCTTATATA TTATTTGGTG GATTGTCAAC	360
AATGGCTCTG AGTATGTTAG TAACTTCATC CCCTCAAAAT ATAATAGAAT TTCTTGCTTT	420
AATTGGCATG ACTGCATGCT TCTTTCTACT GATATGTCA TCGGTTCTAG ATAAAAAAT	480
TCATGTTATT TTAAAAACAA ATAAGTAGTA AAATTGATTA ACTTAGGTAG TATCGGATAC	540
TTAAATGTTG GTTCATAAAA AGCAATGATT TTAAATCGAG GAGCTATCTT AGAAcAGGGA	600
AATAAAACAG CCAAAGTTAT AAAAAGTGAA TTAATAACTA ATTATATTAT GTTAGC CA G	660
CTTCAAATAA AAnATAATTA GAATAAGGTG GGATTGATAA TCAAnGCTAn GCGAATCTAA	720
AATCATCAAT AAAAACCCCA AATATAG	747

(2) INFORMATION FOR SEQ ID NO: 891:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891:

ATTTTGAAAT TTTAGCAGAT ACTGATAATG GTCTCGATGC AATGAAACTT ATTGAAGAAT	60
ATAATCCTAA CGTTGTTATT TTAGATATAG AAATGCCAGG CATGACTGGA CTTGAAGTTT	120
TAGCGGAAAT TAGAAAAAAG CATTTGAATA TTAAAGTGAT TATTGTAACA ACTTTTAAAA	180
GACCGGGATA CTTTGAAAAA GCAGTTGTGA ATGAtGTGGA TGCATATGTT TTAAAAGAAC	240
GTTCTATAGA AGAATTGGTG GAAACCATTA ATAAAGTAAA TAACGGAGAG AAAGAATATA	300
GCGCCACATT GATGACTTCA TTTTTTGTAG ATAAAAACCC ATTAACGCCC AAAGAACAAA	360
TTGTATTAAG GGAAATTGGC AaTGGTTTAA GTAGTAAAGA AATAAGTGAA AAATTATTTT	420
TGACAGAnGG AACAGTTAGA AATTATACAT CTGTTATAAT TGATAAATTA TTTGCAGATA	480
ATCGTTTTGA TGCTTGGGAA AAGGCAAATG AAAAAGGCTG GACCTA	526

(2) INFORMATION FOR SEQ ID NO: 892:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892:

TATTTGATGT AAAAGCGAAn GAACCATACA ATGTAACAAT TACTAGTGAT AAATACATCC	60
CTAATACTGA TTTGAAACGT GGGCAAGCTG ATTTATTTGT AGCGGAAGGT TCTATCAAAG	120
ATTTAGTGAA ACATAAGAAG CATGGTAAGG CAATTATAGG AACGAAAAAA CATCATGTTA	180
ATATTAAGTT ACGTAAAGAT ATTAATAAAA TCTATTTTAT GACAGATGTT GATTTAGGTG	240
GACCAACGTT TGTCTTAAAT GACAAAGACT ATCAAGAAAT AAGAAAGTAT ACAAAGGCAA	300
AGCATATCGT CTCTCAATTT GGATTTCGATT TGAAACATAAAAAAGATGCT TTAGCATTAG	360
AAAAAGCGAA AAATAAAGTT GATAAATCTA TTGAAACAAG AAGTGAAGCG ATAAGCTCAA	420
TATCAAGTTT AACCGGAATA TTATTATTTG TAACATCATT TTTAGGTATT ACATTCTTGA	480
TTGCTGTATG TTGCATTATA TACATAAAGC AAATAGATGA AACCGAAGAT GAGTTAGAGA	540
ATTATAGTAT TTTGAGAAAG CTTGGATTTA CACAAAAAGA TATGGCAAGG GGACTAAAGT	600
TTAAAATTAT GTTTAATTTT GGGTTACCTT TAGTTATTGC ACTATCACAT GCATATTTTA	660
CATCATTAGC ATATATGAAA TTAATGGGTA CAACGAATCA AATACCGGTT TTCATAGTAA	720
TGGGATTATA CATTTGTATG TATGCTGTTT T	751

(2) INFORMATION FOR SEQ ID NO: 893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893:

GGATGTTGTA CATTATTCAG ATTACTTTGA AGGGGCACAA AAATATTTGA GCTATTTAAA	60
ATCAACAGTA GATGTTAACT TTGAAGGTTT GAAAATTGCT TTAGATGGTG CAAATGGTTC	120
AACATCATCA CTAGCGCCAT TCTTATTTGG TGA C TTAGAA GC A ATACTG AAACAATTGG	180
ATGTAGTCCT GATGGATATA ATATCAATGA GAAATGTGGC TCTACACATC CTGGAAAAAT	240
TAGCTGAAAA AGTAGTTGAA ACTGAAATGA TTTTGGGGTT AGCATTGGA CGGCGATGGG	300
AGACAGAnCC ATAGCAGTAA GATGGAGAnG GnCCAATCCG TTGACGGTGG ACCCAAT	357

(2) INFORMATION FOR SEQ ID NO: 894:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894:

GCTAACCTGC AAAATTTCGAT AAGCGATTCA ATaCTGAcGC CTGcATTTCG CAAATTTTTC	60
ACTAAATAAA TCCAATTTAA ATCACTATCA TTATATATTC TATATCCATT TTCATCTCGA	120
TTAACTGGTG GAATCACACC AACCTTTTCA TAATATCTTA AAGTGTCTTG AGATATATTC	180
ATGAGCGCTA CGACTTCTTT AGTTTTTCATT GCGACTATCC TTTCAGTTAT GTTTGGTCGT	240
CTAAAGTAAT GTTGCTTTAT ATATTGTCAT CTTCGTTTGA AACTTCTTA TTTTATTACT	300
CAAATTTAAA TTTGTCTCTT TTTTAACATT TTACATTTCA TCGTTTTTAA TTACTTTAAA	360
AATTGTATAA CTkAAATATT TAAAATGATA TAAwCACTAA GATTGa E AT AtTTAATTnT	420
TTGGAAAATT ATnTTAAGTT GCCAATTTTG GGGGGATGCG GAAA	464

(2) INFORMATION FOR SEQ ID NO: 895:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895:

AnAATGAAAG AGTTACAGGA CTTTATTGCT CGTTTCTCAG TAACGCTTCT AAATCTAAAC	60
AAGCAACAAG TCGTAAAAAA CAACTCGAGA AAATTGAATT AGATGATATT CAACCATCAT	120
CAAGAAGATA TCCTTTCGTT AAATTCACAC CTGAGCGCGA AATCGGTAAT GACTTACTAA	180
TCGTTCAAaA TCTATCTAAA aCGATTGACG GTGAAAAAGT ATTAGATAAT ATTTCAATCA	240
CAATGAATCC AAATGATAAA GCAATTTTAA TTGGGGATAG TGAAATTGCG AAAACCACAT	300
TGCTTAAAAAT ATTAGCCGGT GAAAT E GAAc CAGACGAAGG TTCATATAAA TGGGGTGTA	360
CAACGTCATT AAGTTACTTC CCTAAAGATA ACTCAGAATT CTTTGAGGGC GTTAATATGA	420
ACCTTGTAGA TTGGTTAAGA CAATACGCAC CAGAAGATGA GCAAACCTGAA ACATTTTTTAC	480
GCGGCTTCTT AGGCCGTATG CTATTTAGTG GAGAAGAAGT TAAGAAAAAAGCTAGTGTAC	540
TTTCAGGTGG AGAAAAAGTA CGTTGTATGC TAAGTAAAAT GATGTTATCA AGTGCAAAC	599

(2) INFORMATION FOR SEQ ID NO: 896:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1057 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896:

TCATTAGTAG AAATCGTTAA AGATGCATCT TGCAATTTAA AATCCGAATC TTTGTATTGT	60
TTGTTACAC TATCTACGTT TAACAATGTT GTCATATCCA TGCTCCTCTT TGTTTAATTT	120
TAATAAAAC GTCTTCTCTT CAATAAATAA CTAAAGGCGT TATATATGAA AATAGCAATG	180
ATAAGTAGCA AACTAAAGCT TTGATTAATT CCAGTAGTAA TTGAATAAAG CCCAATTACT	240
ACAATGGCTA GTATCAATAT TGATAAGTTG ATCGCATATG TTTTAAATAA TGCAATTAAT	300
TCTATATGGC GTTCACCTTC ATCCAATAT TCCAATCGCT TTTCAGTGTA ATTCTTATCT	360
GCAATTTTTG GTATTCTGTC ATCAAACCTT CTATTAAACA GTGTAAATTG TGTATTGAAA	420
ATAGCACTAG CAAAAAATGG TATTAAAAAG AATAGTATTG CATTTGCTGC AGCGTGCCCT	480
ACCACAAAAA TAAGCAATAC TAAAAAAGCA ATAAGTGTCT GCAGAATACT TAAATACTT	540
CCATTTAAAA CATAACGATT CGCAAGCAAC TCATATTGAT CTGTTGCATC GATATCTACC	600
TCTTTATCTA CAAGTTGCTT ATACTTCAAT GCACGTCTTT GATTCATCAA AACAATGGCT	660
TCTACCAATA TGATAATAAT CGTCGCAACA ATCGATATTA CAACGACATT GTTATATGTC	720
GCAAACGTCA AGTTCTCAAT ACCAAATCCA TCAAATTAC CTAAAATTCC ACCTATGATA	780
CCCCCTACAA GTCCACCCAG TAAAAGATAT CCGATATATC TTAGTATTTT CATGCCTCAT	840
CCTCCTCAAT AATAAAAACA GTTCCACCG TTTCATTGAA AATGCGAGCA ATTTTTATTG	900
CCGTTAATAC TGATGGCATA AAATTGTTTC GCTCATTAG CGATATGGTT TGTCTTGAAA	960
CGCCCGCTTG TTTAGCAAGT TGCGTTTGGT TTAAGCCATC TCGTGCTCGT AATTCTTTCA	1020
ATCGATTACG CACATCGCAT CAACTCCnTA ATTACAC	1057

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897:

AAATTATTGA GTTAACAAAT CATTACGGAG CACATAATTA TTTACCATTG nCAATTECA	60
TTTCAGAAGC CGAnGGGGTA TGGGTAAAG ATCCTGAAGG CAATAAATAT ATGGATATGT	120
GAnCTGCATA TTCCGCTGTT AACCAAGGTC ATAGACATCC GAAAGGTATT CAAGCATTA	180
AAGATCAAGC TGATAAAGTG ACTTTACTCT CACGTGCTTT TCATAGTGAT AACTTAGGTG	240
AATGGTACGA AAAAATTTGT AACTGGCAG GTAAAGATAA AGCTTTACCA ATGTAATACA	300
GGTGCTGTAA GCAGTAGAAA CAGCTTTGAA AGCAGC	336

(2) INFORMATION FOR SEQ ID NO: 898:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898:

TGnTGnTTTC TTATTGTTGA CCAATTATTT TGCATACCAA ATCCAAATCA TGTATTTATC	60
AATCACATCC TAATGCTAAA TCCAATGTAT TACATGTTT AATGGTATAG CACAATCTAT	120
CATATTTGGT ATATCAAGTA TGGAAAACAT TCCATATCAT TTTTACTTTA TTTTATTCTT	180
ATGTTTAATA GCTGCAGTAA ATTTTCGTATT AGCAGGTATA CGACACACGG CAATTTATAA	240
TAAACATCT AAAGTGACAC AAACGTATAA TCAACAGGGA GTTTCAAAGA TAGTCAGACG	300
GG	302

(2) INFORMATION FOR SEQ ID NO: 899:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899:

CCACTAGCTG ATACAGTAGG TATACCAAGA TTCGTCATCG TTACGACATA TCAATTTGGT	60
CAATATGCGA TGTTATTCTT AGCGCCGACT GGACTTGTTA TGGCCACACT ACAAATGTTA	120
AACATGCGAT ATTCACATTG GTTCCGATTT GTATGGCCGG TAGTTGCTTT TGTATTGATT	180
TTCGGTGGCG GAGTACTAAT TACGCAAGTA CTAATTTATT CATAATTTGA AATGCTATAT	240
TATAAAAAAT ACTAATGGGG TTTTATGCAT CTCGTAGGTT TGTAGAAATA CTAACTAAG	300
CGAGGTGCAT TATTATTTTT GATTAAGAAA ATAATGACG TAATGATAAC ACTAGTAAGT	360
AATTGATACA ATGCTCTATT TAATAATGAT ATTTTAAAAA TTTGTTTTTA ATGTAATGTT	420
AGATCTATGG TATATTATAT TTAACGTGGT AAATATGTAT TTGCTGTAA	469

(2) INFORMATION FOR SEQ ID NO: 900:

- (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900:

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CTTTATTGGT AACTCTCTAT aATATtTTaA CATTTTTACG CTATCGTGCA AACGCAAcCa      60
CTTTGAATTy TCTGATATTT TTAGCATATA ATTTACACCC TGCACGATGA ATTGTTAATC      120
CAGTTGTATA AATATCGTCA ACGAGTAATA TTTCTTACC ATTTAAATCT AATTCCGTAT      180
CAATAATAAA TGGATTTTCA TCTGCCAGAC GCTCTTTCTT AGTTAAATGA GACTGTTTTG      240
GTCTATTTGA CATCTTTAAA ATCTTATCaA AGCGAATCCC TTTAGCTTTT AGTACTGCTT      300
CTACCGGGT AAATGTTCTA GATAAATCAT GTGCCGGCGA AGAAGGAATT GGCACAATAT      360
AGTCATAAGA TGTTTGTGGT ATTTCAATCA AATGTGCCAA TAATTCACAT AAATAATAGT      420
CTTTCAAAAA TTTATACTGA TGTATCATCT CTTTCATTAA ACGTCATAT TGAAATTGAC      480
AATATAATTG TTCCATTAAA TTAAAGTGTG CCGATAGAAA CTTGCAGTCT AAACAATACG      540
CTTCATCTTG ATTTAAGTGT TTTAAGCACC TTGAACATCG CCTTGCTTTA ATATCAAGTT      600
TAATATTGTC CCAATTCTCT TTGCATCTGT CACATAATCT ATTAGGTTTC TTGAACAAAT      660
TATAAATGGT TATATTTTCA TATAACTTAG CACCACAACCT CAAACAATTA TTCATCAATC      720
CAACCTCTTT TTAATGCTAA TTTGTTTCATC CTTTGAATCT CTTTTTTAGC TTGAATCATA      780
TTCATACTTA CCCCTTnCAT GAAAAAACAA TACTTTTTCC A                          821
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(2) INFORMATION FOR SEQ ID NO: 901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 901:

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TGATGCTATT AAAAAGTTAA TTGTGCGGTC TGTTTTGATA ATTTTAATAA TAACTTCAGG      60
TAACTAAAAA TCCTAATATT GAAAAAACAA AGCCATTTAA AACATAACCT AGTATATTCC      120
ATGTATGATT GTAACTCATT TGCCAGTTnT GTACTGACTT GCATAATTCT GTCACGTnCG      180
AACCATGTAC AAGCCTGCAA CTACTGCTGA ATGATTCCTG ATGCGEAAC AATTCAGCAA      240
TTAAATACGT AACAAATGGT GTTACAATTG AATAATTGAA ACATATTAAT GTTTCATATC      300
CTCGACGnCA TCAATGTTAA TCCGGACCTT ACTAATGCAT ACCTATAAG                  349
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(2) INFORMATION FOR SEQ ID NO: 902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902:

CAAGTGGTAT AAATTTACCT GGTGAAATGT AGGTCGTGGT GGCGATGATA CATTATTCGC	60
TAAAATCGAC GCGTTGTTA AATTCGAACG TAAAGGTCGC GACAAAAAAC AAGTTTCTGT	120
ATATGCAGTT AGCTGAATAA TTTTGTCTAG TTAACACCAG AAAGTGAATC TTCTGGTGTT	180
TTTTACTTTT TATAAAATGT TTTTCATTAT TATTTTCATT ATGnTATTTA AAAATGGGGA	240
TTTTAGACGT TATACTAAAT GTGACTGTA TAGGGGCCCT AATCACTAAC TATAGGGGGA	300
CAAGGATACA GTGCAGCGTT AAGGATAACT GnCCACATTG GTCTGGGAAT ATAGGATTTA	360
AGCAAGGTTA TAAAGTACTC nTAGGCCCTA	390

(2) INFORMATION FOR SEQ ID NO: 903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903:

GGAATAGACG TATATGCGCG TTGAATTTAA TCCTAATAAG CTTTCGATG ATGAAGTGCT	60
TTGGTTAAAA CAAAATATCA TCAGTTATTT GGACGATGTT AGTTTTACGA GATTAGATTT	120
GGCTTTTGAT TTTGAATTTG ATTTAAAAATG ACTATTATGC ATTGTCAGAT AAGnCGGTAA	180
AAGAACTAT ATTTTATGGC CGAATGTAAA ACCAGAACAA AATATTTTGG TGnCGAATA	240
GTGAAGGTTT ATnCGGATTT ATAATAAAAC AAGACGTAAA GATAATGCAG ATGTTGAATT	300
GATTCACATT CTATGCGGTG GAATTGATTA AACG	334

(2) INFORMATION FOR SEQ ID NO: 904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904:

CAAGTTGGGG AACTGTTTC AAATGAAACA ACAGTGTGTA TTTTAGAGGC AATGAACTA	60
TTTAATGAAA TTCAAGCAGA AATTCAGGT GAAATTGTTG AAATCTTAGT AGAAGACGGA	120
CAAATGGTAG AGTATGGCCA ACCGTTATTT AAGGTGAAAT AATGAAAAAG GTTTAATTGC	180

AAACCGCGGT GAnTCGCAGT TAGGATTATT CGCGCTTGTC GTGATTTAGG CATCCAAACT	240
GTTGCATCTT TCTGAGGGGA TAAAGATCGC TACATCTCAA ATGCTGATGAGGCATATnCG	300
TGGGCCnCTT GTCTAAGGTC ATATTTAATA TCCG	334

(2) INFORMATION FOR SEQ ID NO: 905:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905:

TTCACCCTGT AATTCTTaAC CGTCAATTGA CCTTTATGCA GATTTAATAT TCCTAAAACG	60
TATAACTCTT CTAATGATAA TTGACACATA TTTAAATAAC ACTTTAGATT CCGCAATAAT	120
TCTTGTGACG ACAATAAATA CGATACATAG TCACAATAA AATCAAATGT ATATTGACCA	180
AAATAACGTT CAATATAGTC ACTAAGCTCA TTATTCATAT ATTCTATTTn ATCTATATGC	240
ATTTTATTAA TCGAAATAGT CAATTTACGT TGATCCCTTT GATCTCTTCC TTTCAATAGC	300
CATTGATGAT TGTnTAAATA ACTTAACnT TGAAGAAGGG CCATCTTAGA TTGGATTTCT	360
TTCATTnTTA ATAACTATC TATTGAAGCG CTATTGGAA	399

(2) INFORMATION FOR SEQ ID NO: 906:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

TACATTTTTT AATTTATGGC AAAATnCACA ATTTTCATCG AAATATTTTG TAnAnAATCA	60
TTGCTAGGTG ATGAGTTATC TCGGTTAATT ACAAACGAT ATCTAAGTT AAATATTAGA	120
TCATAAAAAA ACTATCTACT GAATATCCCT CCATAGCATC ATTTTTCTAA GCAAAAGTTA	180
AACTTAGTTA GATAAAATGC AAATGAGATT ATTGTAGATA GTCTCTTTTT AATGTTTAAA	240
AATGATTAAT GCCaTAAACA TAAATAATTC CaAAGAATGC CGCGCCACTA AGCACTGTTA	300
ATATAAGACT TAGTAACAAT GTGCGTTTAT AATGTTTaAC AAATGCTATG AACAAAATGA	360
CTACATTATA CGCAAAGAAA AGTCCGAATA ATGTCATTGT TATTTTCAA TCAGAATAGA	420
AAATATTTAA TAGTAATACA ATGACTGCAT AAATTAAATA CGGAATAACT ATAAATTTGC	480
GTTCAAATCT TAATTGTTTCG AAaCGtTTAT CTTGTTTGT CATGATATGC TCCTTTATGA	540

TTTAAAAGTA AATAAGTTTA CGGAAtATCT TGTCCGaTAA TAGCGGTGTA AAtGTCAAAC	600
CACGACTGAT CATCtAAATT AAGTkGTAGC CcTTCGATTG CTTGATCAAT ACGCTTTAAC	660
TGACTTG TTC CAAGTATCCG GCATGATACG ATGCGGTATT TTTACTAACC ACGCTACAT	720
CACAGCTGTG TCACTyACAC mATATTTGTC AGCTATTGAT TGAACAACCTT TCATAATACG	780
TTGCGCTTTA ATATCTTCCT TGTCGAAAAT TTTACCGCCT GCAAAAGGAC TCCAAGCCAT	840
GATTTGAACA TGGTTTTGAT ACATTGAATC CATTGTTCCA TCTTGTAAC TATCAACGTG	900
ATATGGCGAT AATTCTAATT GATTGATGCT AATATGTAGT CTTTCTTTCA TAATATATTG	960
ATTTAACAAT TGGTATTGTG AATGATTAAA ATTTCGACACC CCGAATGACT TCAACTTACC	1020
TTGTTTAAACA AGTTTAGTTA ATGCATCAGC AACTTGTTCT GGaTCCATCA ATGGTGaAgG	1080
ACGATGAATG AGTAGACTAT CTAAATAATC TACATTCAA TTGATTAATG ACTGTTCAAC	1140
AGATTTACAG ATGTGCTTAC TACTCAAATC ATAACGATGT CCATTTGTAA AATCAAATTG	1200
CTTAGAAGGC AAAATGATAC CACATTTTCGT AACAAATTTGA ATTTTATTTT TTAATTCGGG	1260
TGATAAATCC AAAGCATTAC CAAACAGTGA TTCACATTGA TAATCTCCAT AAATATCAGC	1320
ATGATCCATC GTTGTAATTC CACGTTCAAC TAATTCATTT ATAAAATAAT TTAACTCTTT	1380
CGCAGTCATC TTCCATTCAT TTGCACGCCA AAAACCTTGT ACAAGCCTAG AAAAATGAAC	1440
ATAGTGATTA ATCATTATTT GTTCCATATn TCATCCAC	1478

(2) INFORMATION FOR SEQ ID NO: 907:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907:

TTCTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTTTATTAT GACAAAAGAA	60
AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAAG	120
CTTAAGAATG AaATTATACG AAAGTATGAT TTTAAACCCT CAATTATCTC AAATTCGATA	180
AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTAAAAAG TGATGAAAAA	240
GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAAA TGGAACATGA TGTTTTAAAG	300
CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTAAAGA TACATTACTT GAAGATTCTA	360
ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTTT	402
AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG ATTGCTTTTA	480